

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:30:52 ; Search time 1652 seconds
(without alignments)
264.251 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cctctcccccctgtt 15

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.hig.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.Other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.Other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	15	100.0	190	9	HSA288489	AL288489 Homo sapi
C 2	15	100.0	600	5	AF506010	AF506010 Gallus ga
C 3	15	100.0	1689	9	AK021867	AK021867 Homo sapi
C 4	15	100.0	1721	4	AF232676	AF232676 Sus scrofa
C 5	15	100.0	3190	9	BC000776	BC000776 Homo sapi
C 6	15	100.0	3347	5	CHK7GFA	L01121 Gallus gall
C 7	15	100.0	3752	9	AF312211	AF312211 Homo sapi
C 8	15	100.0	4353	9	AB018279	AB018279 Homo sapi
C 9	15	100.0	11001	5	FR092H06	AF035357 Fugu rubr
C 10	15	100.0	11896	1	AE009810	AE009810 Pyrobacul
C 11	15	100.0	12602	14	AF144617	AF144617 Pestivirus
C 12	15	100.0	32802	1	BSSRFAP	X70356 B subtilis
C 13	15	100.0	34578	9	AC107069	AC107069 Homo sapi
C 14	15	100.0	43347	9	AL138734	AL138734 Human DNA
C 15	15	100.0	56701	9	AL583852	AL583852 Human DNA
C 16	15	100.0	61720	2	AC131033	AC131033 Mus muscu
C 17	15	100.0	62755	2	AC097798	AC097798 Rattus no
C 18	15	100.0	64209	2	AC120156	AC120156 Mus muscu
C 19	15	100.0	65377	9	AL391356	AL391356 Human DNA
C 20	15	100.0	65421	2	AC129736	AC129736 Rattus no
C 21	15	100.0	66283	2	AC108314	AC108314 Rattus no
C 22	15	100.0	68171	9	AL158205	AL158205 Human DNA
C 23	15	100.0	71117	9	HSJ132F21	AL079335 Human DNA
C 24	15	100.0	88502	2	AC021967	AC021967 Homo sapi
C 25	15	100.0	99752	2	AC111526	AC111526 Rattus no
C 26	15	100.0	102853	2	AC116184	AC116184 Rattus no
C 27	15	100.0	106186	2	AC105876	AC105876 Rattus no
C 28	15	100.0	110000	2	AC103237_2	Continuation (3 of
C 29	15	100.0	110000	2	AC125066_2	Continuation (2 of
C 30	15	100.0	110000	2	AC125102_1	Continuation (2 of
C 31	15	100.0	113370	9	AL591493	AL591493 Human DNA
C 32	15	100.0	126392	2	AC018785	AC018785 Homo sapi
C 33	15	100.0	132526	2	AC120946	AC120946 Rattus no
C 34	15	100.0	141105	2	AC117134	AC117134 Rattus no
C 35	15	100.0	141289	9	AL449363	AL449363 Human DNA
C 36	15	100.0	142059	2	AC121163	AC121163 Rattus no
C 37	15	100.0	142662	2	AC118810	AC118810 Rattus no
C 38	15	100.0	142682	2	AC128133	AC128133 Rattus no
C 39	15	100.0	144201	9	HS230119	293942 Human DNA s
C 40	15	100.0	146191	1	D50453	D50453 Bacillus su
C 41	15	100.0	146427	2	AC124033	AC124033 Rattus no
C 42	15	100.0	148500	2	AC094249	AC094249 Rattus no
C 43	15	100.0	151514	2	AC113827	AC113827 Rattus no
C 44	15	100.0	154023	2	AC112466	AC112466 Rattus no
C 45	15	100.0	154888	2	AC114830	AC114830 Rattus no
C 46	15	100.0	155497	2	AC096300	AC096300 Rattus no
C 47	15	100.0	158374	2	AC120953	AC120953 Rattus no
C 48	15	100.0	159070	2	AL354939	AL354939 Homo sapi
C 49	15	100.0	161802	2	AC095162	AC095162 Rattus no
C 50	15	100.0	166475	2	AC130756	AC130756 Rattus no
C 51	15	100.0	166845	2	AC103006	AC103006 Rattus no
C 52	15	100.0	167098	5	AL590149	AL590149 zebrafish
C 53	15	100.0	167161	2	AL645945	AL645945 Mus muscu
C 54	15	100.0	167230	2	AC107010	AC107010 Rattus no
C 55	15	100.0	167264	2	AC095776	AC095776 Rattus no
C 56	15	100.0	167441	9	AC012084	AC012084 Homo sapi
C 57	15	100.0	167862	9	AC011966	AC011966 Homo sapi
C 58	15	100.0	167898	10	AL645630	AL645630 Mouse DNA
C 59	15	100.0	171864	2	AC016248	AC016248 Homo sapi
C 60	15	100.0	172803	2	AC130990	AC130990 Rattus no
C 61	15	100.0	176688	2	AC084696	AC084696 Mus muscu
C 62	15	100.0	177717	9	AC060788	AC060788 Homo sapi
C 63	15	100.0	179290	2	AC097041	AC097041 Rattus no
C 64	15	100.0	182301	9	AC012498	AC012498 Homo sapi
C 65	15	100.0	183783	2	AC109410	AC109410 Rattus no

c	66	15	100.0	184203	9	AC008249	AC008249 Homo sapi	139	14	93.3	90992	2	AC098357	AC098357 Rattus no
c	67	15	100.0	190687	2	AC094723	AC094723 Rattus no	140	14	93.3	93329	2	AC097393	AC097393 Rattus no
c	68	15	100.0	192428	10	AL672015	AL672015 Mouse DNA	141	14	93.3	93805	9	HS42485	AL035468 Human DNA
c	69	15	100.0	194364	9	AC016820	AC016820 Homo sapi	142	14	93.3	93821	9	AC004254	AC004254 Homo sapi
c	70	15	100.0	195523	2	AC103103	AC103103 Rattus no	143	14	93.3	95747	9	AL358175	AL358175 Human DNA
c	71	15	100.0	195524	2	AC055756	AC055756 Homo sapi	144	14	93.3	98533	2	AP003828	AP003828 Oryza sat
c	72	15	100.0	195529	2	AC114417	AC114417 Mus muscu	145	14	93.3	98688	2	AC108245	AC108245 Rattus no
c	73	15	100.0	197706	2	AL772232	AL772232 Mus muscu	146	14	93.3	98713	9	AC002511	AC002511 Human DNA
c	74	15	100.0	198148	2	AC101933	AC101933 Mus muscu	147	14	93.3	99213	2	AC126466	AC126466 Rattus no
c	75	15	100.0	209100	1	BSUB0003	Z99106 Bacillus su	148	14	93.3	100000	9	AP000019	AP000019 Homo sapi
c	76	15	100.0	209404	2	AC124688	AC124688 Mus muscu	149	14	93.3	100000	9	AP000160	AP000160 Homo sapi
c	77	15	100.0	211397	10	AC098887	AC098887 Mus muscu	150	14	93.3	100016	2	HSS171M_3	Continuation (4 of
c	78	15	100.0	212232	2	AL845485	AL845485 Homo sapi	151	14	93.3	100740	2	AC131216	AC131216 Rattus no
c	79	15	100.0	212237	2	AC079235	AC079235 Homo sapi	152	14	93.3	103184	2	AC111427	AC111427 Rattus no
c	80	15	100.0	212727	2	AC131110	AC131110 Mus muscu	153	14	93.3	103184	9	AC111940	AC111940 Homo sapi
c	81	15	100.0	214186	2	AC078933	Z99105 Bacillus su	154	14	93.3	104418	2	AC126312	AC126312 Rattus no
c	82	15	100.0	221160	1	BSUB0002	AC126130 Rattus no	155	14	93.3	106684	2	AC095126	AC095126 Rattus no
c	83	15	100.0	221203	2	AC126130	AL732510 Danio rer	156	14	93.3	106747	2	AC098415	AC098415 Rattus no
c	84	15	100.0	228208	2	AL732510	AC087420 Mus muscu	157	14	93.3	107372	2	AC095333	AC095333 Homo sapi
c	85	15	100.0	228856	2	AC087420	AC073823 Mus muscu	158	14	93.3	108660	10	AL671863	AL671863 Mouse DNA
c	86	15	100.0	261498	2	AC073823	AC124422 Mus muscu	159	14	93.3	110000	2	AC108692_2	Continuation (3 of
c	87	15	100.0	267982	2	AC124422	AC073371 Homo sapi	160	14	93.3	110004	2	AC106477	AC106477 Rattus no
c	88	15	100.0	325518	2	AC073371	UI3613 Human aggre	161	14	93.3	110220	9	AL591415	AL591415 Human DNA
c	89	14	93.3	316	9	HSU13613	AX334095 Sequence	162	14	93.3	110758	2	AC108534	AC108534 Rattus no
c	90	14	93.3	389	6	AX334095	AX410588 Sequence	163	14	93.3	112059	2	AC130641	AC130641 Rattus no
c	91	14	93.3	389	6	AX410588	AL115377 Botrytis	164	14	93.3	113248	2	AC094145	AC094145 Rattus no
c	92	14	93.3	720	8	CNS01CDS	AX005964 faba bean	165	14	93.3	113530	9	AC073216	AC073216 Homo sapi
c	93	14	93.3	1014	14	NVS964	AL132185 faba bean	166	14	93.3	115604	2	AC123175	AC123175 Rattus no
c	94	14	93.3	1015	14	FBEL132185	MI7156 Human vitam	167	14	93.3	116172	2	AC103371	AC103371 Mus muscu
c	95	14	93.3	1805	9	HUMDBPG	BC021386 Mus muscu	168	14	93.3	116177	2	HS265A22	HS265A22 Homo sapi
c	96	14	93.3	1998	10	BC021386	AF222345 Homo sapi	169	14	93.3	116948	2	AC128008	AC128008 Rattus no
c	97	14	93.3	2601	9	AF222345	AK001146 Homo sapi	170	14	93.3	117928	9	AC024722	AC024722 Homo sapi
c	98	14	93.3	2775	9	AB002110	AB002310 Human mRN	171	14	93.3	119721	9	AC093655	AC093655 Homo sapi
c	99	14	93.3	5842	9	AB002210	AF090693 Homo sapi	172	14	93.3	120835	2	AC110644	AC110644 Rattus no
c	100	14	93.3	6905	9	AB090693	AB071605 Homo sapi	173	14	93.3	121046	8	OSJN00203	OSJN00203 Oryza sat
c	101	14	93.3	10348	9	AB071605	AF321003 Homo sapi	174	14	93.3	125528	2	AC027389	AC027389 Homo sapi
c	102	14	93.3	11906	1	AE009851	AE009851 Pyrobacul	175	14	93.3	125528	2	AC110644	AC110644 Rattus no
c	103	14	93.3	12016	1	AE009851	AC131186 Mus muscu	176	14	93.3	128164	8	AP004912	AP004912 Lotus jap
c	104	14	93.3	17920	9	AC131186	AL034450 Human DNA	177	14	93.3	134203	2	AC094055	AC094055 Rattus no
c	105	14	93.3	18890	9	HS115K14	Z19155 Caenorhabdi	178	14	93.3	134203	2	AC116864	AC116864 Mus muscu
c	106	14	93.3	31613	3	CSEF5468	Z68165 Human DNA s	179	14	93.3	135259	9	HS127B20	HS127B20 Homo sapi
c	107	14	93.3	35281	9	HS196A2	AC005945 Homo sapi	180	14	93.3	135259	9	AC068279	AC068279 Human DNA
c	108	14	93.3	38876	9	AL0731802	AL731802 Mouse DNA	181	14	93.3	135751	9	AL596089	AL596089 Homo sapi
c	109	14	93.3	39985	10	AL731802	AC005787 Homo sapi	182	14	93.3	137054	2	AC011920	AC011920 Homo sapi
c	110	14	93.3	43346	9	AC005787	AL713912 Mouse DNA	183	14	93.3	139043	2	AC090974	AC090974 Oryza sat
c	111	14	93.3	46478	10	AL713912	AL713912 Mouse DNA	184	14	93.3	140369	2	AC104925	AC104925 Mus muscu
c	112	14	93.3	49738	2	AC015752	IL0641 Human vitam	185	14	93.3	140369	2	AP005618	AP005618 Oryza sat
c	113	14	93.3	55136	9	HUMVITDBP	AC118706 Mus muscu	186	14	93.3	140899	2	AC083769	AC083769 Homo sapi
c	114	14	93.3	56099	2	AC118706	AL33658 Human DNA	187	14	93.3	141287	2	AC093404	AC093404 Pan trogl
c	115	14	93.3	56475	9	AL33658	AC125016 Mus muscu	188	14	93.3	141293	2	AP004337	AP004337 Oryza sat
c	116	14	93.3	56520	2	AC125016	AL133473 Human DNA	189	14	93.3	142559	2	AC112559	AC112559 Rattus no
c	117	14	93.3	57423	9	AL133473	AC117755 Mus muscu	190	14	93.3	142559	2	AC123281	AC123281 Rattus no
c	118	14	93.3	59828	2	AC117755	AC113482 Mus muscu	191	14	93.3	144555	2	AC119116	AC119116 Rattus no
c	119	14	93.3	60855	2	AC113482	AC083935 Homo sapi	192	14	93.3	144963	2	AC108521	AC108521 Homo sapi
c	120	14	93.3	62309	2	AC083935	AC083935 Homo sapi	193	14	93.3	147803	9	AL356867	AL356867 Human DNA
c	121	14	93.3	62309	2	AC083935	AC096816 Rattus no	194	14	93.3	148678	2	AC131169	AC131169 Rattus no
c	122	14	93.3	67605	2	AC096816	283845 Human DNA s	195	14	93.3	148900	2	AC113769	AC113769 Rattus no
c	123	14	93.3	69660	9	HS407F17	AC073029 Homo sapi	196	14	93.3	150014	2	AC113607	AC113607 Oryza sat
c	124	14	93.3	71157	2	AC073029	AC124990 Mus muscu	197	14	93.3	150151	2	AC116339	AC116339 Rattus no
c	125	14	93.3	74002	2	AC124990	AC034115 Homo sapi	198	14	93.3	151008	2	AP004261	AP004261 Oryza sat
c	126	14	93.3	74912	2	AC034115	AC112044 Rattus no	199	14	93.3	151090	9	AC026720	AC026720 Homo sapi
c	127	14	93.3	76276	9	AF314199S7	AF295068 Homo sapi	200	14	93.3	151091	2	AC125871	AC125871 Rattus no
c	128	14	93.3	78359	9	AF314199S7	AL033376 Human DNA	201	14	93.3	151207	2	AP001031	AP001031 Homo sapi
c	129	14	93.3	78533	9	HS454G6	Z98750 Human DNA s	202	14	93.3	151438	2	AC103516	AC103516 Rattus no
c	130	14	93.3	79376	9	HS454G6	AC111937 Rattus no	203	14	93.3	152150	2	AC116247	AC116247 Rattus no
c	131	14	93.3	80135	2	AC111937	AC016354 Homo sapi	204	14	93.3	153097	2	AC096715	AC096715 Homo sapi
c	132	14	93.3	81675	2	AC016354	AL592046 Human DNA	205	14	93.3	153182	8	AC051632	AC051632 Oryza sat
c	133	14	93.3	86196	9	AL592046	AL390776 Human DNA	206	14	93.3	153258	2	AC127736	AC127736 Rattus no
c	134	14	93.3	86428	9	AL390776	AL161744 Human DNA	207	14	93.3	153344	2	AC104160	AC104160 Canis fam
c	135	14	93.3	87187	9	AL161744	AP001417 Homo sapi	208	14	93.3	153710	2	AC119778	AC119778 Rattus no
c	136	14	93.3	89723	9	AP001417	AC095836 Rattus no	209	14	93.3	153937	2	AC023953	AC023953 Homo sapi
c	137	14	93.3	90049	2	AC095836	AC117060 Rattus no	210	14	93.3	154028	9	HSAC002087	HSAC002087 Human BAC
c	138	14	93.3	90575	2	AC117060		211	14					

c 212	14	93.3 154120	2	AP002472	AP002472 Homo sapi	c 285	14	93.3 180895	2	AC110552	AC110552 Mus muscu
c 213	14	93.3 154260	2	AC123292	AC123292 Rattus no	286	14	93.3 181204	2	AC119576	AC119576 Rattus no
c 214	14	93.3 155843	2	AC106772	AC106772 Homo sapi	c 287	14	93.3 181343	10	AL671882	AL671882 Mouse DNA
c 215	14	93.3 156602	9	AC012487	AC012487 Homo sapi	c 288	14	93.3 181507	2	AC015907	AC015907 Homo sapi
c 216	14	93.3 157227	2	AC118442	AC118442 Rattus no	c 289	14	93.3 181808	9	AL356267	AL356267 Human DNA
c 217	14	93.3 157430	2	AC108975	AC108975 Rattus no	290	14	93.3 182017	2	AL824710	AL824710 Mus muscu
c 218	14	93.3 157979	9	CNS0501D4	AL355922 Human chr	291	14	93.3 182166	2	AC098066	AC098066 Rattus no
c 219	14	93.3 158016	2	AC026570	AC026570 Homo sapi	292	14	93.3 182441	2	AC121709	AC121709 Rattus no
c 220	14	93.3 158179	2	OSJN00106	AL606669 Oryza sat	293	14	93.3 182659	2	AC120130	AC120130 Mus muscu
c 221	14	93.3 159295	2	AC096444	AC096444 Rattus no	294	14	93.3 182806	2	AC098902	AC098902 Rattus no
c 222	14	93.3 159983	2	AC128001	AC128001 Rattus no	c 295	14	93.3 182898	2	AC079122	AC079122 Homo sapi
c 223	14	93.3 160008	2	AC022823	AC022823 Homo sapi	296	14	93.3 183036	2	AC074174	AC074174 Mus muscu
c 224	14	93.3 160331	2	AC129612	AC129612 Rattus no	297	14	93.3 183580	8	AP003561	AP003561 Oryza sat
c 225	14	93.3 160385	2	AC120080	AC120080 Rattus no	c 298	14	93.3 183714	2	AC103508	AC103508 Rattus no
c 226	14	93.3 161363	10	AL645535	AL645535 Mouse DNA	c 299	14	93.3 184245	2	AC120488	AC120488 Rattus no
c 227	14	93.3 161546	2	AC108270	AC108270 Rattus no	c 300	14	93.3 184245	2	AC127355	AC127355 Mus muscu
c 228	14	93.3 161840	9	AC023430	AC023430 Homo sapi	301	14	93.3 184427	14	EHV020824	U20824 Equine herp
c 229	14	93.3 162518	2	AC094485	AC094485 Rattus no	c 302	14	93.3 185181	2	AP005620	AP005620 Oryza sat
c 230	14	93.3 162900	2	AC123889	AC123889 Rattus no	c 303	14	93.3 186449	9	AC111954	AC111954 Rattus no
c 231	14	93.3 163121	2	AC114255	AC114255 Rattus no	c 304	14	93.3 187495	9	AC026887	AC026887 Homo sapi
c 232	14	93.3 163258	2	AP003514	AP003514 Oryza sat	c 305	14	93.3 188158	9	AC092465	AC092465 Homo sapi
c 233	14	93.3 163475	9	AC092619	AC092619 Homo sapi	c 306	14	93.3 189188	9	AC040965	AC040965 Homo sapi
c 234	14	93.3 163537	2	AC102348	AC102348 Mus muscu	c 307	14	93.3 189385	9	CNS06C7Y	AL391152 Human chr
c 235	14	93.3 163623	9	AP005203	AP005203 Homo sapi	c 308	14	93.3 189665	2	AC113066	AC113066 Mus muscu
c 236	14	93.3 163657	2	AC120645	AC120645 Rattus no	c 309	14	93.3 189904	2	AL845451	AL845451 Mus muscu
c 237	14	93.3 164518	2	OSJN00128	AL607001 Oryza sat	310	14	93.3 189939	2	AL831715	AL831715 Mus muscu
c 238	14	93.3 165318	2	AC126747	AC126747 Rattus no	311	14	93.3 190105	2	AC111599	AC111599 Rattus no
c 239	14	93.3 165330	2	AC121372	AC121372 Rattus no	c 312	14	93.3 191052	10	AL683814	AL683814 Mouse DNA
c 240	14	93.3 165491	2	AP004273	AP004273 Oryza sat	c 313	14	93.3 192192	2	AC129342	AC129342 Rattus no
c 241	14	93.3 165959	2	AC109706	AC109706 Rattus no	c 314	14	93.3 192309	2	AC115642	AC115642 Rattus no
c 242	14	93.3 166294	2	AC122113	AC122113 Atelerix	315	14	93.3 193136	2	AC125683	AC125683 Rattus no
c 243	14	93.3 166486	9	CNS0101DWC	AL137100 Human chr	c 316	14	93.3 193389	2	AL645531	AL645531 Mus muscu
c 244	14	93.3 166595	9	AC108215	AC108215 Homo sapi	317	14	93.3 194197	9	AC064871	AC064871 Homo sapi
c 245	14	93.3 166601	2	AC097684	AC097684 Rattus no	c 318	14	93.3 196283	10	AL672215	AL672215 Mouse DNA
c 246	14	93.3 167123	2	AP001495	AP001495 Homo sapi	319	14	93.3 196437	2	AC131036	AC131036 Mus muscu
c 247	14	93.3 167428	2	AC114343	AC114343 Rattus no	c 320	14	93.3 196715	2	AC094874	AC094874 Rattus no
c 248	14	93.3 167694	2	AC103113	AC103113 Rattus no	c 321	14	93.3 196744	2	AC120667	AC120667 Rattus no
c 249	14	93.3 167651	2	AC068969	AC068969 Homo sapi	c 322	14	93.3 196938	10	AL672218	AL672218 Mouse DNA
c 250	14	93.3 168751	2	AC109716	AC109716 Rattus no	c 323	14	93.3 197063	2	AC129280	AC129280 Rattus no
c 251	14	93.3 169410	2	AC031980	AC031980 Homo sapi	c 324	14	93.3 197423	2	AC107448	AC107448 Rattus no
c 252	14	93.3 169913	2	AC129774	AC129774 Mus muscu	c 325	14	93.3 200021	2	AC117635	AC117635 Mus muscu
c 253	14	93.3 170082	2	AB026295	AB026295 Oryza sat	c 326	14	93.3 200146	2	AC073774	AC073774 Mus muscu
c 254	14	93.3 170371	8	AC024490	AC024490 Homo sapi	c 327	14	93.3 200257	2	AC124472	AC124472 Mus muscu
c 255	14	93.3 170425	2	AC114199	AC114199 Rattus no	c 328	14	93.3 200843	2	AC102311	AC102311 Mus muscu
c 256	14	93.3 170491	9	AC067805	AC067805 Homo sapi	c 329	14	93.3 201050	2	AC128356	AC128356 Rattus no
c 257	14	93.3 170883	2	AL356740	AL356740 Human DNA	c 330	14	93.3 201390	2	AC098182	AC098182 Rattus no
c 258	14	93.3 170928	9	AL356740	AL356740 Human DNA	c 331	14	93.3 201465	2	AC122424	AC122424 Mus muscu
c 259	14	93.3 171363	2	AC084863	AC084863 Papio cyn	c 332	14	93.3 201990	9	AC002385	AC002385 Human BAC
c 260	14	93.3 172524	2	AC097314	AC097314 Homo sapi	c 333	14	93.3 203363	9	CNS01RHB	AL161668 Human chr
c 261	14	93.3 172664	9	AC119609	AC119609 Rattus no	c 334	14	93.3 203568	2	AC008693	AC008693 Homo sapi
c 262	14	93.3 172738	9	AC091953	AC091953 Homo sapi	c 335	14	93.3 203756	2	AL772132	AL772132 Danio rer
c 263	14	93.3 173185	9	AP004606	AP004606 Homo sapi	c 336	14	93.3 205662	9	AC017002	AC017002 Homo sapi
c 264	14	93.3 173331	2	AC083903	AC083903 Homo sapi	c 337	14	93.3 205688	2	AC107344	AC107344 Rattus no
c 265	14	93.3 173346	2	AL773561	AL773561 Mus muscu	c 338	14	93.3 207245	2	AC123552	AC123552 Mus muscu
c 266	14	93.3 174534	9	AL672138	AL672138 Human DNA	c 339	14	93.3 209693	2	AC113363	AC113363 Homo sapi
c 267	14	93.3 174631	2	AC069059	AC069059 Homo sapi	c 340	14	93.3 209882	2	AC103554	AC103554 Rattus no
c 268	14	93.3 174693	2	AL732588	AL732588 Mus muscu	c 341	14	93.3 211308	2	AC094850	AC094850 Rattus no
c 269	14	93.3 175439	8	AP001111	AP001111 Oryza sat	c 342	14	93.3 213097	2	AL672180	AL672180 Mus muscu
c 270	14	93.3 175694	9	AC016753	AC016753 Homo sapi	c 343	14	93.3 213473	2	AC094371	AC094371 Rattus no
c 271	14	93.3 176975	2	AC098753	AC098753 Rattus no	c 344	14	93.3 215528	2	AC099105	AC099105 Rattus no
c 272	14	93.3 177293	2	AC069525	AC069525 Homo sapi	c 345	14	93.3 217141	2	AC073998	AC073998 Homo sapi
c 273	14	93.3 177433	9	AL691476	AL691476 Mus muscu	c 346	14	93.3 217421	9	AC006211	AC006211 Homo sapi
c 274	14	93.3 177829	9	AC026392	AC026392 Homo sapi	c 347	14	93.3 219175	9	AC092641	AC092641 Homo sapi
c 275	14	93.3 178049	2	AL672146	AL672146 Mus muscu	c 348	14	93.3 220809	2	AC123955	AC123955 Mus muscu
c 276	14	93.3 178892	2	AC096931	AC096931 Rattus no	c 349	14	93.3 220820	2	AC126962	AC126962 Rattus no
c 277	14	93.3 178975	2	AP001500	AP001500 Homo sapi	c 350	14	93.3 221941	2	AC099391	AC099391 Rattus no
c 278	14	93.3 179198	2	AC130729	AC130729 Oryza sat	c 351	14	93.3 223977	2	AC124199	AC124199 Mus muscu
c 279	14	93.3 179324	2	AC101874	AC101874 Mus muscu	c 352	14	93.3 224560	2	AC115725	AC115725 Mus muscu
c 280	14	93.3 179430	2	AC103238	AC103238 Rattus no	c 353	14	93.3 226191	2	AC115665	AC115665 Rattus no
c 281	14	93.3 180538	2	AC073514	AC073514 Homo sapi	c 354	14	93.3 226608	2	AC105612	AC105612 Rattus no
c 282	14	93.3 180722	9	AC012169	AC012169 Homo sapi	c 355	14	93.3 227364	2	AC105604	AC105604 Rattus no
c 283	14	93.3 180744	2	AC094049	AC094049 Rattus no	c 356	14	93.3 228878	2	AC090652	AC090652 Mus muscu
c 284	14	93.3 180819	2	AC126857	AC126857 Rattus no	c 357	14	93.3 230571	2	AC026911	AC026911 Mus muscu

C 358	14	93.3	232089	2	AC130222	AC130222 Mus muscu	C 431	13	86.7	86.7	867	9	AB079246S6	AB079251 Homo sapi
C 359	14	93.3	232860	2	AL808123	AL808123 Mus muscu	C 432	13	86.7	86.7	884	11	CNS06K3X	AL402403 T7 end of
C 360	14	93.3	235559	2	AC105824	Rattus no	C 433	13	86.7	86.7	957	6	AX226440	AX226440 Sequence
C 361	14	93.3	237896	2	AC096317	Rattus no	C 434	13	86.7	86.7	966	6	AX241571	AX241571 Sequence
C 362	14	93.3	238551	2	AC095726	Rattus no	C 435	13	86.7	86.7	1014	5	HS1LGF52	U13801 Human insul
C 363	14	93.3	239685	2	AC096310	Rattus no	C 436	13	86.7	86.7	1041	5	CP091420	U91420 Carharinul
C 364	14	93.3	247462	3	LMFLCHRA4B	AL139794 Leishmani	C 437	13	86.7	86.7	1047	5	AB018982	AB018982 Rhinogobi
C 365	14	93.3	248160	3	AC122000	Mus muscu	C 438	13	86.7	86.7	1047	5	AF412173	AF412173 Peccillop
C 366	14	93.3	249243	2	AC114544	Mus muscu	C 439	13	86.7	86.7	1077	6	AX226363	AX226363 Sequence
C 367	14	93.3	270516	2	AC096350	Rattus no	C 440	13	86.7	86.7	1085	1	ECNHSITEN	X89444 E.chrysanth
C 368	14	93.3	270852	2	AC125346	Mus muscu	C 441	13	86.7	86.7	1094	8	BNCHITIN	X61488 B.napus mRN
C 369	14	93.3	283765	2	AL672224	AL672224 Mus muscu	C 442	13	86.7	86.7	1194	8	AY072009	AY072009 Arabidops
C 370	14	93.3	300189	2	AC121683	Rattus no	C 443	13	86.7	86.7	1284	4	AF509590	AF509590 Bos tauru
C 371	14	93.3	309662	2	AC004469	AP003009 Mesorhizo	C 444	13	86.7	86.7	1356	6	AX194096	AX194096 Sequence
C 372	14	93.3	339681	1	AP003009	AP003009 Mesorhizo	C 445	13	86.7	86.7	1369	9	AB065758	AB065758 Homo sapi
C 373	14	93.3	340000	9	AP001730	Homo sapi	C 446	13	86.7	86.7	1380	6	AX194318	AX194318 Sequence
C 374	14	93.3	340000	9	HS21C009	AL163302 Homo sapi	C 447	13	86.7	86.7	1419	6	AR051312	AR051312 Sequence
C 375	14	93.3	340000	9	HS21C102	AL163302 Homo sapi	C 448	13	86.7	86.7	1419	6	HUMCH13GEN	L13388 Human genom
C 376	14	93.3	347750	1	AP002998	AP002998 Mesorhizo	C 449	13	86.7	86.7	1458	8	AF223358	AF223358 Mesembrya
C 377	14	93.3	349116	1	AP003003	AP003003 Mesorhizo	C 450	13	86.7	86.7	1458	8	AK026359	AK026359 Homo sapi
C 378	14	93.3	349116	1	AP003003	AP003003 Mesorhizo	C 451	13	86.7	86.7	1506	5	CHKMARKS	M31650 Chicken myr
C 379	13	86.7	92	10	MMV51NM26	Z12520 M.musculus	C 452	13	86.7	86.7	1595	10	BC022727	BC022727 Mus muscu
C 380	13	86.7	119	1	AF503927	AF503927 Geobacter	C 453	13	86.7	86.7	1632	8	AB001578	AB001578 Lentinus
C 381	13	86.7	189	8	AF164378	AF164378 Oryza sat	C 454	13	86.7	86.7	1634	10	BC011067	BC011067 Mus muscu
C 382	13	86.7	201	11	AF098957	AF098957 Ovis arie	C 455	13	86.7	86.7	1670	9	BC008030	BC008030 Homo sapi
C 383	13	86.7	210	6	AX193049	AX193049 Sequence	C 456	13	86.7	86.7	1769	9	BC025749	BC025749 Homo sapi
C 384	13	86.7	231	9	HS190G11R	Z55080 H.sapiens C	C 457	13	86.7	86.7	1905	6	AR198640	AR198640 Sequence
C 385	13	86.7	239	11	G45463	G45463 Z23659_1 Ze	C 458	13	86.7	86.7	1937	8	RICOCs	M29259 Rice oryzac
C 386	13	86.7	260	9	HSU35893	U35893 Human throm	C 459	13	86.7	86.7	1974	10	BC027376	BC027376 Mus muscu
C 387	13	86.7	306	6	AX186927	AX186927 Sequence	C 460	13	86.7	86.7	1975	9	AK054700	AK054700 Homo sapi
C 388	13	86.7	308	8	HVU234775	AJ234775 Hordeum v	C 461	13	86.7	86.7	2007	6	AX431590	AX431590 Sequence
C 389	13	86.7	341	11	G47380	G47380 Z24275_1 Ze	C 462	13	86.7	86.7	2007	9	HSU19111	HSU19111 Human HOXB6
C 390	13	86.7	383	6	AX333410	AX333410 Sequence	C 463	13	86.7	86.7	2017	9	HSU802377	HSU802377 Sequence
C 391	13	86.7	383	6	AX408430	AX408430 Sequence	C 464	13	86.7	86.7	2040	6	AX460885	AX460885 Sequence
C 392	13	86.7	396	11	G64359	G64359 B47614/T7	C 465	13	86.7	86.7	2041	8	THA243799	AJ243799 Trichoder
C 393	13	86.7	430	3	LPY422074	LPY422074 Limatula	C 466	13	86.7	86.7	2050	3	AF234189	AF234189 Trypanoso
C 394	13	86.7	435	9	AF009305	AF009305 Homo sapi	C 467	13	86.7	86.7	2050	8	AB007849	AB007849 Lentinula
C 395	13	86.7	447	14	G45806	G45806 Z4452_1 Zeb	C 468	13	86.7	86.7	2088	9	HS4420478	HS4420478 Homo sapi
C 396	13	86.7	447	14	AF233147	AF233147 Human pol	C 469	13	86.7	86.7	2090	9	AK092728	AK092728 Homo sapi
C 397	13	86.7	480	9	HS4309474	GJ309474 Homo sapi	C 470	13	86.7	86.7	2103	9	AK092728	AK092728 Homo sapi
C 398	13	86.7	500	11	G34590	G34590 human SFS S	C 471	13	86.7	86.7	2135	9	AF279649S6	AF279649S6 Homo sapi
C 399	13	86.7	529	6	AX194651	AX194651 Sequence	C 472	13	86.7	86.7	2141	8	AF105110	AF105110 Nymphaea
C 400	13	86.7	530	9	HS4327382	AJ327382 Homo sapi	C 473	13	86.7	86.7	2141	9	AK056318	AK056318 Homo sapi
C 401	13	86.7	561	11	G54558	G54558 SHGC-100153	C 474	13	86.7	86.7	2164	10	AB03719S08	AB03719S08 Mus muscu
C 402	13	86.7	564	11	G54961	G54961 SHGC-100157	C 475	13	86.7	86.7	2219	3	AF144214	AF144214 Leptodora
C 403	13	86.7	594	6	AX320062	AX320062 Sequence	C 476	13	86.7	86.7	2307	3	AK055277	AK055277 Homo sapi
C 404	13	86.7	597	6	A51316	A51316 Sequence 1	C 477	13	86.7	86.7	2325	9	AK093602	AK093602 Homo sapi
C 405	13	86.7	598	8	RICCP1	J03469 Rice cystei	C 478	13	86.7	86.7	2364	9	AK022631	AK022631 Homo sapi
C 406	13	86.7	643	9	S49967	S49967 oryzacystat	C 479	13	86.7	86.7	2451	14	AF357218S1	AF357218 Deer tick
C 407	13	86.7	647	9	AF399565	AF399565 Homo sapi	C 480	13	86.7	86.7	2486	9	BC018702	BC018702 Homo sapi
C 408	13	86.7	685	9	HUMDAS12S2	M62750 Homo sapien	C 481	13	86.7	86.7	2496	9	HUMTGAS102	HUMTGAS102 Human trans
C 409	13	86.7	695	11	G34888	G34888 STS SHGC-95	C 482	13	86.7	86.7	2539	10	BC027155	BC027155 Mus muscu
C 410	13	86.7	705	6	AX437493	AX437493 Sequence	C 483	13	86.7	86.7	2616	14	AF383234	AF383234 HIV-1 98C
C 411	13	86.7	705	6	AX437494	AX437494 Sequence	C 484	13	86.7	86.7	2630	9	AK027086	AK027086 Homo sapi
C 412	13	86.7	745	9	HS4337047	AJ337047 Homo sapi	C 485	13	86.7	86.7	2675	9	AK054809	AK054809 Homo sapi
C 413	13	86.7	776	11	G75117	G75117 MARC 13236-	C 486	13	86.7	86.7	2683	10	BC003260	BC003260 Mus muscu
C 414	13	86.7	778	8	AF435976	AF435976 Oryza sat	C 487	13	86.7	86.7	2687	6	I24726	I24726 Sequence 8
C 415	13	86.7	792	8	AX3424918	AJ324918 Homo sapi	C 488	13	86.7	86.7	2708	10	HUMAM11AA	HUMAM11AA Mus muscu
C 416	13	86.7	831	11	PM12F10G	AL684404 Penicilli	C 489	13	86.7	86.7	2722	9	AK056158	AK056158 Homo sapi
C 417	13	86.7	832	9	GU019115	U19115 Gorilla gor	C 490	13	86.7	86.7	2759	9	AK056158	AK056158 Homo sapi
C 418	13	86.7	846	3	AB050862	AB050862 Carabus h	C 491	13	86.7	86.7	2809	8	MTHAHE	MTHAHE H.annuus m1
C 419	13	86.7	846	3	AB050863	AB050863 Carabus i	C 492	13	86.7	86.7	2830	10	MGGRK115	MGGRK115 Mus muscu
C 420	13	86.7	846	3	AB050864	AB050864 Carabus r	C 493	13	86.7	86.7	2863	10	BC024859	BC024859 Mus muscu
C 421	13	86.7	846	3	AB050865	AB050865 Carabus p	C 494	13	86.7	86.7	2873	6	I11774	I11774 Sequence 1
C 422	13	86.7	846	3	AB050866	AB050866 Carabus q	C 495	13	86.7	86.7	2877	6	I24719	I24719 Sequence 1
C 423	13	86.7	846	3	AB050867	AB050867 Carabus g	C 496	13	86.7	86.7	2877	6	E03372	E03372 gdna encodi
C 424	13	86.7	848	3	AB031400	AB031400 Leptocara	C 497	13	86.7	86.7	2900	9	AF277094	AF277094 Homo sapi
C 425	13	86.7	848	3	AB031401	AB031401 Leptocara	C 498	13	86.7	86.7	2902	9	HSU81262	HSU81262 Homo sapien
C 426	13	86.7	851	3	AB031399	AB031399 Leptocara	C 499	13	86.7	86.7	2941	1	AB026631	AB026631 Streptomy
C 427	13	86.7	858	9	HKU19112	U19112 Hylobates k	C 500	13	86.7	86.7	2944	9	AF312028	AF312028 Homo sapi
C 428	13	86.7	858	9	HLU19113	U19117 Hylobates l	C 501	13	86.7	86.7	2982	1	ATLEUCD	ATLEUCD A.teichomyc
C 429	13	86.7	858	9	SSU19113	U19113 Hylobates s	C 502	13	86.7	86.7	2982	1	ATLEUCD	ATLEUCD A.teichomyc
C 430	13	86.7	860	8	OSU54702	U54702 Oryza sativ	C 503	13	86.7	86.7	2982	1	ATLEUCD	ATLEUCD A.teichomyc

650	13	86.7	57103	2	AC087467	AC087467 Homo sapi	c 723	13	86.7	71699	2	AC027378	Homo sapi
651	13	86.7	57353	2	AC124318	Homo sapi	c 724	13	86.7	72038	2	AC023768	Homo sapi
c 652	13	86.7	57969	2	AC100083	Mus muscu	c 725	13	86.7	72591	2	AC080137	Homo sapi
c 653	13	86.7	58097	9	AL157758	Human DNA	c 726	13	86.7	72788	8	NCB2A19	Neurospor
c 654	13	86.7	58132	2	AC101310	Mus muscu	c 727	13	86.7	72969	2	AC027724	Homo sapi
c 655	13	86.7	58190	2	AC124329	Mus muscu	c 728	13	86.7	73048	2	AC103741	Homo sapi
c 656	13	86.7	58712	2	AC102832	Mus muscu	c 729	13	86.7	73052	2	AC013538	Homo sapi
c 657	13	86.7	59084	2	AC131506	Lytechinu	c 730	13	86.7	73141	2	AC120902	Rattus no
c 658	13	86.7	59320	3	AC024746	Caenorhab	c 731	13	86.7	73148	2	AC123731	Mus muscu
c 659	13	86.7	59339	9	AF287967	Homo sapi	c 732	13	86.7	73228	2	AC111529	Rattus no
c 660	13	86.7	59499	2	AC115550	Rattus no	c 733	13	86.7	73322	2	AC069380	Homo sapi
c 661	13	86.7	59942	2	AC130768	Human DNA	c 734	13	86.7	73605	9	AL136309	Human DNA
c 662	13	86.7	60016	2	AC126381	Homo sapi	c 735	13	86.7	73666	2	AC130343	Homo sapi
c 663	13	86.7	60042	2	AC100484	Mus muscu	c 736	13	86.7	73782	2	AC123702	Mus muscu
c 664	13	86.7	60163	9	AC012018	Homo sapi	c 737	13	86.7	73782	2	AC123702	Mus muscu
c 665	13	86.7	60609	2	AC023519	Homo sapi	c 738	13	86.7	73852	2	AC101524	Mus muscu
c 666	13	86.7	60661	2	AC120009	Mus muscu	c 739	13	86.7	74510	2	AC101683	Mus muscu
c 667	13	86.7	61212	9	AL391812	Human DNA	c 740	13	86.7	74521	9	AC112710	Homo sapi
c 668	13	86.7	61245	2	AC069449	Mus muscu	c 741	13	86.7	74600	9	AP000275	Homo sapi
c 669	13	86.7	61309	2	AC090748	Homo sapi	c 742	13	86.7	74905	2	AC097836	Rattus no
c 670	13	86.7	61412	2	AC021493	Homo sapi	c 743	13	86.7	75106	8	ATFL6M2	Arabidops
c 671	13	86.7	61588	10	AL611970	Mouse DNA	c 744	13	86.7	75254	2	AC016176	Homo sapi
c 672	13	86.7	61958	2	AC121467	Rattus no	c 745	13	86.7	75306	2	AC100494	Mus muscu
c 673	13	86.7	61977	2	AC100640	Mus muscu	c 746	13	86.7	75939	9	AL606519	Human DNA
c 674	13	86.7	62076	2	AC091416	Rattus no	c 747	13	86.7	76556	2	AL691517_3	Continuation (4 of
c 675	13	86.7	62078	2	AC013711	Homo sapi	c 748	13	86.7	76730	2	AC114105	Rattus no
c 676	13	86.7	62499	2	AC091183	Homo sapi	c 749	13	86.7	77730	9	AC105760	Homo sapi
c 677	13	86.7	62649	2	AC022552	Homo sapi	c 750	13	86.7	77830	10	AL672057	Mouse DNA
c 678	13	86.7	62791	2	AC026350	Homo sapi	c 751	13	86.7	78197	10	AL671896	Mouse DNA
c 679	13	86.7	63170	10	AL645799	Mouse DNA	c 752	13	86.7	78423	2	AC094380	Rattus no
c 680	13	86.7	63403	10	AL611923	Mouse DNA	c 753	13	86.7	78843	2	AC015455	Homo sapi
c 681	13	86.7	63427	2	AC130366	Homo sapi	c 754	13	86.7	79199	2	AC097165	Rattus no
c 682	13	86.7	63528	2	AC091196	Homo sapi	c 755	13	86.7	79202	8	AP005165	Oryza sat
c 683	13	86.7	63596	2	AC108913	Mus muscu	c 756	13	86.7	79877	2	AC131495	Lytechinu
c 684	13	86.7	63600	2	AC101405	Mus muscu	c 757	13	86.7	79899	2	AC109972	Rattus no
c 685	13	86.7	63668	2	AC116754	Mus muscu	c 758	13	86.7	79991	2	AC096336	Rattus no
c 686	13	86.7	64260	2	AC112046	Rattus no	c 759	13	86.7	80218	2	AC084700	Homo sapi
c 687	13	86.7	64326	9	AP000331	Homo sapi	c 760	13	86.7	80478	2	AC107331	Rattus no
c 688	13	86.7	64638	2	AC103116	Rattus no	c 761	13	86.7	80600	9	AL589941	Human DNA
c 689	13	86.7	64776	2	AC101127	Mus muscu	c 762	13	86.7	80609	2	AC128424	Rattus no
c 690	13	86.7	65147	2	AC101675	Mus muscu	c 763	13	86.7	80803	9	AL139084	Human DNA
c 691	13	86.7	65174	2	AC025214	Homo sapi	c 764	13	86.7	81120	2	AC022851	Homo sapi
c 692	13	86.7	65356	2	AC109800	Mus muscu	c 765	13	86.7	81374	9	HSJ300H18	Human DNA
c 693	13	86.7	65612	2	AC087452	Homo sapi	c 766	13	86.7	81878	2	AC013647	Homo sapi
c 694	13	86.7	65612	2	AC087452	Homo sapi	c 767	13	86.7	83001	2	AC015632	Homo sapi
c 695	13	86.7	65762	2	AC118238	Mus muscu	c 768	13	86.7	83379	2	AC092113	Homo sapi
c 696	13	86.7	65762	2	AC118238	Mus muscu	c 769	13	86.7	83453	2	AC111885	Rattus no
c 697	13	86.7	65762	10	AC093315	Mus muscu	c 770	13	86.7	83783	2	AC016513	Homo sapi
c 698	13	86.7	66206	2	AC102041	Mus muscu	c 771	13	86.7	84003	2	AC110461	Rattus no
c 699	13	86.7	66624	2	AC101520	Mus muscu	c 772	13	86.7	84163	2	AC013510	Homo sapi
c 700	13	86.7	66666	2	AC123639	Mus muscu	c 773	13	86.7	84906	2	AC019750	Drosophil
c 701	13	86.7	67045	2	AC118213	Mus muscu	c 774	13	86.7	85022	2	AC121484	Rattus no
c 702	13	86.7	67346	10	AL732624	Mouse DNA	c 775	13	86.7	85545	9	HS833B7	Human DNA
c 703	13	86.7	67645	10	AL645583	Mouse DNA	c 776	13	86.7	85574	9	AP01349	Human DNA
c 704	13	86.7	67808	2	AC114539	Mus muscu	c 777	13	86.7	87065	9	HSJ1174H9	Human DNA
c 705	13	86.7	68419	2	AC016014	Homo sapi	c 778	13	86.7	87834	9	AP002957	Homo sapi
c 706	13	86.7	68543	9	AC115779	Mus muscu	c 779	13	86.7	88295	9	AC004612	Homo sapi
c 707	13	86.7	68651	2	AC027343	Homo sapi	c 780	13	86.7	89259	9	AL137076	Human DNA
c 708	13	86.7	68899	2	AC034301	Homo sapi	c 781	13	86.7	89937	2	AC096092	Rattus no
c 709	13	86.7	68946	2	AC128842	Rattus no	c 782	13	86.7	90378	2	AC097566	Rattus no
c 710	13	86.7	69314	2	AC108417	Mus muscu	c 783	13	86.7	90513	9	AC107627	Homo sapi
c 711	13	86.7	69734	2	AC010953	Homo sapi	c 784	13	86.7	90608	2	AC128541	Rattus no
c 712	13	86.7	69894	2	AC123604	Mus muscu	c 785	13	86.7	90701	2	AC094040	Human DNA
c 713	13	86.7	70310	9	AC079839	Homo sapi	c 786	13	86.7	91025	9	AL359270	Human DNA
c 714	13	86.7	70511	2	AC091083	Homo sapi	c 787	13	86.7	91098	2	AC111605	Rattus no
c 715	13	86.7	70556	2	AC113141	Homo sapi	c 788	13	86.7	91202	2	AC007609	Homo sapi
c 716	13	86.7	70866	2	AC114419	Mus muscu	c 789	13	86.7	91410	2	AC095538	Rattus no
c 717	13	86.7	70878	2	AC100628	Mus muscu	c 790	13	86.7	91503	9	AL592488	Human DNA
c 718	13	86.7	70982	2	AC107577	Rattus no	c 791	13	86.7	91927	9	AC004771	Homo sapi
c 719	13	86.7	71166	2	AC023783	Homo sapi	c 792	13	86.7	92276	2	AC023646	Homo sapi
c 720	13	86.7	71464	2	AC124296	Homo sapi	c 793	13	86.7	92337	2	AC108839	Mus muscu
c 721	13	86.7	71544	9	AC093792	Homo sapi	c 794	13	86.7	93001	2	AC007286	Homo sapi
c 722	13	86.7	71605	2	AC119332	Rattus no	c 795	13	86.7	93329	2	AC097393	Rattus no

796	13	86.7	93423	2	AC120035	AC120035 Homo sapi	869	13	86.7	106604	9	HSXKSRPX	AJ239329 Homo sapi
C 797	13	86.7	93526	2	AC128218	Rattus no	870	13	86.7	106866	10	AL7332550	AL7332550 Mouse DNA
C 798	13	86.7	93610	2	AC127757	Rattus no	871	13	86.7	107092	2	AC094284	AC094284 Rattus no
C 799	13	86.7	93701	8	AC006954	Arabidops	C 872	13	86.7	107163	9	AL449105	AL449105 Human DNA
C 800	13	86.7	93721	2	AC122625	Rattus no	C 873	13	86.7	107133	9	AL354702	AL354702 Human DNA
C 801	13	86.7	94533	2	AC058788_3	Continuation (4 of	C 874	13	86.7	107422	9	AL354681	AL354681 Human DNA
C 802	13	86.7	94625	9	AC011337	Homo sapi	C 875	13	86.7	107689	9	AC008631	AC008631 Homo sapi
C 803	13	86.7	94770	9	HSJ570F3	Human DNA	C 876	13	86.7	107857	9	AP000057	AP000057 Homo sapi
C 804	13	86.7	95092	2	AC129002	Rattus no	C 877	13	86.7	107947	8	NCB7N14	AL669886 Neurospor
C 805	13	86.7	95594	2	AC122615	Rattus no	C 878	13	86.7	108287	2	AP003814	AP003814 Oryza sat
C 806	13	86.7	96676	2	AC099305	Rattus no	C 879	13	86.7	108315	9	HS41P2	AL049748 Human DNA
C 807	13	86.7	96741	2	AC109685	Rattus no	C 880	13	86.7	108579	2	AC091566	AC091566 Homo sapi
C 808	13	86.7	96975	9	AC004975	Homo sapi	881	13	86.7	108685	2	AL157383	AL157383 Homo sapi
C 809	13	86.7	97464	2	AC095194	Rattus no	C 882	13	86.7	109043	5	CNS08CA7	AL808032 BAC 30B15
C 810	13	86.7	97468	2	AC111394	Rattus no	C 883	13	86.7	109270	2	AC107541	AC107541 Rattus no
C 811	13	86.7	97792	2	AC097881	Rattus no	884	13	86.7	109351	2	AL831758	AL831758 Dantio rer
C 812	13	86.7	98031	2	AC105808	Rattus no	C 885	13	86.7	109394	9	AC010979	AC010979 Homo sapi
C 813	13	86.7	98145	2	AC126313	Rattus no	C 886	13	86.7	109626	9	AC010346	AC010346 Homo sapi
C 814	13	86.7	98340	2	HS344J2	AL449213 Homo sapi	C 887	13	86.7	109626	9	AC010346	AC010346 Homo sapi
C 815	13	86.7	98490	9	HS1018D12	AL031650 Human DNA	C 888	13	86.7	110000	2	AC112065_0	AC112065 Rattus no
C 816	13	86.7	98562	2	AC098628	Rattus no	C 889	13	86.7	110000	2	AC112065_2	Continuation (3 of
C 817	13	86.7	98597	9	AC008416	Homo sapi	C 890	13	86.7	110000	2	AC115817_1	Continuation (2 of
C 818	13	86.7	99141	8	AP003704	AP003704 Oryza sat	C 891	13	86.7	110000	2	AC122235_0	AC122235 Mus muscu
C 819	13	86.7	99156	8	AF466932	AF466932 Zea mays	C 892	13	86.7	110000	2	AC125228_0	AC125228 Mus muscu
C 820	13	86.7	99156	8	AF466932	AF466932 Zea mays	C 893	13	86.7	110000	2	AL772293_0	AL772293 Mus muscu
C 821	13	86.7	99657	2	AC106957	AL078461 Rattus no	C 894	13	86.7	110000	2	LMFLCHR18_03	Continuation (4 of
C 822	13	86.7	99876	9	HSJ901O8	AL078461 Rattus no	C 895	13	86.7	110000	2	LMFLCHR31_04	Continuation (5 of
C 823	13	86.7	99920	2	AC096218	AC096218 Rattus no	896	13	86.7	110000	2	LMFLCHR31_04	Continuation (30 o
C 824	13	86.7	100000	9	AP000037	AP000037 Homo sapi	897	13	86.7	110000	2	LMFLCHR36_29	Continuation (30 o
C 825	13	86.7	100000	9	AP000105	AP000105 Homo sapi	898	13	86.7	110000	2	AC055726_0	AC055726 Homo sapi
C 826	13	86.7	100000	9	AP000172	AP000172 Homo sapi	C 899	13	86.7	110000	10	AE008685_0	AE008685 Mus muscu
C 827	13	86.7	100000	9	AP000181	AP000181 Homo sapi	C 900	13	86.7	110000	10	AE008684_0	AE008684 Mus muscu
C 828	13	86.7	100000	9	AP000508	AP000508 Homo sapi	C 901	13	86.7	110000	10	AE008685_0	AE008685 Mus muscu
C 829	13	86.7	100025	2	AC130913	AC130913 Rattus no	C 902	13	86.7	110276	9	AC010169	AC010169 Homo sapi
C 830	13	86.7	100079	9	AC108002	AC108002 Homo sapi	C 903	13	86.7	111016	2	AC099129	AC099129 Rattus no
C 831	13	86.7	100241	2	AC115168	AC115168 Rattus no	C 904	13	86.7	111295	2	AC098255	AC098255 Rattus no
C 832	13	86.7	100644	2	AC105511	AC105511 Rattus no	C 905	13	86.7	111659	2	AC128720	AC128720 Rattus no
C 833	13	86.7	100644	2	AC105511	AC105511 Rattus no	C 906	13	86.7	111723	9	HSJ101K10	AL080276 Human DNA
C 834	13	86.7	100674	2	AC126873	AC126873 Rattus no	C 907	13	86.7	111855	8	AF267176	AF267176 Pyricular
C 835	13	86.7	101199	2	AC120605	AC120605 Rattus no	C 908	13	86.7	111948	2	AC094563	AC094563 Rattus no
C 836	13	86.7	101737	2	AC130446	AC130446 Rattus no	C 909	13	86.7	112311	9	AL358780	AL358780 Human DNA
C 837	13	86.7	102057	2	AC122587	AC122587 Rattus no	C 910	13	86.7	112428	2	AP003906	AP003906 Oryza sat
C 838	13	86.7	102271	2	AC097693	AC097693 Rattus no	C 911	13	86.7	112442	9	AL355340	AL355340 Human DNA
C 839	13	86.7	102319	9	AL159153	AL159153 Human DNA	C 912	13	86.7	112662	9	AC104453	AC104453 Homo sapi
C 840	13	86.7	102326	9	AC087407	AC087407 Homo sapi	C 913	13	86.7	112686	2	AC002086	AC002086 Human PAC
C 841	13	86.7	102377	2	AC004086	AC004086 Homo sapi	C 914	13	86.7	112813	9	AC102504	AC102504 Mus muscu
C 842	13	86.7	102390	2	AC104712	AC104712 Oryza sat	C 915	13	86.7	112846	9	AC004991	AC004991 Homo sapi
C 843	13	86.7	102422	2	AC129557	AC129557 Mus muscu	C 916	13	86.7	112876	9	AC122138	AC122138 Homo sapi
C 844	13	86.7	102488	9	AP005231	AP005231 Homo sapi	C 917	13	86.7	112917	2	AC096013	AC096013 Rattus no
C 845	13	86.7	102515	2	AC112323	AC112323 Rattus no	C 918	13	86.7	112968	9	AC093833	AC093833 Homo sapi
C 846	13	86.7	102515	2	AC099466	AC099466 Rattus no	C 919	13	86.7	113164	10	AL731688	AL731688 Mouse DNA
C 847	13	86.7	102704	5	AL672216	AL672216 Zebrafish	C 920	13	86.7	113248	2	AC094145	AC094145 Rattus no
C 848	13	86.7	103190	5	AF016020	AF016020 Gallus ga	C 921	13	86.7	113468	2	AC113911	AC113911 Rattus no
C 849	13	86.7	103247	2	AF176678	AF176678 Homo sapi	C 922	13	86.7	113513	2	AC115368	AC115368 Rattus no
C 850	13	86.7	103409	5	AL662880	AL662880 Zebrafish	C 923	13	86.7	113633	2	AC094512	AC094512 Rattus no
C 851	13	86.7	103616	9	AL138689	AL138689 Human DNA	C 924	13	86.7	113704	2	AC119345	AC119345 Rattus no
C 852	13	86.7	103694	9	AC004836	AC004836 Homo sapi	C 925	13	86.7	114356	8	AP003700	AP003700 Oryza sat
C 853	13	86.7	103699	9	AC034305	AC034305 Homo sapi	C 926	13	86.7	114576	9	AC074397	AC074397 Human sapi
C 854	13	86.7	103720	9	AL161717	AL161717 Human DNA	C 927	13	86.7	115009	9	HSJ092C4	AL132875 Human DNA
C 855	13	86.7	103894	2	AC119635	AC119635 Rattus no	C 928	13	86.7	115043	9	AL663070	AL663070 Human DNA
C 856	13	86.7	104481	2	AP003844	AP003844 Oryza sat	C 929	13	86.7	115468	2	AC011820	AC011820 Homo sapi
C 857	13	86.7	104509	2	AL356429	AL356429 Homo sapi	C 930	13	86.7	115583	2	AC115470	AC115470 Rattus no
C 858	13	86.7	104983	2	AC119590	AC119590 Rattus no	C 931	13	86.7	115793	2	AC025166	AC025166 Homo sapi
C 859	13	86.7	105027	9	AC118563	AC118563 Homo sapi	C 932	13	86.7	116245	2	AC110842	AC110842 Rattus no
C 860	13	86.7	105156	2	AF235094	AF235094 Homo sapi	C 933	13	86.7	116736	2	AC095745	AC095745 Rattus no
C 861	13	86.7	105507	2	AC109113	AC109113 Rattus no	C 934	13	86.7	117035	2	AL391418	AL391418 Homo sapi
C 862	13	86.7	105565	2	AC104103	AC104103 Mus muscu	C 935	13	86.7	117048	2	AC118902	AC118902 Rattus no
C 863	13	86.7	105899	2	AC098634	AC098634 Rattus no	C 936	13	86.7	117082	2	AC126076	AC126076 Rattus no
C 864	13	86.7	105967	2	AC114148	AC114148 Rattus no	C 937	13	86.7	117199	17	AP000125	AP000125 Homo sapi
C 865	13	86.7	106093	9	AC007561	AC007561 Homo sapi	C 938	13	86.7	117602	2	AC087055	AC087055 Homo sapi
C 866	13	86.7	106140	2	AC098002	AC098002 Rattus no	C 939	13	86.7	118053	2	AC125919	AC125919 Rattus no
C 867	13	86.7	106392	9	AC007316	AC007316 Homo sapi	C 940	13	86.7	118247	2	AC109841	AC109841 Rattus no
C 868	13	86.7	106580	9	AL683834	AL683834 Human DNA	C 941	13	86.7	118361	2	AC109383	AC109383 Rattus no

942	13	86.7	118873	9	HSJ1017F8	AL132822	Human DNA	ORGANISM	Homo sapiens
943	13	86.7	119000	2	AP001482	AC127841	Rattus no	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
944	13	86.7	119164	2	AC127841	AC127841	Rattus no	AUTHORS	1 (bases 1 to 190)
945	13	86.7	119238	2	AC098424	AC107227	Mus muscu	TITLE	Heidet.L., Arrondel.C., Forestier.L., Cohen-Solal,L., Mollet,G., Gutierrez.B., Stavrou,C., Gubler,M.C. and Antignac,C.
946	13	86.7	119494	2	AC107227	AC107227	Mus muscu	JOURNAL	Structure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome
947	13	86.7	119574	2	AC107284	AC107284	Rattus no	MEDLINE	J. Am. Soc. Nephrol. 12 (1), 97-106 (2001)
948	13	86.7	119821	2	CNS07YP6	AL713929	Ryza sat	PUBMED	11134255
949	13	86.7	119971	2	AC120331	AC120331	Rattus no	REFERENCE	2 (bases 1 to 190)
950	13	86.7	119977	2	AC094827	AC094827	Rattus no	AUTHORS	Antignac,C.
951	13	86.7	120048	2	AC110849	AC110849	Rattus no	TITLE	Direct Submission
952	13	86.7	120197	9	AL671883	AL671883	Human DNA	JOURNAL	Submitted (28-MAR-2000) Antignac C., U423, INSERM, Hopital Necker-Enfants malades 149 rue de Sevres, 75015 Paris, FRANCE
953	13	86.7	120487	9	HSJ247G22	AL096866	Human DNA	FEATURES	Location/Qualifiers
954	13	86.7	120606	2	AC105474	AC105474	Rattus no	source	1..190
955	13	86.7	120629	2	AC097995	AC097995	Rattus no	gene	/organism="Homo sapiens"
956	13	86.7	120773	9	AL139322	AL139322	Human DNA	exon	/db_xref="taxon:9606"
957	13	86.7	120864	2	AL672161	AL672161	Danio rer		51..140
958	13	86.7	121080	2	AC120314	AC120314	Rattus no		/gene="COL4A3"
959	13	86.7	121304	2	AC126973	AC126973	Rattus no		51..140
960	13	86.7	121349	2	AC094313	AC094313	Rattus no		/gene="COL4A3"
961	13	86.7	121601	9	AL592406	AL592406	Human DNA		/number=3
962	13	86.7	121777	9	AC093381	AC093381	Homo sapi		/usedin="AJ288487:cal_mRNA"
963	13	86.7	121777	9	AC093381	AC093381	Homo sapi		/usedin="AJ288487:cal_CDS"
964	13	86.7	122223	9	AC007880	AC007880	Homo sapi	BASE COUNT	37 a 55 c 49 g 49 t
965	13	86.7	122547	2	AC121162	AC121162	Mus muscu	ORIGIN	
966	13	86.7	122674	9	AC007021	AC007021	Homo sapi		1 CCTCTCCCCCTGTT 15
967	13	86.7	122882	9	AC023163	AC023163	Homo sapi		
968	13	86.7	122903	9	AC005833	AC005833	Homo sapi		60 CCTCTCCCCCTGTT 46
969	13	86.7	123007	2	AC094437	AC094437	Rattus no	Query Match	100.0%; Score 15; DB 9; Length 190;
970	13	86.7	123360	9	HS222E13	HS222E13	Human DNA	Best Local Similarity	100.0%; Pred. No. 52;
971	13	86.7	123755	2	AC120682	AC120682	Rattus no	Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
972	13	86.7	123916	2	AC128031	AC128031	Rattus no	Qy	1 CCTCTCCCCCTGTT 15
973	13	86.7	124518	9	AL138962	AL138962	Human DNA	Db	60 CCTCTCCCCCTGTT 46
974	13	86.7	124541	9	AC068288	AC068288	Homo sapi	RESULT 2	
975	13	86.7	124675	9	AC004933	AC004933	Homo sapi	AF506010/c	
976	13	86.7	124995	2	AC115286	AC115286	Homo sapi	LOCUS	AF506010
977	13	86.7	125212	2	AC123201	AC123201	Rattus no	DEFINITION	Gallus gallus TNF family B cell activation factor (BAFF) mRNA,
978	13	86.7	125224	2	AC094403	AC094403	Rattus no	ACCESSION	AF506010
979	13	86.7	125287	9	HS159A19	HS159A19	Human DNA	VERSION	AF506010.1 GI:22087370
980	13	86.7	125508	2	AC006345	AC006345	Homo sapi	KEYWORDS	chicken.
981	13	86.7	125766	2	AC013137	AC013137	Drosophil	ORGANISM	Gallus gallus
982	13	86.7	126352	9	HS23K20	AL022153	Human DNA	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
983	13	86.7	126452	2	AC118313	AC118313	Rattus no	AUTHORS	1 (bases 1 to 600)
984	13	86.7	126864	2	AC130199	AC130199	Gallus ga	TITLE	Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and Staeheli,P.
985	13	86.7	126906	2	AC112012	AC112012	Rattus no	JOURNAL	A chicken homolog of the B cell activating factor of the TNF family (BAFF)
986	13	86.7	127051	2	AC114895	AC114895	Tetraodon	REFERENCE	2 (bases 1 to 600)
987	13	86.7	127144	9	AC008883	AC008883	Homo sapi	AUTHORS	Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and Staeheli,P.
988	13	86.7	127356	2	AC109534	AC109534	Rattus no	TITLE	Direct Submission
989	13	86.7	127402	2	AC114021	AC114021	Rattus no	JOURNAL	Submitted (24-APR-2002) Virology, University of Freiburg, Hermann-Herder-Str.11, Freiburg 79104, Germany
990	13	86.7	127665	2	AC128777	AC128777	Rattus no	FEATURES	Location/Qualifiers
991	13	86.7	127722	2	AC123891	AC123891	Rattus no	source	1..600
992	13	86.7	127953	2	AC022835	AC022835	Homo sapi	gene	/organism="Gallus gallus"
993	13	86.7	127953	2	AC022835	AC022835	Homo sapi		/db_xref="taxon:9031"
994	13	86.7	127992	2	AC105036	AC105036	Homo sapi		<1..600
995	13	86.7	128090	2	AC108372	AC108372	Pan trogl		/gene="BAFF"
996	13	86.7	128329	2	AC112014	AC112014	Rattus no	CDS	<1..534
997	13	86.7	128468	9	AL139090	AL139090	Human DNA		/gene="BAFF"
998	13	86.7	128962	2	AC099273	AC099273	Rattus no		/codon_start=1
999	13	86.7	129169	2	AC032038	AC032038	Homo sapi		
1000	13	86.7	129396	9	AC091113	AC091113	Homo sapi		

ALIGNMENTS

HSA288489 190 bp DNA linear PRI 04-APR-2001

LOCUS HSA288489.1 GI:13559182

DEFINITION Homo sapiens partial COL4A3 gene for alpha3 type IV collagen, exon 3.

ACCESSION AJ288489

VERSION AJ288489.1

KEYWORDS alpha3 type IV collagen; col4a3 gene.

SOURCE human.

/product="TNF family B cell activation factor"
/protein_id="AM90951.1"
/db_xref="GI:22087371"
/translation="RLPGSPAESFQTEIWRNRNRGRSIVNAETVLQACLIAD
SKSDIQKDDSSIVPWLKFKRGTALEQGNKIVIKETGYFFIYGVLYDTDTFMGH
LQIRKKAHVGGDLSLAVLFRCLQNMPQSPNNSCYTAGIAKLEEGDELQTLTPRRRA
KISLDGDCGTFCAVRLI"
186 a 117 c 133 g 164 t

BASE COUNT
ORIGIN
Query Match 100.0%; Score 15; DB 5; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTCCCTCCCTGTT 15
|||||
Db 75 CTTCTCCCTCCCTGTT 61

RESULT 3
AK021867/c
LOCUS
DEFINITION Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately
similar to POLY(A) POLYMERASE (EC 2.7.7.19).
ACCESSION AK021867
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
mRNA, clone_lib:HEMBAL clone:HEMBAL006278.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,K., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.
NEDO human cDNA sequencing project
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
Location/Qualifiers
1..1689
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBAL006278"
/tissue_type="whole embryo, mainly head"
/clone_lib="HEMBAL"
/dev_stage="embryo, 10 weeks"
/note="cloning vector: pME18SFL3"
186..>1689
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB13919.1"
/db_xref="GI:10433147"

Translati
/translation="MKMSANTVLDQRQKKHYGITSPLASPKEDHIYTKLIDA
MKPGVFDEDELNRLVYVGLNNLVKREWISDSKSNLPSPVATVGKLTFGSY
RLGVHTKADIDALCAVRHVSDFQSFEEKLKHQDGIKRLRAVEDAFVPIKFEF
DGIEDILVFARLAQTISDNLDRDSRLSLDICIIRSLNGRCRVDEILHLPNKET
FRLTLRAVWAKRGIYSNMLGVLGGVSWAMLVARTCOLYPNAASTLVHKKFFLVFS
KWEVNPVLLKQPEESNLPVWDPVRVNPDSRYHLMPIITPAIPQONSTYNVSTSTR

BASE COUNT
ORIGIN
Query Match 100.0%; Score 15; DB 5; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTCCCTCCCTGTT 15
|||||
Db 75 CTTCTCCCTCCCTGTT 61

RESULT 3
AK021867/c
LOCUS
DEFINITION Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately
similar to POLY(A) POLYMERASE (EC 2.7.7.19).
ACCESSION AK021867
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
mRNA, clone_lib:HEMBAL clone:HEMBAL006278.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,K., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.
NEDO human cDNA sequencing project
Unpublished

VMVEEFQGLAVTDEILQKSDSKLLEPPNFPNFQKRYHYIVLTASASTENHLEWGL
VESKIRVLGNLERNETITLAHVQSPFGNKEHKKONNYYVSMFGLGIFIRRVNAES
VNIDLTDIQSFTDVTYVRQANNINLKEGMIKIEATHVKKKQLHYLPAEIL"
BASE COUNT 555 a 309 c 366 g 459 t
ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 1689;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTCCCTCCCTGTT 15
|||||
Db 123 CTTCTCCCTCCCTGTT 109

RESULT 4
AF232676/c
LOCUS
DEFINITION Sus scrofa prophet of pit-1 (prop-1) mRNA, complete cds.
ACCESSION AF232676
VERSION AF232676.1 GI:11275672
KEYWORDS
SOURCE Sus scrofa.

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS Sloop,K.W., McCutchan Schiller,A., Smith,T.P., Blanton,J.R. Jr.,
Rohrer,G.A., Meier,B.C. and Rhodes,S.J.
TITLE Biochemical and genetic characterization of the porcine Prophet of
Pit-1 pituitary transcription factor
Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)

JOURNAL
MEDLINE 20519384
PUBMED 11064154
REFERENCE
AUTHORS McCutchan Schiller,A.L., Sloop,K.W., Blanton,J.R. Jr., Meier,B.C.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Biology, Indiana University Purdue
University Indianapolis, 723 West Michigan Street, Indianapolis, IN
46202-5132, USA

FEATURES
Location/Qualifiers
1..1721
/organism="Sus scrofa"
/db_xref="taxon:9823"
1..1721
/gene="Prop-1"
333..1013
/gene="Prop-1"
/note="transcription factor"
/codon_start=1
/product="prophet of pit-1"
/protein_id="AAG33702.1"
/db_xref="GI:11275673"
/translation="MEAEGRREQKPRKRVCSLLWPPEGYPAGTTLTARVDISTRPYR
NLSGVAGRPRLSPQGGQRGRPHSRHRHTFSPAQLQESAFGRNQYPDIIWAREGL
ARDTGLSEARIQVWFKRAKORAKORERSLLQLAHLSPATSGFLPEPPACPYSVPTP
PPMWTCEPHYPNHALPSPQSTGGSFARHQSDEWYPIHPTTGHLPCPPAPPVPLLS
LEPPKSNW"

BASE COUNT 457 a 460 c 469 g 333 t 2 others
ORIGIN
Query Match 100.0%; Score 15; DB 4; Length 1721;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTCCCTCCCTGTT 15
|||||
Db 236 CTTCTCCCTCCCTGTT 222

RESULT 5
BC000776
LOCUS
DEFINITION Sus scrofa prophet of pit-1 (prop-1) mRNA, complete cds.
ACCESSION BC000776
VERSION BC000776.1 GI:11275672
KEYWORDS
SOURCE Sus scrofa.

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS Sloop,K.W., McCutchan Schiller,A.L., Sloop,K.W., Blanton,J.R. Jr., Meier,B.C.
TITLE Biochemical and genetic characterization of the porcine Prophet of
Pit-1 pituitary transcription factor
Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)

JOURNAL
MEDLINE 20519384
PUBMED 11064154
REFERENCE
AUTHORS McCutchan Schiller,A.L., Sloop,K.W., Blanton,J.R. Jr., Meier,B.C.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Biology, Indiana University Purdue
University Indianapolis, 723 West Michigan Street, Indianapolis, IN
46202-5132, USA

FEATURES
Location/Qualifiers
1..1721
/organism="Sus scrofa"
/db_xref="taxon:9823"
1..1721
/gene="Prop-1"
333..1013
/gene="Prop-1"
/note="transcription factor"
/codon_start=1
/product="prophet of pit-1"
/protein_id="AAG33702.1"
/db_xref="GI:11275673"
/translation="MEAEGRREQKPRKRVCSLLWPPEGYPAGTTLTARVDISTRPYR
NLSGVAGRPRLSPQGGQRGRPHSRHRHTFSPAQLQESAFGRNQYPDIIWAREGL
ARDTGLSEARIQVWFKRAKORAKORERSLLQLAHLSPATSGFLPEPPACPYSVPTP
PPMWTCEPHYPNHALPSPQSTGGSFARHQSDEWYPIHPTTGHLPCPPAPPVPLLS
LEPPKSNW"

BASE COUNT 457 a 460 c 469 g 333 t 2 others
ORIGIN
Query Match 100.0%; Score 15; DB 4; Length 1721;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTCCCTCCCTGTT 15
|||||
Db 236 CTTCTCCCTCCCTGTT 222

LOCUS BC000776 3190 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, Similar to KIAA0736 gene product, clone
IMAGE:3509807, mRNA, partial cds.
ACCESSION BC000776
VERSION GI:12653962
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 7 Row: 1 Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES
source
1. 3190
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3509807"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
<1..1824
/codon_start=1
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/protein_id="AAH00776.1"
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GVFVGVFLPSAEKDCLSNKGMLGLIVLGMVGAFLWGLADLRGRQCILLI
SLSVNSVAFSSFGQGTFLFCRLSCVGIGGSIPIVFSVEFLAQEKRGELSW
LCMFWMIGVYAAAWALPHYIGWSFGMSAYQFHSRVFLVCAFPVFAIGALTT
QPESPRFFLENGKDEAMVLKOVHDTNMRKGPVSVTHIKTHQDEDELIQOS
DTGTWQWGRVRLSGQVGNFLSCFGPEYRRITLMGMVMTFMSFYGLTWFP
DMRIHQADVASRTKVQGERVHVTFNFTLENQIHRGQYFNDKFIQLKSVSFE
DSLRECFEDVTSNTFPRNCTFINVYNTDLPFYKFVNSRLINSTFLHNKGCPL
DYTGCEGAYWYFVSFGLTAVLPGNIVSALIMDKIGRLMLAGSSVMSCVSCFFLS
FQNSGSMALLCULCGGVSIASWALDVLTVELYPSDKRTTAFGLNALCKLAALVGI
SIFTSFVGTAKAPILFASALALGSSALKALPETFQGVQLQ"

BASE COUNT 662 a 850 c 868 g 810 t
ORIGIN
Query Match 100.0%; Score 15; DB 9; Length 3190;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCTGTT 15
|||||
Db 2096 CCTTCTCCCTGTT 2110

RESULT 6

CHKTGFBPBA/c
LOCUS
DEFINITION Gallus gallus transforming growth factor-beta type III receptor
mRNA, complete CDS.
L01121
ACCESSION L01121.1 GI:511842
VERSION
KEYWORDS TGF-beta; betaglycan; plasma membrane; transforming growth
factor-beta receptor; transforming growth factor-beta type III
receptor.
SOURCE Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3347)
AUTHORS Barnett,J.V., Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y.,
Galper,J.B. and Maas,R.L.
TITLE Cloning and developmental expression of the chick type II and type
III TGF beta receptors
JOURNAL Dev. Dyn. 199 (1), 12-27 (1994)
MEDLINE 94220749
PUBMED 8167376
FEATURES
source
Location/Qualifiers
1..3347
/organism="Gallus gallus"
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/tissue_type="brain"
/dev_stage="embryonic"
/germline
/tissue_lib="lambda zap"
152..2677
/codon_start=1
/product="transforming growth factor-beta type III
receptor"
/protein_id="AAA49090.1"
/db_xref="GI:511843"
/translation="MSSSCVTVPFALMILCFADAGPVPRSECVLSPVNSSHPVHALLE
SFTVLGSCASRGTTGLPQEVHVLNLRNPDEGLDHERETLHLTPISVHHHQKPLVF
LLNSPLVWKLTERLAPGIRRVFVSSGSIYVMEKGNFSLSAETEPNEHHL
LOWAKKEYGAVTSFTELKISNIYIKVGEDQVFPPTCNIEKNFSLNLAGYLPQKRA
EGCLMSNLQVREHVIITLTPNSNYSAFOVDIIVDKPQPGAKLRNVVLILKCK
KSNWVTKSHDVQGLKLVITNSIGFGKTERSMTSKSVIPDIPSSHESLKGWYEH
KYSPTSYTKAPVANRHLQLTEENDEEDHSLPELTLLHGAKNPALSDGLTFP
FHINRGHETGGEGIFPFRSDVDTLINHDFHLSKHKKEPEVOGSDAVLSIKDDK
VMTVAEKDLSQASGYTRTSLSDHSCARMNGHTFILESPLNKCGRTRSTILDQIV
YFNSIVQLSPAESGSDDDMESGDNFGPDADGDGVTFSNMPEAFNCTLHQPEK
LGFALOTCFVSPFSPNDRMSDYTIENICPKDSVKFYSTEKLNPIAHAKDKKRFIS
FVKPFINISLLFLHCELTCTLTNIDKDTORLPKCPVPEACTSLNVDMLAMHMKKT
FTPLVITHGKPEDSSLPKSNVRQPSVFGYGLDILTIVYVGAFAAFVIGALLTGALWFI
YSTHTGAAGRQVRVTPSPASNSAAHSIGSTQSTPCSSSAI"

BASE COUNT 996 a 712 c 708 g 931 t
ORIGIN
Query Match 100.0%; Score 15; DB 5; Length 3347;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCTGTT 15
|||||
Db 1368 CCTTCTCCCTGTT 1354

RESULT 7
AF312211/c
LOCUS AF312211
DEFINITION Homo sapiens neo-poly(A) polymerase mRNA, complete cds.
ACCESSION AF312211
VERSION AF312211.1 GI:15080910
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 3752)
              Topalian,S.L., Kaneko,S., Gonzales,M.I., Bond,G.L., Ward,Y. and
              Manley,J.L.
TITLE        Identification and functional characterization of neo-poly(A)
              polymerase, an RNA processing enzyme overexpressed in human tumors
JOURNAL      Mol. Cell. Biol. 21 (16), 5614-5623 (2001)
MEDLINE      21356984
PUBMED       11463842
REFERENCE     2 (bases 1 to 3752)
              Topalian,S.L., Gonzales,M.I., Wang,X. and Wang,R.-F.
AUTHORS      Direct Submission
TITLE        Submitted (09-OCT-2000) Surgery Branch, NCI, National Institutes of
              Health, Building 10, Room 2B47, Bethesda, MD 20892, USA
JOURNAL      Location/Qualifiers
FEATURES     source
              1..3752
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              /db_xref="taxon:9606"
              /cell_type="malignant melanoma"
              232..2442
              /note="similar to Homo sapiens poly(A) polymerase protein
              (PAP) encoded by GenBank Accession Number X76770"
              /codon_start=1
              /product="neo-poly(A) polymerase"
              /protein_id="AAK83701.1"
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              /translation="MKMSANTVLDQRQKHGVTSPISLASPKRIDHYTQKLIDA
              MKPGVFDEELNRLVGLKLNLYKWNISDVSESKNLPVSVAATVGKTFIFS
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              DGIEDLVFADIAIQTISDNLDRLSDIRICIRSLGCRVTEILHLVPKET
              FLTLRAVLAQKRGYISNMLGFLGGVSWAMLVARTCOLYPNAAATLVHKKFLVFS
              KWENPVLLKQPEESNLNLPVMDRPNVSDRYHLMPIITPAYPOONSTYNYSTSTRT
              VMVEEFKGLAVTDELQCKSDMSKLEPPNPFQKYRHVILVTASATRENHLEWGL
              VESKTRVLGNLNEFTITLAVNPQSEPGNKEHKHNNVSWMFLGILFRRVENAES
              VNIDYDIQSDTIVYQANNINMLKGMKLEATHVKKKQLHHYLPALIELQKKKQ
              LSDVNRSGGQKRLSDSLSDSDTNGTDPNSPASKSDSPSGVETERNASAP
              AVIVEKPLSPQAQGLSPIVIGAKVDSITVKTVPPTVCTIPTVGNVPIRTTHNP
              AQGPGLNGMSNITVTPTPKRSHSPSIDGTPKRLKDVKEFIRLESFKDPRTAEERK
              KSVDAIGGSEMPITDTSRKKRLPSKELPDSSSPVANNIRVIKNSIRLTNR"
BASE COUNT   1175 a 709 c 738 g 1130 t
ORIGIN
Query Match   100.0%; Score 15; DB 9; Length 3752;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||||
DB 169 CCTTCTCCCCCTGTT 155

RESULT 8
AB018279
LOCUS        AB018279 Homo sapiens mRNA for KIAA0736 protein, complete cds.
DEFINITION   Homo sapiens mRNA for KIAA0736 protein, complete cds.
ACCESSION    AB018279
VERSION      AB018279.1 GI:3882192
KEYWORDS     Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII
SOURCE       SK plus clone:hk03846.
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (sites)
AUTHORS      Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Miyajima,N.,
              Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
TITLE        Prediction of the coding sequences of unidentified human genes. XI.
              The complete sequences of 100 new cDNA clones from brain which code
              for large proteins in vitro
JOURNAL      DNA Res. 5 (5), 277-286 (1998)
MEDLINE      99087487
REFERENCE     2 (bases 1 to 4353)
AUTHORS      Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.

Direct Submission
Submitted (08-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdna@infokazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
Location/Qualifiers
source       1..4353
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="hk03846"
              /sex="male"
              /tissue_type="brain"
              /clone_lib="pBluescriptII SK plus"
              /dev_stage="adult"
              1..4353
              /gene="KIAA0736"
              435..2663
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              /protein_id="BAA34456.1"
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              /translation="MESGFDRAAAFIRGAKDIAKEVKKHAAKVVVKGLDRVODEYSRR
              SYSRFEEDDDDFPAPSDGYIRGEGTQDEEGGASDATEGHDEDDIYEGEQGIP
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              HGFOWTLYFVGLALMADGVEFVGVFLPSAKDKMCLSDSNKMLGLIVLGMVVG
              AFLWGLADRLGRQCLLISLVNSVFAFTSFVQGVGTFLFCRLLSGVGGISPIV
              FSTFSELAQEKREHLSWLCMFNMIGVYANAWALIPHYFSQFMSQSAIQHSWR
              FVFLVCAFPVFVAIGALTQPSRFFLENGKHDENAMVLQVHDTNNRKGHPERVE
              SVTHIKTHIEDELIETQSTGTWYQWGRVRLSGQVWGNFLSCFGEYRRITLMM
              MGVMTFVYGLTVFVPMRIHQADVASRTKVPFGEVHVTFNFTLENOIHRG
              GQVFNDFIGLRKLSVFSFSLPEECYFEDVTSNTFPRNCTFNTVFYNTDLFEYKF
              VNSRLNSTLHNKEGCPDVTGTGEGAYVYVFSFLGTAVLPCGNIVSALLMDKIGR
              LRLAGSVVSCVFLSFGNSAMIALICLLKFGVSIAWNALDVLTVELIYPSDKR
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              LQ"
BASE COUNT   914 a 1181 c 1192 g 1066 t
ORIGIN
Query Match   100.0%; Score 15; DB 9; Length 4353;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
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DB 2935 CCTTCTCCCCCTGTT 2949

RESULT 9
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LOCUS        FR092H06 11001 bp DNA linear VRT 21-SEP-2001
DEFINITION   Fugu rubripes cosmid 092H06 genomic DNA fragment, top1alpha gene.
ACCESSION    AL035357
VERSION      AL035357.1 GI:157233143
KEYWORDS     top1alpha gene; topoisomerase I.
SOURCE       Takifugu rubripes.
ORGANISM     Takifugu rubripes
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
              Tetraodontidae; Takifugu.
REFERENCE    1 (bases 1 to 11001)
              Smith,S.F., Metcalfe,J. and Elgar,G.
AUTHORS      Unpublished
JOURNAL      2 (bases 1 to 11001)
              Smith,S.F.
REFERENCE     Direct Submission
TITLE        Submitted (01-FEB-1999) Smith S.F., Fugu Group, UK HGMP Resource
              Centre, Wellcome Genome Campus, Hinxton Hall, Hinxton,
              Cambridgeshire, CB10 1SB, UNITED KINGDOM
JOURNAL      Location/Qualifiers
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Query Match 100.0%; Score 15; DB 5; Length 11001;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6409 CCTTCTCCCCCTGTT 6395

RESULT 10
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LOCUS 11896 bp DNA linear BCT 16-JAN-2002
DEFINITION Pyrobaculum aerophilum strain IM2 section 65 of the complete genome.
ACCESSION AE009810 AE009441
VERSION AE009810.1 GI:18159943
KEYWORDS Pyrobaculum aerophilum.
SOURCE Pyrobaculum aerophilum.
ORGANISM Pyrobaculum aerophilum
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
REFERENCE 1 (bases 1 to 11896)
AUTHORS Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and Miller,J.H.
TITLE Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002)
PUBMED 11792869
REFERENCE 2 (bases 1 to 11896)
AUTHORS Fitz-Gibbon,S.T., Ladner,H., Kim,U.-J., Stetter,K.O., Simon,M.I. and Miller,J.H.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA
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Query Match 100.0%; Score 15; DB 1; Length 11896;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTCTCCCCCTGTT 15
Db 6661 CCTTCTCCCCCTGTT 6647
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RESULT 11
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LOCUS Pestivirus giraffe-1 H138 complete genome.
DEFINITION
ACCESSION AF144617
VERSION AF144617.2 GI:15282441
KEYWORDS
SOURCE pestivirus giraffe-1 H138.
ORGANISM pestivirus giraffe-1 H138
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Pestivirus.
REFERENCE 1 (bases 1 to 12602)
AUTHORS Becher,P., Orlich,M., Kosmidou,A., Konig,M., Baroth,M. and
Thiel,H.J.
TITLE Genetic diversity of pestiviruses: identification of novel groups
and implications for classification
MEDLINE 99420379
PUBMED 10489341
REFERENCE 2 (bases 1 to 12602)
AUTHORS Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
TITLE Evidence for the presence of two novel pestivirus species
MEDLINE 21378881
PUBMED 11485413
REFERENCE 3 (bases 1 to 12602)
AUTHORS Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
TITLE Complete genomic sequences of pestiviruses from giraffe and
reindeer: evidence for the presence of two novel species within the
genus pestivirus
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 12602)
AUTHORS Becher,P. and Orlich,M.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1999) Justus-Liebig-Universitaet Giessen,
Institut fuer Virologie (Fachbereich Veterinaermedizin),
Frankfurter Str. 107, Giessen D-35392, Germany
REFERENCE 5 (bases 1 to 12602)
AUTHORS Avalos-Ramirez,R., Orlich,M. and Becher,P.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2001) Justus-Liebig-Universitaet Giessen,
Institut fuer Virologie (Fachbereich Veterinaermedizin),
Frankfurter Str. 107, Giessen D-35392, Germany
REMARK Sequence update by submitter
COMMENT On Aug 23, 2001 this sequence version replaced gi:6049239.
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ORIGIN
Query Match 100.0%; Score 15; DB 14; Length 12602;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCTGTT 15
DB 10231 CCTTCTCCCTGTT 10245
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B.subtilis srfA-sfp gene region for surfactin synthetase.
ACCESSION X70356 X70357 X70358 X70359
VERSION X70356.1 GI:396480
KEYWORDS surfactin synthetase.
SOURCE Bacillus subtilis.
ORGANISM Bacillus subtilis.
REFERENCE 1 (bases 1 to 32802)
AUTHORS Grandi,G.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1993) G. Grandi, Enricerche, Via F Maritano 26,
20097, S Donato Milanese (MI), ITALY
REFERENCE 2 (bases 1 to 32802)
AUTHORS Cosmina,P., Rodriguez,F., de Ferra,F., Grandi,G., Perego,M.,
Venema,G. and van Sinderen,D.
TITLE Sequence and analysis of the genetic locus responsible for
surfactin synthesis in Bacillus subtilis
JOURNAL Mol. Microbiol. 8 (5), 821-831 (1993)
MEDLINE 93360813
PUBMED 8355609
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Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCGTGT 15

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Db 29177 CCTTCTCCCTGTT 29163
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RESULT 13
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LOCUS          34578 bp      DNA      linear      PRI 29-MAY-2002
DEFINITION    Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.
ACCESSION     AC107069
VERSION       AC107069.5  GI:20146820
KEYWORDS      HTG.
SOURCE        Homo sapiens.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 34578)
AUTHORS      Sulston, J.E. and Waterston, R.
TITLE        Toward a complete human genome sequence
JOURNAL      Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE      99063792
PUBMED       9847074
REFERENCE     2 (bases 1 to 34578)
AUTHORS      Scott, K., Kozlowski, A., Spalding, L. and Trani, L.
TITLE        The sequence of Homo sapiens BAC clone RP11-249A8
JOURNAL      Unpublished (2001)
REFERENCE     3 (bases 1 to 34578)
AUTHORS      Waterston, R.H.
TITLE        Direct Submission
JOURNAL      Submitted (15-JAN-2002) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE     4 (bases 1 to 34578)
AUTHORS      Waterston, R.H.
TITLE        Direct Submission
JOURNAL      Submitted (04-APR-2002) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE     5 (bases 1 to 34578)
AUTHORS      Waterston, R.H.
TITLE        Direct Submission
JOURNAL      Submitted (13-APR-2002) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE     6 (bases 1 to 34578)
AUTHORS      Waterston, R.
TITLE        Direct Submission
JOURNAL      Submitted (29-MAY-2002) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              On Apr 13, 2002 this sequence version replaced gi:19924179.
COMMENT      -----
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu/gsc
              Contact: saplens@watson.wustl.edu
              -----
              Summary Statistics
              -----
              Center project name: H_NH0249A08
              -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
```

McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-495023, 2000 bp overlap; the clone sequenced to the right is RP11-563C6, 2000 bp overlap. Actual start of this clone is at base position 126621 of RP11-495023.

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Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||
Db 1831 CCTTCTCCCTGTT 1817

RESULT 14
AL138734/c ALL138734 43347 bp DNA linear PRI 16-AUG-2000
LOCUS

DEFINITION

Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains GSSs, complete sequence.

ACCESSION

AL138734

VERSION

AL138734.6 GI:8388469

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 43347)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Tromans/A.

AUTHORS

Direct Submission

TITLE

Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

JOURNAL

COMMENT

On Jun 8, 2000 this sequence version replaced gi:8247412.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6

RP1-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/VECTOR: PCYPAC2
IMPORTANT: This sequence is not the entire insert of clone RP1-310P17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP1-310P17 is at 1 in this sequence. The true left end of clone RP3-413H6 is at 43244 in this sequence.

FEATURES

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/note="MIR repeat: matches 20..146 of consensus"

1924..2090

/note="L1MB8 repeat: matches 6005..6171 of consensus"

repeat_region

2151..2266

/note="L1MB8 repeat: matches 5874..5991 of consensus"

repeat_region

2281..2431

/note="AluY repeat: matches 158..308 of consensus"

repeat_region

2432..2878

/note="L1MB8 repeat: matches 5429..5879 of consensus"

repeat_region

2879..3641

/note="LTR17 repeat: matches 1..780 of consensus"

misc_feature

3516..4013

/note="match: GSS: Em:AQ112069"

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repeat_region 3642. .3924
/note="L1MB8 repeat: matches 5147. .5429 of consensus"
misc_feature 4063. .4518
/note="match: GSS: Em:AQ508138"
misc_feature complement(4129. .4662)
/note="match: GSS: Em:AQ316392"
misc_feature 4657. .5169
/note="match: GSS: Em:AQ484379"
misc_feature 4665. .5178
/note="match: GSS: Em:AQ432756"
repeat_region 5449. .5596
/note="L2 repeat: matches 2580. .2750 of consensus"
repeat_region 6304. .6577
/note="AluX repeat: matches 9. .282 of consensus"
repeat_region 6589. .6721
/note="AluSg/x repeat: matches 1. .133 of consensus"
repeat_region 6732. .7036
/note="AluSp repeat: matches 1. .305 of consensus"
repeat_region 7164. .7253
/note="MIR repeat: matches 47. .147 of consensus"
repeat_region 7584. .7643
/note="30 copies 2 mer gt 96% conserved"
repeat_region 7969. .8079
/note="MIR repeat: matches 28. .143 of consensus"
repeat_region 8265. .8544
/note="AluJo repeat: matches 2. .289 of consensus"
repeat_region 8711. .8799
/note="MIR repeat: matches 59. .145 of consensus"
repeat_region 9753. .9893
/note="AluY repeat: matches 168. .311 of consensus"
repeat_region 10697. .11158
/note="L2 repeat: matches 2290. .2750 of consensus"
repeat_region 11255. .11286
/note="16 copies 2 mer ac 100% conserved"
repeat_region 11352. .11558
/note="HERVL repeat: matches 1757. .1969 of consensus"
repeat_region 12998. .13299
/note="AluX repeat: matches 1. .311 of consensus"
repeat_region 14005. .14200
/note="MIR repeat: matches 1. .208 of consensus"
repeat_region 14674. .14748
/note="L1ME3 repeat: matches 5872. .5956 of consensus"
repeat_region 15052. .15480
/note="L1M4 repeat: matches 3375. .3822 of consensus"
repeat_region 15481. .15498
/note="AluS repeat: matches 152. .170 of consensus"
repeat_region 15499. .15731
/note="AluSg/x repeat: matches 71. .308 of consensus"
repeat_region 15732. .15790
/note="AluS repeat: matches 1. .152 of consensus"
repeat_region 15822. .16105
/note="L1PA16 repeat: matches 5830. .6110 of consensus"
repeat_region 16106. .16416
/note="AluSp repeat: matches 1. .313 of consensus"
repeat_region 16417. .17711
/note="L1PA16 repeat: matches 4517. .5830 of consensus"
repeat_region 17737. .18032
/note="WER61A repeat: matches 7. .314 of consensus"
repeat_region 18038. .18426
/note="L1PA16 repeat: matches 4125. .4510 of consensus"
repeat_region 18427. .18706
/note="L1M4 repeat: matches 3826. .4124 of consensus"
repeat_region 18703. .19271
/note="L1MD2 repeat: matches 5774. .6331 of consensus"
repeat_region 19272. .19892
/note="L2 repeat: matches 1452. .2147 of consensus"
repeat_region 19893. .19948
/note="WADE1 repeat: matches 5. .80 of consensus"
repeat_region 19949. .20211
/note="L2 repeat: matches 1194. .1452 of consensus"
repeat_region 20944. .21113
/note="AluSg/x repeat: matches 129. .299 of consensus"
repeat_region 21140. .21264

/note="AluSc repeat: matches 1. .125 of consensus"
21581. .21650
/note="35 copies 2 mer tt 68% conserved"
21747. .21896
/note="L1MD3 repeat: matches 7476. .7579 of consensus"
complement(21823. .22281)
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22304. .22755
/note="match: GSS: Em:AQ357726"
22608. .22697
/note="L2 repeat: matches 2620. .2710 of consensus"
22829. .22868
/note="20 copies 2 mer aa 80% conserved"
22998. .23085
/note="L1R22 repeat: matches 413. .509 of consensus"
23148. .23417
/note="L1R22 repeat: matches 38. .312 of consensus"
23454. .23569
/note="L2 repeat: matches 2005. .2146 of consensus"
23645. .23819
/note="MIR repeat: matches 61. .243 of consensus"
24043. .25714
/note="L1MEC repeat: matches 281. .1953 of consensus"
25721. .26938
/note="L1MEC repeat: matches 2151. .3045 of consensus"
complement(26913. .27340)
/note="match: GSS: Em:AQ225006"
28135. .28460
/note="MER7A repeat: matches 4. .346 of consensus"
28538. .29022
/note="L1MC3 repeat: matches 7250. .7739 of consensus"
29898. .30315
/note="MLT1B repeat: matches 6. .390 of consensus"
30318. .31382
/note="Charlie2 repeat: matches 2658. .3755 of consensus"
31290. .31766
/note="match: GSS: Em:AQ735362"
31390. .31669
/note="L1R16C repeat: matches 102. .387 of consensus"
32151. .32455
/note="AluJb repeat: matches 1. .304 of consensus"
33318. .33468
/note="Charlie2 repeat: matches 327. .504 of consensus"
34076. .34305
/note="MIR repeat: matches 6. .260 of consensus"
34434. .34535
/note="L2 repeat: matches 2574. .2687 of consensus"
34633. .35136
/note="MER9 repeat: matches 1. .511 of consensus"
36692. .37186
/note="Cheshire repeat: matches 27. .548 of consensus"
37183. .38826
/note="Cheshire repeat: matches 723. .2420 of consensus"

Query Match 100.0%; Score 15; DB 9; Length 43347;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
Db 27556 CCTTCTCCCCCTGTT 27542
|||||

RESULT 15
AL583852 LOCUS
DEFINITION Human DNA sequence from clone RP11-17G2 on chromosome 10, complete
sequence.
ACCESSION AL583852 AC011691
VERSION AL583852.6 GI:14702147
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 56701)
 AUTHORS Chapman,J.
 TITLE Direct Submission
 JOURNAL Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hamquerry@sanger.ac.uk
 COMMENT On or before Jul 12, 2001 this sequence version replaced gi:7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>
 RP11-17G2 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6
 IMPORTANT: This sequence is not the entire insert of clone RP11-17G2 it may be shorter because we sequence overlapping sections only once, except for a short overlap.
 The true right end of clone RP11-17G2 is at 56701 in this sequence.
 The true right end of clone RP11-397115 is at 2000 in this sequence.

FEATURES

source	Location/Qualifiers
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/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/chromosome="10"	
/clone="RP11-17G2"	
/clone_lib="RPC1-11.1"	
1..284	
/note="MER1B repeat: matches 1..285 of consensus"	
285..400	
/note="MER20 repeat: matches 103..218 of consensus"	
1266..1301	
/note="L2 repeat: matches 2580..2615 of consensus"	
1305..1352	
/note="24 copies 2 mer ga 75% conserved"	
complement(2038..2454)	
/note="match: GSS: Em:AQ358591"	
2479..2823	
/note="match: GSS: Em:AQ812738"	
2586..2791	
/note="MIR repeat: matches 45..258 of consensus"	
2979..3119	
/note="MIR repeat: matches 61..212 of consensus"	
complement(3478..3937)	
/note="match: GSS: Em:AQ475942"	
4218..4317	
/note="L2 repeat: matches 2645..2749 of consensus"	
5477..5644	
/note="MLT1F repeat: matches 68..240 of consensus"	
complement(5738..6110)	
/note="match: STS: Em:G53244"	
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6206..6292	
/note="MER91A repeat: matches 5..95 of consensus"	
6293..6521	
/note="MIR repeat: matches 9..234 of consensus"	
8688..8929	
/note="L2 repeat: matches 2284..2534 of consensus"	
8947..9112	
/note="MIR repeat: matches 70..248 of consensus"	
9173..9416	
/note="MLT1A repeat: matches 337..568 of consensus"	
9753..10220	
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10458..10642	
/note="L2 repeat: matches 2129..2318 of consensus"	
13448..13763	
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15428..15572	
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16288..16546	
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16664..16777	
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16779..16842	
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16817..16938	
/note="7 copies 26 mer 62% conserved"	
16861..16944	
/note="21 copies 4 mer gga 75% conserved"	
16951..16994	
/note="11 copies 4 mer gga 81% conserved"	
17973..18165	
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18174..18509	
/note="MER46C repeat: matches 7..338 of consensus"	
18670..18785	
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18833..19044	
/note="MIR repeat: matches 28..260 of consensus"	
21936..22145	
/note="TIME repeat: matches 5599..5820 of consensus"	
22148..22199	
/note="13 copies 4 mer caca 82% conserved"	
22199..22596	
/note="MSTA repeat: matches 1..426 of consensus"	
22480..22743	
/note="match: STS: Em:HS094YH3"	
22597..22638	
/note="21 copies 2 mer ca 92% conserved"	
22599..22638	
/note="10 copies 4 mer caca 92% conserved"	
22770..22846	
/note="MIR repeat: matches 87..165 of consensus"	
22959..23149	
/note="MER3 repeat: matches 1..200 of consensus"	
23508..23698	
/note="L2 repeat: matches 2539..2748 of consensus"	
24378..24458	
/note="L1 repeat: matches 2136..2213 of consensus"	
24486..24581	
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25073..25451	
/note="MLT1F repeat: matches 1..371 of consensus"	
complement(25325..25729)	
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26471..26619	
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26933..27097	
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27101..27219	
/note="MIR repeat: matches 13..134 of consensus"	


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repeat_region 27767..27813
               /note="MIR repeat: matches 49..103 of consensus"
repeat_region 28697..28879
               /note="MIR repeat: matches 31..225 of consensus"
repeat_region 29356..29488
               /note="MIR repeat: matches 50..184 of consensus"
repeat_region 29578..29664
               /note="MIR repeat: matches 82..175 of consensus"
repeat_region 31386..31508
               /note="MIR repeat: matches 42..164 of consensus"
repeat_region 31974..32354
               /note="MIR repeat: matches 1..410 of consensus"
misc_feature 32596..33015
               /note="MLTII repeat: matches 1..410 of consensus"
repeat_region 33407..33823
               /note="match: GSS: Em:AQ604754"
repeat_region 33833..34015
               /note="MLTII repeat: matches 128..547 of consensus"
misc_feature 34122..34214
               /note="MIR repeat: matches 50..251 of consensus"
repeat_region 35380..35474
               /note="match: GSS: Em:AQ551831"
repeat_region 37028..37195
               /note="MIR repeat: matches 46..140 of consensus"
repeat_region 37274..37413
               /note="MER63A repeat: matches 45..210 of consensus"
repeat_region 37801..38057
               /note="L2 repeat: matches 2137..2276 of consensus"
repeat_region 38541..39465
               /note="L2 repeat: matches 2469..2750 of consensus"
repeat_region 39625..39782
               /note="L2 repeat: matches 1655..2599 of consensus"
repeat_region 41102..41277
               /note="MIR repeat: matches 59..220 of consensus"
repeat_region 41278..41718
               /note="L2 repeat: matches 2517..2691 of consensus"
repeat_region 41719..41924
               /note="MLTIC repeat: matches 5..462 of consensus"
repeat_region 42387..42468
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repeat_region 42496..42577
               /note="MIR repeat: matches 162..246 of consensus"
repeat_region 43328..43400
               /note="L2 repeat: matches 2605..2692 of consensus"
repeat_region 43505..43769
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Query Match      100.0%; Score 15; DB 9; Length 56701;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCTTCTCCCCCTGTT 15
    |||||
Db 2530 CCTTCTCCCCCTGTT 2544
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Search completed: December 11, 2002, 18:08:27
Job time : 1740 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:29:02 ; Search time 213 Seconds
(without alignments)
158.591 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cctctcccccgtgtt 15

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	AAH28085
2	15	100.0	352	21	AAC09241
3	15	100.0	445	23	ABV50337
4	15	100.0	549	23	AAS66052
5	15	100.0	827	22	AAH04051
6	15	100.0	1689	22	AAH15437
7	15	100.0	1854	22	AAH28083
8	15	100.0	1854	22	AAH28087
9	15	100.0	2159	23	ABK43728
					Probe for human no
					Human secreted pro
					Human prostate exp
					DNA encoding novel
					Human CDNA clone (
					Human CDNA sequenc
					DNA encoding human
					DNA encoding human
					DNA encoding novel

15	100.0	2451	23	AAS83288	DNA encoding novel
15	100.0	2520	24	ABL90474	Human polynucleoti
15	100.0	2522	23	ABK44004	DNA encoding novel
15	100.0	3580	21	AAI16697	Human secreted pro
15	100.0	3580	24	ABK35630	cDNA sequence #21
15	100.0	4215	23	ABV22746	Human prostate exp
15	100.0	4215	23	ABV28574	Human prostate exp
15	100.0	4366	22	AAH57556	Human brain cell s
15	100.0	15857	22	AAH26730	Human genomic DNA
15	100.0	31122	14	AAQ40706	Bacillus subtilis
15	93.3	389	24	ABN96737	Gene #3235 used to
14	93.3	389	24	ABL66267	Lung cancer relate
14	93.3	482	24	ABT04065	Human ovary specif
14	93.3	594	22	ABA62115	Human foetal liver
14	93.3	594	22	AAK10435	Human brain expres
14	93.3	594	22	AAK36337	Human bone marrow
14	93.3	594	22	AAI42060	Probe #10746 used
14	93.3	599	23	AAS85439	DNA encoding novel
14	93.3	2349	21	AAA26376	Human secreted pro
14	93.3	2415	18	AAT62067	Fission yeast prot
14	93.3	2775	22	AAH13954	Human cDNA sequenc
14	93.3	6959	23	AAS85443	DNA encoding novel
14	93.3	8894	22	AAL36698	Human musculoskele
14	93.3	8894	22	ABA20494	Human nervous syst
14	93.3	16877	22	AAI36984	Human musculoskele
14	93.3	61710	22	AAK83782	Human immune/haema
13	86.7	193	16	AAT21956	Human gene signatu
13	86.7	209	22	ABA75403	Human foetal liver
13	86.7	209	22	ABA40037	Probe #18503 for g
13	86.7	209	22	AAK23963	Human brain expres
13	86.7	209	22	AAK50031	Human bone marrow
13	86.7	209	22	AAI27125	Probe #17058 for g
13	86.7	209	22	AAI55970	Probe #24656 used
13	86.7	209	22	ABS23521	Human genome-deriv
13	86.7	210	22	AAI29067	Colon tumour relat
13	86.7	285	24	ABL81791	Human ovarian canc
13	86.7	306	22	AAH71347	Human cervical can
13	86.7	315	22	AAH52042	Mycobacterium tube
13	86.7	322	22	ABA07823	Human ovarian and
13	86.7	322	22	AAL03625	Human reproductive
13	86.7	337	21	AAI11522	Human secreted pro
13	86.7	337	24	ABL87132	Human ovarian canc
13	86.7	373	22	AAK56539	Human immune/haema
13	86.7	381	23	AAK64315	Human immune/haema
13	86.7	383	24	ABN94579	DNA encoding novel
13	86.7	383	24	ABL65582	Gene #1077 used to
13	86.7	401	22	ABA08339	Lung cancer relate
13	86.7	435	22	AAK68265	Human protein-tyr
13	86.7	435	22	AAK68266	Human immune/haema
13	86.7	435	22	AAK68267	Human immune/haema
13	86.7	444	20	AAV88767	Human immune/haema
13	86.7	449	24	AAJ37354	EST clone HM280.
13	86.7	467	22	ABA07414	A2R20 adenylate ur
13	86.7	467	22	AAK91145	Human pancreatic c
13	86.7	469	22	ABA52284	Human digestive sy
13	86.7	469	22	ABA22085	Human foetal liver
13	86.7	469	22	ABA22085	Probe #551 for gen
13	86.7	469	22	ABA07060	Human pancreatic c
13	86.7	469	22	AAK00559	Human brain expres
13	86.7	469	22	AAK26008	Human bone marrow
13	86.7	469	22	AAK88801	Human digestive sy
13	86.7	469	22	AAI10637	Probe #570 for gen
13	86.7	469	22	AAI1891	Probe #577 used to
13	86.7	469	22	AAI00568	Probe #559 used to
13	86.7	469	24	ABS00589	Human genome-deriv
13	86.7	494	24	ABL83753	Human ovarian canc
13	86.7	500	22	ABA62303	Human foetal liver
13	86.7	500	22	ABA29646	Probe #8112 for ge
13	86.7	500	22	AAK10639	Human brain expres
13	86.7	500	22	AAK36525	Human bone marrow
13	86.7	500	22	AAI17384	Probe #7317 for ge
13	86.7	500	22	AAI42281	Probe #10967 used
13	86.7	500	24	ABS10523	Human genome-deriv

c 83	13	86.7	529	23	AAB88281	CNS disorder-relat	156	13	86.7	5514	23	ABL10818	Drosophila melanog
c 84	13	86.7	561	22	AAH13181	Human cDNA clone (157	13	86.7	5728	20	ABK62572	Rat sequence diffe
c 85	13	86.7	565	22	ABA64032	Human foetal liver	c 158	13	86.7	5828	24	AAK84592	AML1-MTG16 fusion
c 86	13	86.7	596	17	AAT33226	Oryzacystatin-I de	c 159	13	86.7	5938	24	ABL66297	Lung cancer relat
c 87	13	86.7	598	22	ABA62898	Human foetal liver	c 160	13	86.7	5938	24	ABL68033	Ovary cancer relat
c 88	13	86.7	598	22	ABA30172	Probe #8638 for ge	161	13	86.7	6004	21	AAA07835	Human homologue of
c 89	13	86.7	598	22	AAK11302	Human brain expres	162	13	86.7	6032	19	AAV30268	Plasmid pMT1802 en
c 90	13	86.7	598	22	AAK37094	Human bone marrow	163	13	86.7	6032	19	AAV12368	Trichoderma harzia
c 91	13	86.7	598	22	AAI17935	Probe #7868 for ge	c 164	13	86.7	6056	20	AAK84593	AML1-MTG16 fusion
c 92	13	86.7	598	22	AA142917	Probe #11603 used	c 165	13	86.7	6864	22	AAI26588	Human breast cance
c 93	13	86.7	598	24	ABSI11096	Human genome-deriv	c 166	13	86.7	7180	23	ABL04344	Drosophila melanog
c 94	13	86.7	616	23	ABV57123	Human prostate exp	167	13	86.7	8267	23	ABL09340	Drosophila melanog
c 95	13	86.7	673	22	AAI01192	Human reproductive	c 168	13	86.7	8448	22	AAK04680	DNA encoding human
c 96	13	86.7	673	23	ABK97085	Human testicular a	c 169	13	86.7	8448	22	AAI06568	Human reproductive
c 97	13	86.7	705	24	ABK78617	Bacillus clausii g	c 170	13	86.7	9566	22	AAK81002	DNA encoding human
c 98	13	86.7	705	24	ABK78618	Bacillus clausii g	c 171	13	86.7	9566	22	AAI06570	Human reproductive
c 99	13	86.7	788	22	AAI21413	Human breast cance	c 172	13	86.7	10828	22	ABA19208	Human nervous syst
c 100	13	86.7	966	22	AAH31746	Human olfactory re	173	13	86.7	10828	22	AAK70743	Human immune/haema
c 101	13	86.7	991	24	ABT04187	Human G-protein co	174	13	86.7	13660	22	AAI199126	Human excretory re
c 102	13	86.7	1044	24	ABQ91421	M. capsulatus gene	175	13	86.7	13660	22	AAK67907	Human immune/haema
c 103	13	86.7	1046	22	AAK76385	T. harzianum alpha	176	13	86.7	13660	22	AAK81002	Human immune/haema
c 104	13	86.7	1059	22	AAK42429	Human cDNA encodin	177	13	86.7	13660	22	AAI63476	Human kidney relat
c 105	13	86.7	1059	24	ABK37715	DNA encoding G-cou	c 178	13	86.7	14221	22	AAK40681	DNA encoding human
c 106	13	86.7	1077	22	AAH75725	Human NOV 10 codin	c 179	13	86.7	14221	22	AAI06569	Human reproductive
c 107	13	86.7	1136	19	AAV37396	Streptococcus pneu	180	13	86.7	14537	24	ABL67781	Oesophagus cancer
c 108	13	86.7	1139	24	AAK51019	Rice 16S RNA-speci	181	13	86.7	21469	22	AAK89568	Human digestive sy
c 109	13	86.7	1167	22	AAK52030	Human polynucleoti	182	13	86.7	21475	22	AAK89569	Human digestive sy
c 110	13	86.7	1229	21	AAK47295	Arabidopsis thalia	183	13	86.7	22813	22	AAK65271	Human immune/haema
c 111	13	86.7	1356	22	AAH90777	CPE 81 coding sequ	184	13	86.7	22813	22	AAK82016	Human immune/haema
c 112	13	86.7	1379	22	AAH90886	2CFE 81 coding seq	185	13	86.7	22813	22	AAK86303	Human immune/haema
c 113	13	86.7	1448	22	AAU05887	Human reproductive	186	13	86.7	22813	22	AAK87333	Human immune/haema
c 114	13	86.7	1448	23	ABU98451	Human testicular a	c 187	13	86.7	23449	21	AAZ35393	Human immune/haema
c 115	13	86.7	1656	23	AAK55580	Streptococcus pneu	c 188	13	86.7	23449	21	AAK87743	Human immune/haema
c 116	13	86.7	1896	24	AAI40132	Isoprenoid related	c 189	13	86.7	24740	21	AAK87743	Human LMP-1 (HLMF-
c 117	13	86.7	1900	21	AAK75509	Human ORFX ORF3064	c 190	13	86.7	30352	22	AAK87743	Human LMP-1 (HLMF-
c 118	13	86.7	2007	24	ABK72714	Bacillus lichenifo	c 191	13	86.7	32217	22	AAK87743	Human LMP-1 (HLMF-
c 119	13	86.7	2037	23	AAK69761	DNA encoding novel	c 192	13	86.7	32217	22	AAK87743	Human LMP-1 (HLMF-
c 120	13	86.7	2037	23	AAK76456	DNA encoding novel	c 193	13	86.7	32217	22	AAK87743	Human LMP-1 (HLMF-
c 121	13	86.7	2037	23	AAK83764	DNA encoding novel	194	13	86.7	112190	22	AAK44801	Human GPCR protein
c 122	13	86.7	2040	24	AAI45342	Human T2 coding se	c 195	13	86.7	143899	24	AAK38336	Genomic sequence e
c 123	13	86.7	2256	22	AAK76384	Trichoderma harzia	c 196	13	86.7	169739	24	ABQ88186	Human osteoblast d
c 124	13	86.7	2339	24	ABQ54676	Human ovarian anti	c 197	13	86.7	349980	22	AAH41223	Pyrococcus abyssi
c 125	13	86.7	2364	22	AAH15873	Human cDNA sequenc	c 198	13	86.7	4411529	22	AAI99682	Mycobacterium tube
c 126	13	86.7	2448	22	AAI58188	Human polynucleoti	199	12	80.0	23	22	AAH48908	Human PAH gene ass
c 127	13	86.7	2499	23	AAK88464	DNA encoding novel	200	12	80.0	23	22	AAH49156	Human PAH gene ass
c 128	13	86.7	2525	21	AAK16144	Human prostate can	201	12	80.0	35	22	AAH48904	Human PAH gene ass
c 129	13	86.7	2687	15	AAO54896	Maize pollen-speci	202	12	80.0	35	22	AAH49154	Human PAH gene ass
c 130	13	86.7	2873	15	AAO54889	Maize pollen-speci	203	12	80.0	51	22	AAH79634	Human DNA containi
c 131	13	86.7	2874	22	AAK58134	Human polynucleoti	c 204	12	80.0	65	24	ABN53494	Mouse spliced tran
c 132	13	86.7	2879	13	AAO23074	Bacterial alpha-1,	c 205	12	80.0	114	22	ABA47639	Human breast cell
c 133	13	86.7	2902	24	AAK27895	DNA encoding novel	c 206	12	80.0	114	22	ABA65533	Human foetal liver
c 134	13	86.7	2943	23	AAK84770	DNA encoding novel	c 207	12	80.0	114	22	ABA32625	Probe #11091 for g
c 135	13	86.7	3045	22	AAI58133	Human polynucleoti	c 208	12	80.0	114	22	AAK13938	Human brain expres
c 136	13	86.7	3069	22	AAI58135	Human polynucleoti	c 209	12	80.0	114	22	AAK39685	Human bone marrow
c 137	13	86.7	3100	23	AAK77867	DNA encoding novel	c 210	12	80.0	114	22	AAI20492	Probe #10425 for g
c 138	13	86.7	3383	24	ABQ72496	Human MDDT encodin	c 211	12	80.0	114	22	AAI45699	Probe #14385 used
c 139	13	86.7	3415	20	ABK28654	Human cDNA encodin	c 212	12	80.0	114	22	AAI06190	Probe #6181 used t
c 140	13	86.7	3419	20	AAK28077	HS2ST coding sequ	c 213	12	80.0	114	22	ABSI3777	Human genome-deriv
c 141	13	86.7	3611	22	AAH18179	Human cDNA sequenc	214	12	80.0	134	21	AAC04726	Human secreted pro
c 142	13	86.7	4254	23	ABK42317	Genomic sequence #	215	12	80.0	152	22	AAK58799	Human immune/haema
c 143	13	86.7	4255	23	ABK42316	Genomic sequence #	216	12	80.0	171	22	ABA74644	Human foetal liver
c 144	13	86.7	4287	15	AAQ58996	AML1-MTG8 fusion.	217	12	80.0	171	22	AAK23115	Human brain expres
c 145	13	86.7	4287	19	AAQ58996	Human AML1/MTG8 on	218	12	80.0	171	22	AAK49290	Human bone marrow
c 146	13	86.7	4440	23	ABV25160	Human prostate exp	219	12	80.0	171	22	AAI55134	Probe #23820 used
c 147	13	86.7	4503	18	AAK64783	Human oxygen regul	220	12	80.0	174	22	ABA50320	Human breast cell
c 148	13	86.7	4503	24	ABK84398	Human cDNA diffe	221	12	80.0	174	22	ABA68263	Human foetal liver
c 149	13	86.7	5118	23	AAK27692	DNA encoding novel	222	12	80.0	174	22	ABA35273	Probe #13739 for g
c 150	13	86.7	5256	21	AAZ98619	RPPI-WSB genomic n	223	12	80.0	174	22	AAK16641	Human brain expres
c 151	13	86.7	5256	23	AAK58296	DNA encoding novel	224	12	80.0	174	22	AAK42403	Human bone marrow
c 152	13	86.7	5342	22	AAK81684	Human immune/haema	225	12	80.0	174	22	AAI23163	Probe #13096 for g
c 153	13	86.7	5345	22	AAK81685	Human immune/haema	226	12	80.0	174	22	AAI48482	Probe #17168 used t
c 154	13	86.7	5345	22	AAK81686	Human immune/haema	227	12	80.0	174	22	AAI08818	Probe #8809 used t
c 155	13	86.7	5416	23	ABL09341	Drosophila melanog	228	12	80.0	198	24	ABK76772	Bacillus lichenifo

c 229	12	80.0	208	22	ABA76330	Human foetal liver	c 302	12	80.0	409	22	AAI81144	Human polynucleoti
c 230	12	80.0	208	22	ABA40860	Probe #19326 for g	c 303	12	80.0	410	22	ABA42506	Human breast cell
c 231	12	80.0	208	22	AAK24980	Human brain expres	c 304	12	80.0	410	22	ABA52935	Human foetal liver
c 232	12	80.0	208	22	AAK50978	Human bone marrow	c 305	12	80.0	410	22	ABA22714	Probe #1180 for ge
c 233	12	80.0	208	22	AAI28012	Probe #17945 for g	c 306	12	80.0	410	22	AAK01185	Human brain expres
c 234	12	80.0	208	22	AAI57003	Probe #25689 used	c 307	12	80.0	410	22	AAK26646	Human bone marrow
c 235	12	80.0	208	24	ABS24487	Human genome-deriv	c 308	12	80.0	410	22	AAI11273	Probe #1206 for ge
c 236	12	80.0	221	24	ABN16126	Human ORFX polynuc	c 309	12	80.0	410	22	AAI32539	Probe #1225 used t
c 237	12	80.0	238	22	ABA71748	Human foetal liver	c 310	12	80.0	410	22	AAI01188	Probe #1179 used t
c 238	12	80.0	238	22	ABA37838	Probe #16304 for g	c 311	12	80.0	410	22	ABS01238	Human genome-deriv
c 239	12	80.0	238	22	AAK20111	Human brain expres	c 312	12	80.0	412	22	ABA12382	Human nervous syst
c 240	12	80.0	238	22	AAK46164	Human bone marrow	c 313	12	80.0	415	22	AAK33940	Human cdna encodin
c 241	12	80.0	238	22	AAI25549	Probe #15482 for g	c 314	12	80.0	419	22	AAI3780	Human polynucleoti
c 242	12	80.0	238	22	AAI52073	Probe #20759 used	c 315	12	80.0	437	23	ABV05483	Human prostate exp
c 243	12	80.0	238	24	ABS20473	Human genome-deriv	c 316	12	80.0	441	23	ABV36664	Human prostate exp
c 244	12	80.0	245	21	AAK29279	Human secreted pro	c 317	12	80.0	449	22	ABA59019	Human foetal liver
c 245	12	80.0	255	20	AAV89836	EST clone CW1150.	c 318	12	80.0	449	22	ABA27849	Probe #6315 for ge
c 246	12	80.0	258	21	AAK12892	Human secreted pro	c 319	12	80.0	449	22	AAK07189	Human brain expres
c 247	12	80.0	268	21	AAK19159	Human secreted pro	c 320	12	80.0	449	22	AAK32940	Human bone marrow
c 248	12	80.0	269	21	AAK45882	Human secreted exp	c 321	12	80.0	449	22	AAI16267	Probe #6200 for ge
c 249	12	80.0	270	24	ABK64644	Human benign prost	c 322	12	80.0	449	22	AAI38746	Probe #7432 used t
c 250	12	80.0	270	24	ABL65692	Lung cancer relate	c 323	12	80.0	449	24	ABS07746	Human genome-deriv
c 251	12	80.0	277	22	AAK36637	Human cardiovascular	c 324	12	80.0	450	22	AAK62933	Human immune/haema
c 252	12	80.0	277	22	AAK06330	Human reproductive	c 325	12	80.0	451	20	AAK40853	Human secreted pro
c 253	12	80.0	277	22	AAI06331	Human reproductive	c 326	12	80.0	460	22	AAK13384	Human nervous syst
c 254	12	80.0	277	22	AAK47445	Human ovarian canc	c 327	12	80.0	461	22	AAK54824	Rice glutamate 1-s
c 255	12	80.0	278	24	ABL83286	DNA encoding novel	c 328	12	80.0	467	22	ABA57318	Human foetal liver
c 256	12	80.0	291	23	AAK571802	Human foetal liver	c 329	12	80.0	467	22	ABA26868	Probe #5334 for ge
c 257	12	80.0	294	22	ABA72856	Probe #16919 for g	c 330	12	80.0	467	22	AAK05354	Human brain expres
c 258	12	80.0	294	22	ABA38453	Human brain expres	c 331	12	80.0	467	22	AAK30948	Human bone marrow
c 259	12	80.0	294	22	AAK21289	Human bone marrow	c 332	12	80.0	467	22	AAI36861	Probe #5547 used t
c 260	12	80.0	294	22	AAK47445	Probe #15871 for g	c 333	12	80.0	467	24	ABS05696	Human genome-deriv
c 261	12	80.0	294	22	AAI25938	Probe #21965 used	c 334	12	80.0	468	24	ABN65232	Human cancer relat
c 262	12	80.0	294	22	AAI53279	Human genome-deriv	c 335	12	80.0	473	22	ABA59228	Human foetal liver
c 263	12	80.0	294	22	ABS21568	Human colon cancer	c 336	12	80.0	473	22	ABA27977	Probe #6443 for ge
c 264	12	80.0	300	21	AAK01000	DNA encoding novel	c 337	12	80.0	473	22	AAK07434	Human brain expres
c 265	12	80.0	318	23	AAK65968	Human cdna encodin	c 338	12	80.0	473	22	AAK33211	Human bone marrow
c 266	12	80.0	324	22	AAK26456	CDNA encoding colo	c 339	12	80.0	473	22	AAI16368	Probe #6301 for ge
c 267	12	80.0	325	24	ABK45574	Human nervous syst	c 340	12	80.0	473	22	AAI39008	Probe #7694 used t
c 268	12	80.0	326	22	ABA12341	Human polynucleoti	c 341	12	80.0	473	24	ABS08041	Human genome-deriv
c 269	12	80.0	330	22	AAI87249	Human foetal liver	c 342	12	80.0	477	24	ABK62794	Rat sequence diffe
c 270	12	80.0	342	22	ABA59241	Probe #6452 for ge	c 343	12	80.0	486	24	ABK55193	Human colon cancer
c 271	12	80.0	342	22	ABA27986	Novel human diagno	c 344	12	80.0	490	23	ABV56974	Human prostate exp
c 272	12	80.0	342	22	AAK38882	Human brain expres	c 345	12	80.0	494	22	AAK33594	Human bone marrow
c 273	12	80.0	342	22	AAK07449	Human bone marrow	c 346	12	80.0	494	22	AAI39329	Probe #8015 used t
c 274	12	80.0	342	22	AAK33231	Probe #6308 for ge	c 347	12	80.0	494	24	ABS08485	Human genome-deriv
c 275	12	80.0	342	22	AAI16375	Probe #7712 used t	c 348	12	80.0	495	23	AAK59941	DNA encoding novel
c 276	12	80.0	342	22	AAI39026	Human genome-deriv	c 349	12	80.0	496	22	ABA57350	Human foetal liver
c 277	12	80.0	342	24	ABS08062	Human ORFX polynuc	c 350	12	80.0	496	22	AAK05386	Human brain expres
c 278	12	80.0	348	21	ABN21180	Human secreted exp	c 351	12	80.0	496	22	AAK30982	Human bone marrow
c 279	12	80.0	349	21	AAK44806	Human polynucleoti	c 352	12	80.0	496	22	AAI36894	Probe #5580 used t
c 280	12	80.0	354	22	AAI81113	SCA2 gene fragment	c 353	12	80.0	496	24	ABS05731	Human genome-deriv
c 281	12	80.0	355	19	AAV17224	Human nervous syst	c 354	12	80.0	506	22	AAK62150	Human foetal liver
c 282	12	80.0	355	22	ABA17378	Human nervous syst	c 355	12	80.0	506	22	AAK10469	Human brain expres
c 283	12	80.0	355	22	ABA17379	Human nervous syst	c 356	12	80.0	506	22	AAK36370	Human bone marrow
c 284	12	80.0	363	22	AAK65614	Novel human polynu	c 357	12	80.0	506	22	AAI42101	Probe #10787 used
c 285	12	80.0	366	22	AAK59344	Human immune/haema	c 358	12	80.0	512	22	ABA47826	Human breast cell
c 286	12	80.0	376	21	AAK15930	Human secreted pro	c 359	12	80.0	512	22	ABA65714	Human foetal liver
c 287	12	80.0	378	22	AAK77411	Human immune/haema	c 360	12	80.0	512	22	ABA32801	Probe #11267 for g
c 288	12	80.0	378	22	AAK60314	Human immune/haema	c 361	12	80.0	512	22	AAK14119	Human brain expres
c 289	12	80.0	379	22	AAK63114	Novel human polynu	c 362	12	80.0	512	22	AAK39860	Human bone marrow
c 290	12	80.0	381	22	AAK64655	Novel human polynu	c 363	12	80.0	512	22	AAI20671	Probe #10604 for g
c 291	12	80.0	386	21	AAK57268	Eucalyptus grandis	c 364	12	80.0	512	22	AAI45882	Probe #14568 used
c 292	12	80.0	388	22	AAI81345	Human polynucleoti	c 365	12	80.0	512	22	AAI06370	Probe #6361 used t
c 293	12	80.0	389	24	ABN76304	Human transcriptio	c 366	12	80.0	512	24	ABK13958	Human genome-deriv
c 294	12	80.0	397	21	AAK09645	Human secreted pro	c 367	12	80.0	516	19	AAV06551	SCA2 gene fragment
c 295	12	80.0	398	22	AAK75100	Human immune/haema	c 368	12	80.0	519	24	ABQ18838	Oligonucleotide fo
c 296	12	80.0	399	22	AAK66792	Novel human polynu	c 369	12	80.0	519	24	ABQ18839	Oligonucleotide fo
c 297	12	80.0	401	22	AAK96121	Human neuregulin g	c 370	12	80.0	522	22	AAH33128	Human colon cancer
c 298	12	80.0	401	22	AAK97614	Human neuregulin g	c 371	12	80.0	522	24	ABL89713	Human polynucleoti
c 299	12	80.0	403	24	ABN16862	Human ORFX polynuc	c 372	12	80.0	537	21	ABL15158	Trichoderma reesei
c 300	12	80.0	406	21	AAK43968	Human secreted exp	c 373	12	80.0	546	24	ABK55070	Human colon cancer
c 301	12	80.0	406	22	AAH89970	Human bone marrow	c 374	12	80.0	557	22	ABA60528	Human foetal liver

c 375	12	80.0	557	22	ABA28694	Probe #7160 for ge	448	12	80.0	839	22	AAI63352	Human kidney relat
c 376	12	80.0	557	22	AAK08809	Human brain expres	449	12	80.0	849	20	AX97676	Extended human sec
c 377	12	80.0	557	22	AAK34696	Human bone marrow	450	12	80.0	852	20	ABA9428	Escherichia coli p
c 378	12	80.0	557	22	AAI16811	Probe #6744 for ge	c 451	12	80.0	870	23	AS76112	DNA encoding novel
c 379	12	80.0	557	22	AAI40417	Probe #9103 used t	452	12	80.0	889	23	ABL56865	Plant resistance g
c 380	12	80.0	557	24	ABS09288	Human genome-deriv	453	12	80.0	895	21	AAF08172	Fusarium venenatum
c 381	12	80.0	558	24	ABQ17980	Oligonucleotide fo	c 454	12	80.0	895	23	AA578132	DNA encoding novel
c 382	12	80.0	558	24	ABQ17981	Oligonucleotide fo	455	12	80.0	899	24	ABL42277	Pancreatic tumour
c 383	12	80.0	559	22	AAH98842	Human EST-derived	456	12	80.0	910	22	ABA06989	Human pancreatic c
c 384	12	80.0	560	22	AAH13526	Human cDNA clone (457	12	80.0	910	22	AAK88474	Human digestive sy
c 385	12	80.0	565	24	ABK79051	Bacillus clausii g	c 458	12	80.0	936	24	ABK73545	Bacillus lichenifo
c 386	12	80.0	576	23	AA568618	DNA encoding novel	c 459	12	80.0	965	24	AAH98528	Canine EST-derived
c 387	12	80.0	582	22	ABA4212	Human foetal liver	c 460	12	80.0	970	24	ABK74580	Bacillus lichenifo
c 388	12	80.0	582	22	ABA31358	Probe #9824 for ge	461	12	80.0	987	22	AAH22670	Mouse Bcl-G polype
c 389	12	80.0	582	22	AAK12692	Human brain expres	462	12	80.0	1001	21	AA527810	Arachidonic acid m
c 390	12	80.0	582	22	AAK38410	Human bone marrow	c 463	12	80.0	1012	22	ABA47193	Human breast cell
c 391	12	80.0	582	22	AAI19204	Probe #9137 for ge	c 464	12	80.0	1012	22	ABA65077	Human foetal liver
c 392	12	80.0	582	22	AAI44365	Probe #13051 used	c 465	12	80.0	1012	22	ABA32183	Probe #10649 for g
c 393	12	80.0	582	24	ABS12465	Human genome-deriv	c 466	12	80.0	1012	22	AAK13500	Human brain expres
c 394	12	80.0	582	24	ABN79151	Human transcriptio	c 467	12	80.0	1012	22	AAK39239	Human bone marrow
c 395	12	80.0	585	24	ABQ16892	Oligonucleotide fo	c 468	12	80.0	1012	22	AAI20049	Probe #9982 for ge
c 396	12	80.0	585	24	ABQ16893	Oligonucleotide fo	c 469	12	80.0	1012	22	AAI45247	Probe #13933 used
c 397	12	80.0	586	24	ABQ50528	Oligonucleotide fo	c 470	12	80.0	1012	22	AAI05756	Probe #5747 used t
c 398	12	80.0	586	24	ABQ50529	Oligonucleotide fo	c 471	12	80.0	1012	22	ABS13323	Human genome-deriv
c 399	12	80.0	594	21	AAA82223	N. meningitidis pa	c 472	12	80.0	1040	21	AA655525	Porcine BAC-PiGF2-
c 400	12	80.0	594	23	AA580695	DNA encoding novel	c 473	12	80.0	1046	23	AA582954	DNA encoding novel
c 401	12	80.0	595	22	ABA60317	Human foetal liver	474	12	80.0	1057	21	AAF13375	Aspergillus oryzae
c 402	12	80.0	595	22	ABA28576	Probe #7042 for ge	c 475	12	80.0	1074	19	AAV23874	Plant OMT enzyme D
c 403	12	80.0	595	22	AAK08597	Human brain expres	c 476	12	80.0	1074	20	AAZ06877	Pine O-methyl tran
c 404	12	80.0	595	22	AAK34479	Human bone marrow	c 477	12	80.0	1074	21	AA67961	Pinus radiata OMT
c 405	12	80.0	595	22	AAI16743	Probe #6676 for ge	c 478	12	80.0	1075	19	AAV23875	Plant OMT enzyme D
c 406	12	80.0	595	22	AAI40200	Probe #8886 used t	c 479	12	80.0	1075	20	AAZ06878	Pine O-methyl tran
c 407	12	80.0	595	24	ABS09136	Human genome-deriv	c 480	12	80.0	1075	21	AA667962	Pinus radiata OMT
c 408	12	80.0	618	23	ABV52614	Human prostate exp	c 481	12	80.0	1089	22	AD07902	Human secreted pro
c 409	12	80.0	621	21	AA280330	Human colon cancer	c 482	12	80.0	1106	24	ABL49511	Sequence #113 used
c 410	12	80.0	623	19	AAV17229	SCA2 gene fragment	c 483	12	80.0	1106	24	ABK30706	Plant dwarfing/stu
c 411	12	80.0	631	23	ABV17219	Human prostate exp	c 484	12	80.0	1136	21	AA47827	Arabidopsis thalia
c 412	12	80.0	638	22	AAH04944	Human cDNA clone (c 485	12	80.0	1149	24	AA55807	S. lavendulae MICH
c 413	12	80.0	638	24	ABQ04944	Oligonucleotide fo	c 486	12	80.0	1169	24	ABQ68781	Listeria monocytog
c 414	12	80.0	638	24	ABQ22262	Oligonucleotide fo	c 487	12	80.0	1189	21	AAAL3953	Resveratrol syntha
c 415	12	80.0	642	23	AA565185	DNA encoding novel	c 488	12	80.0	1192	24	ABQ68954	Listeria monocytog
c 416	12	80.0	642	23	AA583320	DNA encoding novel	c 489	12	80.0	1197	23	AA565911	DNA encoding novel
c 417	12	80.0	680	22	AA817163	Human ion channel-	c 490	12	80.0	1203	18	AA64815	Tumour suppressor
c 418	12	80.0	682	24	ABQ44992	Oligonucleotide fo	c 491	12	80.0	1208	22	AAF32760	Human secreted pro
c 419	12	80.0	682	24	ABQ44993	Oligonucleotide fo	c 492	12	80.0	1235	24	AA515005	Rice 4-CL-specific
c 420	12	80.0	685	22	AAC86047	CABF-1 partial seq	c 493	12	80.0	1242	22	AAI19045	Human excretory re
c 421	12	80.0	686	22	AAS31375	Human cDNA encodin	c 494	12	80.0	1242	22	AAI63395	Human kidney relat
c 422	12	80.0	686	24	ABQ66699	Human polynucleoti	c 495	12	80.0	1244	24	ABK94958	Human novel polynu
c 423	12	80.0	695	21	AA061719	N. meningitidis pa	c 496	12	80.0	1250	9	AAH80316	Transcription cont
c 424	12	80.0	704	24	ABQ36594	Oligonucleotide fo	c 497	12	80.0	1260	16	AAAT00618	Megakaryocyte kina
c 425	12	80.0	704	24	ABQ36595	Oligonucleotide fo	c 498	12	80.0	1273	22	AAK60835	Human immune/haema
c 426	12	80.0	719	24	ABK53743	Human eosinophil-m	c 499	12	80.0	1274	19	AAV34215	Human secreted pro
c 427	12	80.0	729	23	AA565912	DNA encoding novel	c 500	12	80.0	1282	20	AAV84597	Human secreted pro
c 428	12	80.0	732	15	AAQ70304	Mouse NF-Atp cDNA	c 501	12	80.0	1282	22	ABA83380	Human secreted pro
c 429	12	80.0	732	15	AAQ70314	Human NF-Atp cDNA	c 502	12	80.0	1296	19	AAV34269	Human secreted pro
c 430	12	80.0	741	22	AAQ60771	Human immune/haema	c 503	12	80.0	1327	24	ABQ68452	Listeria monocytog
c 431	12	80.0	742	22	AAAL01395	Human reproductive	c 504	12	80.0	1343	21	AAF16344	Human prostate can
c 432	12	80.0	742	22	AAH33660	Human colon cancer	c 505	12	80.0	1347	22	AAH86035	CABF-1 coding sequ
c 433	12	80.0	742	23	ABL96848	Human testicular a	c 506	12	80.0	1352	22	AAH46065	Sigma-34 factor 9
c 434	12	80.0	747	23	AA582292	DNA encoding novel	c 507	12	80.0	1389	23	AA559778	Propionibacterium
c 435	12	80.0	748	20	AAZ00430	Human secreted pro	c 508	12	80.0	1424	22	AAK78381	Human immune/haema
c 436	12	80.0	753	22	AA580395	Nucleotide sequenc	c 509	12	80.0	1449	22	AA544882	Human contig polyn
c 437	12	80.0	761	20	AA216588	Human gene express	c 510	12	80.0	1458	23	ABL27923	Drosophila melanog
c 438	12	80.0	768	22	AAK80034	Human immune/haema	c 511	12	80.0	1459	23	AA573909	DNA encoding novel
c 439	12	80.0	768	22	AAK86147	Human immune/haema	c 512	12	80.0	1474	15	AAQ70311	Mouse NF-Atp. Mus
c 440	12	80.0	776	22	AAAL17954	Human breast cance	c 513	12	80.0	1486	21	AAF18228	Lung cancer associ
c 441	12	80.0	783	22	AAU23724	Human breast cance	c 514	12	80.0	1492	24	ABK30508	Human glioma-assoc
c 442	12	80.0	784	21	AAA02448	Human colon cancer	c 515	12	80.0	1493	19	AAV27207	cDNA clone ethb001
c 443	12	80.0	788	22	AAH07874	Human cDNA clone (c 516	12	80.0	1494	23	ABL28079	Drosophila melanog
c 444	12	80.0	791	24	AA520988	DNA sequence #19 r	c 517	12	80.0	1522	23	AA590487	DNA encoding novel
c 445	12	80.0	815	20	AA216195	Human gene express	c 518	12	80.0	1539	23	ABV23163	Human prostate exp
c 446	12	80.0	834	22	AA580394	Nucleotide sequenc	c 519	12	80.0	1539	23	ABV29003	Human prostate exp
c 447	12	80.0	839	22	AA199002	Human excretory re	c 520	12	80.0	1551	21	AAZ35757	Strongylocentrotus

521	12	80.0	1561	21	AAF21032	Human low adenosin	c 594	12	80.0	2545	22	AAS63205	Human purified sec
522	12	80.0	1561	21	AAA34910	Human adenosine re	595	12	80.0	2549	22	AAH15872	Human cDNA sequenc
c 523	12	80.0	1584	24	ABK72940	Bacillus lichenifo	c 596	12	80.0	2563	19	AAV28617	Nucleotide sequenc
c 524	12	80.0	1608	22	AAS23120	DNA encoding novel	597	12	80.0	2576	22	AAI59194	Human polynucleoti
c 525	12	80.0	1613	23	AAS94510	DNA encoding novel	598	12	80.0	2590	24	AAH99062	Murine muscle ring
c 526	12	80.0	1622	24	ABK09766	Human ovarian tumo	c 599	12	80.0	2642	22	AAH99048	Human EST-derived
c 527	12	80.0	1634	22	AAF59613	Human cell cycle a	c 600	12	80.0	2656	22	AAH16132	Human cDNA sequenc
c 528	12	80.0	1643	22	AAF54825	Rice glutamate 1-s	601	12	80.0	2675	15	AAQ70312	Human NF-ATP. Hom
529	12	80.0	1650	21	AAZ90020	Human phenylalanin	602	12	80.0	2679	24	ABN95721	Gene #2219 used to
c 530	12	80.0	1650	23	AAZ67603	DNA encoding novel	c 603	12	80.0	2689	22	AAK78265	Human immune/haema
c 531	12	80.0	1650	23	AAZ76471	DNA encoding novel	c 604	12	80.0	2714	22	AAK89167	Rat p-HYDE coding
c 532	12	80.0	1652	22	AAAC88072	Human FLEXHT-3 nuc	c 605	12	80.0	2720	24	AAAC98072	Human DNA for pote
c 533	12	80.0	1667	22	AAAS31214	Human cDNA encodin	c 606	12	80.0	2753	21	AAAC76804	Human ORF ORF2359
c 534	12	80.0	1667	24	ABQ66538	Human polynucleoti	c 607	12	80.0	2806	24	ABA94778	Human BSTP-CAD pol
c 535	12	80.0	1672	24	ABK13773	DNA encoding huma	c 608	12	80.0	2807	22	AAAF81528	Human LTC4 recepto
c 536	12	80.0	1690	22	AAH01056	Streptococcus pneu	c 609	12	80.0	2863	22	AAAD07837	Human secreted pro
c 537	12	80.0	1715	24	ABK63724	Rat sequence diffie	c 610	12	80.0	2872	22	AAAI60426	Human polynucleoti
c 538	12	80.0	1724	20	AAAX20442	Human secreted pro	c 611	12	80.0	2885	22	AAK78266	Human immune/haema
c 539	12	80.0	1735	21	AAZ77448	Human ORFX ORF3003	c 612	12	80.0	2920	23	AAAS87293	DNA encoding novel
540	12	80.0	1746	22	AAI58640	Human polynucleoti	613	12	80.0	2957	22	AAH14691	Human cDNA sequenc
541	12	80.0	1756	21	AAAC98993	Human pancreatic c	c 614	12	80.0	2969	24	ABN85026	Murine Tumour Supp
c 542	12	80.0	1761	20	AAAX20412	Human secreted pro	c 615	12	80.0	2980	6	AAAS50139	Sequence of Hepati
c 543	12	80.0	1776	23	AAZ74532	DNA encoding novel	c 616	12	80.0	2980	6	AAAS50274	Partial sequence o
c 544	12	80.0	1777	23	AAZ74532	Canine IgA gene.	617	12	80.0	2983	19	AAV69281	Mouse chromodomain
c 545	12	80.0	1789	17	AAAT29825	Human cDNA sequenc	618	12	80.0	2998	21	AAF21180	Human low adenosin
546	12	80.0	1820	22	AAI60980	Human polynucleoti	619	12	80.0	2998	21	AAA35058	Human adenosine re
c 547	12	80.0	1834	22	AAH18015	DNA encoding novel	c 620	12	80.0	3063	23	AAAS88981	DNA encoding novel
c 548	12	80.0	1848	23	AAAS90056	Heat resistant car	c 621	12	80.0	3097	19	AAV19609	Homo sapiens EPCR
c 549	12	80.0	1860	13	AAQ26728	C glutamicum codin	c 622	12	80.0	3113	22	AAAL02892	Human reproductive
c 550	12	80.0	1866	22	AAH67164	Nuclear matrix-ass	c 623	12	80.0	3125	22	AAH17859	Human cDNA sequenc
551	12	80.0	1909	20	AAV84356	Human EST-derived	624	12	80.0	3160	24	ABK84122	Human cDNA differe
552	12	80.0	1909	22	AAH98561	AML 1 gene. Homo	c 625	12	80.0	3262	21	AAA16623	Human secreted pro
553	12	80.0	1912	14	AAQ43443	Human polynucleoti	c 626	12	80.0	3343	23	AAI60763	Human polynucleoti
554	12	80.0	1922	22	AAI93648	Human cDNA sequenc	c 627	12	80.0	3360	19	AAV19608	Mus musculus EPCR
555	12	80.0	1934	22	AAH16761	Human cDNA sequenc	c 628	12	80.0	3372	9	AAH80755	Encodes all HAV st
c 556	12	80.0	1941	22	AAH13893	Human cancer cell	629	12	80.0	3380	24	ABK15372	DNA encoding huma
c 557	12	80.0	1949	24	AAAL45652	Human cancer cell	c 630	12	80.0	3394	18	AAAT84484	Human alpha-1 coll
558	12	80.0	1949	24	AAAL45653	Human cancer cell	c 631	12	80.0	3394	20	AAV78379	Human alpha-1 coll
559	12	80.0	1981	22	AAAD04172	Human Her-2/neu ov	c 632	12	80.0	3394	24	ABN95680	Gene #2178 used to
560	12	80.0	1989	24	ABL41076	A. oryzae pacC (Ao	c 633	12	80.0	3399	24	ABL41071	Gene #2178 used to
c 561	12	80.0	2002	22	AAI58794	Human polynucleoti	c 634	12	80.0	3402	23	AAAS88989	A. oryzae pacC (Ao
c 562	12	80.0	2013	24	ABK49349	RNA polymerase II	c 635	12	80.0	3402	23	AAAS88989	DNA encoding novel
563	12	80.0	2016	22	AAK89499	Human digestive sy	c 636	12	80.0	3414	24	ABL41081	A. oryzae pacC (Sp
c 564	12	80.0	2020	14	AAQ40092	PHD1 gene. Saccha	c 637	12	80.0	3458	23	ABL27922	Drosophila melanog
565	12	80.0	2040	24	ABQ54224	Human ovarian anti	c 638	12	80.0	3478	17	AAAT36866	Human transcriptio
c 566	12	80.0	2057	22	AAAF72803	Secreted protein g	c 639	12	80.0	3483	22	AAH62757	Shrimp white spot
c 567	12	80.0	2065	23	AAZ73478	DNA encoding novel	c 640	12	80.0	3512	20	AAH59396	Mouse topoisomeras
c 568	12	80.0	2067	21	AAAC59065	Human secreted pro	641	12	80.0	3512	24	ABI99291	Mouse ischaemic co
569	12	80.0	2084	21	AAAC76364	Human ORFX ORF1919	c 642	12	80.0	3516	19	AAV71082	Green fluorescent
c 570	12	80.0	2087	21	AAAC77154	Human ORFX ORF2709	c 643	12	80.0	3526	21	AAAT77511	Human ORFX ORF3066
c 571	12	80.0	2103	22	AAK79464	Human immune/haema	c 644	12	80.0	3546	19	AAV71083	NFAT1-green fluore
c 572	12	80.0	2108	22	AAI60580	Human polynucleoti	c 645	12	80.0	3616	20	AAV73924	Human SAHH DNA #1.
573	12	80.0	2127	17	AAAT12461	Human K+ channel 1	646	12	80.0	3617	22	AAI99001	Human excretory re
c 574	12	80.0	2127	19	AAV04873	DNA sequence of t	c 647	12	80.0	3617	22	AAI63351	Human kidney relat
c 575	12	80.0	2137	22	AAH15653	Human cDNA sequenc	c 648	12	80.0	3634	23	ABV23195	Human prostate exp
c 576	12	80.0	2152	22	ABAI5445	Human nervous syst	c 649	12	80.0	3634	23	ABV29032	Human prostate exp
c 577	12	80.0	2211	24	ABK12859	DNA encoding huma	c 650	12	80.0	3656	17	AAAT36751	VLDL receptor gene
c 578	12	80.0	2238	23	AAZ71124	DNA encoding novel	c 651	12	80.0	3741	22	AAI99573	Human expressed po
c 579	12	80.0	2259	23	AAZ79424	DNA encoding novel	c 652	12	80.0	3747	23	ABK43741	DNA encoding novel
c 580	12	80.0	2310	22	AAAS46734	Tumour suppressor	c 653	12	80.0	3799	23	ABL20995	Drosophila melanog
c 581	12	80.0	2322	22	AAH75165	Nucleotide sequenc	c 654	12	80.0	3885	22	AAAC99169	ADRSYPHYDE region
c 582	12	80.0	2356	11	AAH80140	Human X chromosome	655	12	80.0	3912	22	AAAF98728	Human late stage o
c 583	12	80.0	2383	21	AAA96495	DNA encoding a hu	c 656	12	80.0	3929	22	ABL26450	Human breast cance
c 584	12	80.0	2387	22	AAH16135	Human cDNA sequenc	c 657	12	80.0	4112	23	ABL08835	Drosophila melanog
c 585	12	80.0	2407	23	AAH68797	DNA encoding novel	c 658	12	80.0	4152	21	AAAF15924	Human prostate can
c 586	12	80.0	2415	22	AAH73802	Phosphatidylyl trans	c 659	12	80.0	4184	23	ABL20999	Drosophila melanog
587	12	80.0	2448	18	AAZ91639	Human phenylalanin	660	12	80.0	4200	18	AAAT78912	Spinocerebellar at
588	12	80.0	2448	20	AAZ30664	Human phenylalanin	c 661	12	80.0	4201	24	ABK83757	Human cDNA differe
c 589	12	80.0	2467	22	AAK94847	Human full-length	c 662	12	80.0	4277	23	ABL20997	Drosophila melanog
c 590	12	80.0	2512	23	AAAS83556	DNA encoding novel	c 663	12	80.0	4278	23	AAAS87531	DNA encoding novel
591	12	80.0	2518	18	AAAT90702	RD114 env gene. S	c 664	12	80.0	4367	23	AAV30270	Gene causative of
592	12	80.0	2523	12	AAQ12712	Phenylalanine hydr	665	12	80.0	4434	23	ABL16404	Drosophila melanog
c 593	12	80.0	2539	24	ABI99857	Mouse ischaemic co	666	12	80.0	4481	19	AAV06552	Human SCA2 DNA. H
	12	80.0						12	80.0	4481	20	AAZ23428	

c 567	12	80.0	4551	24	ABN05301	Human collagen XVI	c 740	12	80.0	7802	24	ABL32765	Human immune syste
c 568	12	80.0	4620	24	ABK30161	Human GLI1 genomic	c 741	12	80.0	7802	24	ABK28184	DNA transcription
c 569	12	80.0	4875	24	ABQ54955	Human ovarian anti	c 742	12	80.0	7911	22	ABS36238	Human cardiovascular
c 570	12	80.0	4881	24	AAD23738	Maize streak gemin	c 743	12	80.0	7911	22	AAO32323	Human reproductive
c 571	12	80.0	4961	24	AAD23740	Maize streak gemin	c 744	12	80.0	7938	23	ABLO4780	Drosophila melanog
c 572	12	80.0	5044	23	ABL03142	Drosophila melanog	c 745	12	80.0	8000	23	ABL07372	Drosophila melanog
c 573	12	80.0	5174	20	AAV65142	Ehrlichia sp. B82	c 746	12	80.0	8043	24	AAD23742	Maize streak gemin
c 574	12	80.0	5212	9	AAH03017	Transcription cont	c 747	12	80.0	8246	22	AAD23742	Maize streak gemin
c 575	12	80.0	5216	20	AAW07548	PKS90 TIR coupling	c 748	12	80.0	8526	22	ABA18356	Human reproductive
c 576	12	80.0	5227	22	ABA20781	Human nervous syst	c 749	12	80.0	8939	22	ABA15471	Human nervous syst
c 577	12	80.0	5230	20	AAW07549	pPREX1 mutant beta	c 750	12	80.0	8939	22	ABA16243	Human nervous syst
c 578	12	80.0	5230	21	AAA15041	Nucleotide sequenc	c 751	12	80.0	8939	22	ABA18915	Human nervous syst
c 579	12	80.0	5231	20	AAW07550	pPREX1A mutant bet	c 752	12	80.0	8965	22	AAK79591	Human immune/haema
c 580	12	80.0	5235	22	ABA20782	Human nervous syst	c 753	12	80.0	9121	21	AAK79591	Human immune/haema
c 581	12	80.0	5271	20	AAK20505	Polynucleotide seq	c 754	12	80.0	9202	8	AAW06008	Human ORFX ORF1956
c 582	12	80.0	5281	22	AAO4261	Human reproductive	c 755	12	80.0	9202	8	AAW06008	VISNA sheep lentiv
c 583	12	80.0	5288	22	AAK52070	Human polynucleoti	c 756	12	80.0	9289	22	AAK90960	Human digestive sy
c 584	12	80.0	5292	21	AAK21374	Human low adenosin	c 757	12	80.0	9289	22	AAK531995	Human liver associ
c 585	12	80.0	5292	21	AAK35252	Human adenosine re	c 758	12	80.0	9289	22	AAK531995	Human liver associ
c 586	12	80.0	5391	24	ABK39938	Human chemically p	c 759	12	80.0	9401	22	AAO86648	Human FLAMINGO 1 h
c 587	12	80.0	5391	24	ABL32242	Human immune syste	c 760	12	80.0	9402	22	AAK46672	Tumour suppressor
c 588	12	80.0	5408	20	AAW77720	Human collagen 18	c 761	12	80.0	9439	19	AAV69284	Human variably cha
c 589	12	80.0	5448	22	AAK78267	Human immune/haema	c 762	12	80.0	9592	17	AAK36752	Adenovirus vector
c 590	12	80.0	5484	24	ABN59750	Novel human coding	c 763	12	80.0	9751	22	AAK18386	Recombinant viral
c 591	12	80.0	5497	22	AAK29646	Plasmid pTINrF1	c 764	12	80.0	9751	24	ABL60796	FIV-Oma3 recombina
c 592	12	80.0	5559	20	AAK02982	Human IL-1ra BAC c	c 765	12	80.0	10695	22	AAK65420	Human immune/haema
c 593	12	80.0	5586	24	ABL32649	Human immune syste	c 766	12	80.0	10766	22	AAK39895	Genomic sequence #
c 594	12	80.0	5704	22	AAO33350	Human reproductive	c 767	12	80.0	10766	22	AAK90312	Human digestive sy
c 595	12	80.0	5736	22	AAO4572	Human reproductive	c 768	12	80.0	10872	24	ABL70336	Chemically treated
c 596	12	80.0	5736	22	AAO5108	Human reproductive	c 769	12	80.0	10872	24	ABK31389	Human gene regulat
c 597	12	80.0	5736	23	ABL97495	Human testicular a	c 770	12	80.0	11172	22	AAH41188	Signal transductio
c 598	12	80.0	5736	23	ABL98000	Human testicular a	c 771	12	80.0	11301	22	AAK71591	Murine oligonucleo
c 599	12	80.0	5770	21	AAK15043	Nucleotide sequenc	c 772	12	80.0	11330	23	AAK59544	Human immune/haema
c 600	12	80.0	5819	22	AAK73716	Human immune/haema	c 773	12	80.0	11330	23	AAK59544	Propionibacterium
c 601	12	80.0	5819	22	AAK73717	Human immune/haema	c 774	12	80.0	11982	23	ABL20994	Drosophila melanog
c 602	12	80.0	5819	22	AAK77589	Human immune/haema	c 775	12	80.0	12020	23	ABL20996	Drosophila melanog
c 603	12	80.0	5819	22	AAK77592	Human immune/haema	c 776	12	80.0	12047	23	ABL20998	Drosophila melanog
c 604	12	80.0	5865	18	AAK90692	Plasmid FBdelPRDSA	c 777	12	80.0	12308	23	AAD23451	Human lung tumour
c 605	12	80.0	5870	21	AAK15044	Nucleotide sequenc	c 778	12	80.0	12309	22	AAK89483	Human digestive sy
c 606	12	80.0	5906	21	AAK15042	Nucleotide sequenc	c 779	12	80.0	12309	22	AAK90834	Human digestive sy
c 607	12	80.0	5954	21	AAK76439	Human ORFX ORF1994	c 780	12	80.0	12328	22	AAK79156	Human immune/haema
c 608	12	80.0	6109	23	AAH78667	Murine Col5a3 cDNA	c 781	12	80.0	12775	23	AAK27700	Drosophila melanog
c 609	12	80.0	6161	23	ABL12556	Drosophila melanog	c 782	12	80.0	12881	22	AAK85861	Human immune/haema
c 610	12	80.0	6167	22	AAK45337	Chemically pretrea	c 783	12	80.0	13123	22	AAO4954	Human reproductive
c 611	12	80.0	6167	24	ABL70194	Chemically treated	c 784	12	80.0	13123	23	ABL97848	Human testicular a
c 612	12	80.0	6167	24	ABL32643	Human immune syste	c 785	12	80.0	13189	22	AAO6063	Human reproductive
c 613	12	80.0	6167	24	AAK61152	Human gene regulat	c 786	12	80.0	13189	23	ABL98628	Human testicular a
c 614	12	80.0	6167	24	ABK28172	DNA transcription	c 787	12	80.0	13202	23	ABL13830	Drosophila melanog
c 615	12	80.0	6211	24	ABL32806	Human immune syste	c 788	12	80.0	13371	22	AAI99114	Human excretory re
c 616	12	80.0	6212	21	AAK21375	Human low adenosin	c 789	12	80.0	13371	22	AAI63464	Human kidney relat
c 617	12	80.0	6212	21	AAK35253	Human adenosine re	c 790	12	80.0	13596	23	ABL02138	Drosophila melanog
c 618	12	80.0	6228	23	ABL11144	Drosophila melanog	c 791	12	80.0	14147	22	AAK46743	Tumour suppressor
c 619	12	80.0	6309	24	AAD23741	Maize streak gemin	c 792	12	80.0	14147	24	ABK33955	Human DNA for stag
c 620	12	80.0	6314	22	AAK90962	Human digestive sy	c 793	12	80.0	14148	22	AAK70926	Human immune/haema
c 621	12	80.0	6314	22	AAK31997	Human liver associ	c 794	12	80.0	14160	22	AAK65583	Human immune/haema
c 622	12	80.0	6314	24	ABN90352	Human liver associ	c 795	12	80.0	14301	23	AAK82709	DNA encoding novel
c 623	12	80.0	6324	24	ABK31543	Signal transductio	c 796	12	80.0	14452	23	ABV22986	Human prostate exp
c 624	12	80.0	6638	22	AAK79592	Human immune/haema	c 797	12	80.0	14456	23	ABV24304	Human prostate exp
c 625	12	80.0	6638	22	AAK83770	Human immune/haema	c 798	12	80.0	14456	23	ABL10220	Drosophila melanog
c 626	12	80.0	6804	23	ABL13824	Drosophila melanog	c 799	12	80.0	14458	22	AAK06039	Angiotensin conver
c 627	12	80.0	6898	24	ABN80223	Human chemically m	c 800	12	80.0	14800	22	AAV59470	Human ryanodin rec
c 628	12	80.0	6911	22	AAK69352	Human immune/haema	c 801	12	80.0	15512	19	AAV59470	DNA encoding novel
c 629	12	80.0	6911	22	AAK82578	Human immune/haema	c 802	12	80.0	15583	23	AAK76501	Drosophila melanog
c 630	12	80.0	7236	22	AAK64793	Human immune/haema	c 803	12	80.0	15662	23	ABL13832	Drosophila melanog
c 631	12	80.0	7404	24	AAD23743	Maize streak gemin	c 804	12	80.0	15820	23	AAK87533	DNA encoding novel
c 632	12	80.0	7408	24	AAK47851	Murine basic helix	c 805	12	80.0	16271	22	ABA19209	Human nervous syst
c 633	12	80.0	7408	24	ABN83211	Mouse transcriptio	c 806	12	80.0	16271	22	ABA19210	Human nervous syst
c 634	12	80.0	7482	22	AAK66961	Human immune/haema	c 807	12	80.0	16676	22	AAK68313	Human immune/haema
c 635	12	80.0	7581	23	ABL10234	Drosophila melanog	c 808	12	80.0	17069	21	AAK21185	Human low adenosin
c 636	12	80.0	7661	22	AAK16545	Human novel protei	c 809	12	80.0	17069	21	AAK35063	Human adenosine re
c 637	12	80.0	7661	22	AAK162954	Human genomic DNA	c 810	12	80.0	17123	22	AAK86738	Human immune/haema
c 638	12	80.0	7661	22	AAK162954	Human polynucleoti	c 811	12	80.0	17150	22	AAK82982	Human DNA methyltr
c 639	12	80.0	7802	22	AAK45351	Chemically pretrea	c 812	12	80.0	17583	22	AAK89484	Human digestive sy
c 640	12	80.0	7802	22	AAK45351	Chemically pretrea	c 813	12	80.0	17865	22	AAK90961	Human digestive sy

813	12	80.0	17865	22	AAS31996	Human liver associ	c 886	12	80.0	160271	22	AAS04858	Human chromosome 1
814	12	80.0	17865	24	ABN90351	Human liver antige	c 887	12	80.0	160271	22	AAS04864	Human chromosome 1
815	12	80.0	18073	20	AVB83948	Bacterial artifici	c 888	12	80.0	160271	22	AAS06667	Human chromosome 1
c 816	12	80.0	18664	22	AK65421	Human immune/haema	c 889	12	80.0	160271	22	AAH40997	160kb fragment of
c 817	12	80.0	18664	22	AK684438	Human immune/haema	c 890	12	80.0	160271	22	AAH23764	Human chromosome 1
c 818	12	80.0	19062	21	AAF21280	Human low adenosin	c 891	12	80.0	160271	22	AAF85116	Nucleotide sequenc
819	12	80.0	19186	20	AXX20620	Polynucleotide seq	c 892	12	80.0	198161	24	ABK83564	Human cDNA differe
820	12	80.0	19334	22	AAS36443	Human cardiovascular	c 893	12	80.0	213251	24	ABQ67193	Listeria innocua c
c 821	12	80.0	19345	22	AAS36444	Human cardiovascular	c 894	12	80.0	235033	19	AAV57926	Hereditary haemoch
c 822	12	80.0	19659	24	ABL32766	Human immune syste	c 895	12	80.0	302250	24	ABL67703	Oesophagus cancer
c 823	12	80.0	19738	23	ABL20992	Drosophila melanog	c 896	12	80.0	305107	22	AAH62689	Shrimp white spot
c 824	12	80.0	19942	22	AAK87416	Human immune/haema	c 897	12	80.0	349980	21	AAF21610	Neisseria meningit
c 825	12	80.0	20155	23	ABL13688	Drosophila melanog	c 898	12	80.0	349980	22	AAH41224	Pyrococcus abyssi
826	12	80.0	20510	23	ABL19710	Drosophila melanog	c 899	12	80.0	349980	22	AAH68530	C glutamicum codin
827	12	80.0	20775	24	AAI47852	Murine basic helix	c 900	12	80.0	349980	22	AAH68531	C glutamicum codin
828	12	80.0	20775	24	ABN83212	Mouse transcriptio	c 901	12	80.0	349980	22	AAH68532	C glutamicum codin
c 829	12	80.0	20829	23	ABL14502	Drosophila melanog	c 902	12	80.0	349980	22	AAH68533	C glutamicum codin
c 830	12	80.0	20933	24	ABQ67124	Human angiogenesis	c 903	12	80.0	611590	21	AAF22303	Arabidopsis thalia
831	12	80.0	21010	22	AAI05888	Human reproductive	c 904	12	80.0	1437668	21	AAH81490	N. meningitidis B
832	12	80.0	21010	22	AAK89247	Human digestive sy	c 905	12	80.0	3011208	24	ABQ69245	Listeria innocua D
833	12	80.0	21010	23	ABL98452	Human testicular a	c 906	11	73.3	13	23	ABH56156	Oligonucleotide SE
834	12	80.0	21024	22	AAI05889	Human reproductive	c 907	11	73.3	13	23	ABH56157	Oligonucleotide SE
835	12	80.0	21024	22	AAK89248	Human digestive sy	c 908	11	73.3	19	21	AAA27545	Fas ligand promote
836	12	80.0	21024	23	ABL98453	Human testicular a	c 909	11	73.3	20	20	AAZ06144	PCR primer used to
837	12	80.0	21729	23	ABL06154	Drosophila melanog	c 910	11	73.3	20	24	ABL59023	Nucleotide sequenc
838	12	80.0	23142	21	AAK35158	Human adenosine re	c 911	11	73.3	20	24	ABK47106	Mouse OTS2-G2 reve
c 839	12	80.0	23532	21	AAK81455	N. meningitidis pa	c 912	11	73.3	23	22	AAH39057	SNP specific upper
c 840	12	80.0	25525	22	ABN19375	Human nervous syst	c 913	11	73.3	27	12	AAQ14480	Consensus tandem r
c 841	12	80.0	25975	22	AAI04955	Human reproductive	c 914	11	73.3	27	12	AAQ14496	Tandem repeat vari
c 842	12	80.0	25975	23	ABL97849	Human testicular a	c 915	11	73.3	27	18	AAH68284	Human flti VEGF re
c 843	12	80.0	26668	24	ABL67771	Oesophagus cancer	c 916	11	73.3	29	20	AAA22249	Integrin subunit b
844	12	80.0	27423	23	ABL04268	Drosophila melanog	c 917	11	73.3	29	20	AAK32249	Primer for amplif
c 845	12	80.0	28444	24	ABK86948	Human glutathione	c 918	11	73.3	29	20	AAK18665	Human p53 gene PCR
c 846	12	80.0	29376	23	ABL08834	Drosophila melanog	c 919	11	73.3	29	21	AAH06694	Hammerhead ribozym
847	12	80.0	30013	22	ABL36932	Human musculoskele	c 920	11	73.3	29	21	AAA04353	Polymorphic fragme
c 848	12	80.0	30013	22	AAS41960	Genomic sequence #	c 921	11	73.3	30	22	AAK87641	Human acetylcholin
849	12	80.0	30352	22	AAS36268	Human cardiovascular	c 922	11	73.3	30	22	AAC90394	Human acetylcholin
850	12	80.0	30417	21	AAF21282	Human low adenosin	c 923	11	73.3	32	19	AAV33214	Fibroblast growth
851	12	80.0	30417	21	AAK35160	Human adenosine re	c 924	11	73.3	32	22	AAC90675	Human FGF-13 PCR p
852	12	80.0	30568	22	AAI37486	Human musculoskele	c 925	11	73.3	33	22	AAI69982	Human peroxidase 1
853	12	80.0	32189	22	AAS30115	Human lung antigen	c 926	11	73.3	35	22	AAC90683	Human FGF-13 PCR p
854	12	80.0	32196	22	ABN18857	Human nervous syst	c 927	11	73.3	40	21	AAZ96111	Polynucleotide seq
855	12	80.0	32221	22	AAS30113	Human lung antigen	c 928	11	73.3	41	22	AAI69984	Human peroxidase 1
856	12	80.0	32222	22	AAS34734	Human DNA for a no	c 929	11	73.3	41	22	AAI69985	Human peroxidase 1
857	12	80.0	32367	19	AAV35620	Human SHOX (short	c 930	11	73.3	49	20	AAK88488	Human MIP-1 beta p
858	12	80.0	33472	23	ABL18792	Drosophila melanog	c 931	11	73.3	50	22	AAH44831	Probe used to dete
c 859	12	80.0	36194	23	ABL20582	Drosophila melanog	c 932	11	73.3	50	23	ABL01061	Human SNP involvin
c 860	12	80.0	39328	24	ABL91800	Human lipase endot	c 933	11	73.3	51	22	AAI27148	Human SNP oligonuc
861	12	80.0	42519	22	AAK81318	Human immune/haema	c 934	11	73.3	51	22	AAI29389	Human SNP oligonuc
c 862	12	80.0	43795	21	AAZ92583	Human DA2 genomic	c 935	11	73.3	52	16	AAI55554	Human rela hairpin
863	12	80.0	50000	20	AAK23517	Human kidney amino	c 936	11	73.3	60	24	ABN39619	Human spliced tran
864	12	80.0	50000	24	AAK26400	Human glutamate re	c 937	11	73.3	60	24	ABN44563	Human spliced tran
865	12	80.0	50000	24	AAK26437	Human GRM3 gene fr	c 938	11	73.3	65	24	ABN56975	Mouse spliced tran
866	12	80.0	50849	24	ABN87883	Human glutathione	c 939	11	73.3	66	16	AAI02938	Human glucose-6-ph
c 867	12	80.0	53500	21	AAS55842	Complete nucleotid	c 940	11	73.3	68	15	AAQ65989	COL2A1 5'-primer (
c 868	12	80.0	53552	22	AAS13655	Genomic DNA sequen	c 941	11	73.3	74	22	AAC90685	Human FGF-13 PCR p
869	12	80.0	54548	21	AAZ45596	DNA sequence of th	c 942	11	73.3	74	22	AAC90692	Human FGF-13 PCR p
c 870	12	80.0	65608	24	ABL62910	Breast cancer rela	c 943	11	73.3	74	22	AAC90695	Human FGF-13 PCR p
c 871	12	80.0	65608	24	ABL64414	Stomach cancer rel	c 944	11	73.3	81	16	AAI06211	HIV-1 reverse tran
c 872	12	80.0	65608	24	ABL67668	Oesophagus cancer	c 945	11	73.3	81	21	AAI19610	Human secreted pro
c 873	12	80.0	74037	24	ABK94412	DNA encoding endot	c 946	11	73.3	87	21	AAC19478	Human secreted pro
874	12	80.0	83946	21	ABQ88101	Human osteoblast d	c 947	11	73.3	93	21	AAC29544	Human secreted pro
875	12	80.0	101786	21	AAK22293	BAC containing rep	c 948	11	73.3	93	18	AAK49246	HVPI region of E2
c 876	12	80.0	107820	22	AAI16230	Human ATP-binding	c 949	11	73.3	96	20	AAV81027	De-immunised 340 v
c 877	12	80.0	112190	22	AAH44801	Human GPCR protein	c 950	11	73.3	104	20	AAH86705	Human single nucle
c 878	12	80.0	113515	24	ABL34175	Human immune syste	c 951	11	73.3	105	21	AAC81453	Chitin-binding apt
879	12	80.0	117574	24	AAI45288	Human KCNB1 gene.	c 952	11	73.3	108	19	AAI10384	Human foetal po
c 880	12	80.0	117574	24	AAI45288	Human KCNB1 gene.	c 953	11	73.3	112	22	ABX76653	Human foetal liver
881	12	80.0	125910	21	AAK64370	Human KCNQ5 (KCN6q	c 954	11	73.3	112	22	ABX41158	Probe #19624 for g
882	12	80.0	134525	11	AAQ04525	Total base sequenc	c 955	11	73.3	112	22	AAK25285	Human brain expres
c 883	12	80.0	134525	11	AAQ04525	Total base sequenc	c 956	11	73.3	112	22	AAK51292	Human bone marrow
c 884	12	80.0	160271	22	AAH85750	Bipolar affective	c 957	11	73.3	112	22	AAI28302	Probe #18235 for g
c 885	12	80.0	160271	22	AAH85756	Human chromosome 1	c 958	11	73.3	112	22	AAI57348	Probe #26034 used

c 959 11 73.3 112 24 ABS24832
 960 11 73.3 114 22 ABA75521
 961 11 73.3 114 22 ABA75521
 962 11 73.3 114 22 ABA40140
 963 11 73.3 114 22 AAK24095
 964 11 73.3 114 22 AAK50155
 965 11 73.3 114 22 AAI27237
 966 11 73.3 114 22 AAI56096
 967 11 73.3 115 24 ABL84209
 968 11 73.3 118 21 AAC29550
 969 11 73.3 120 23 ABV01834
 970 11 73.3 121 22 ABA77503
 971 11 73.3 121 22 ABA77504
 972 11 73.3 130 21 AAC20669
 973 11 73.3 135 22 ABA12275
 974 11 73.3 135 22 AAL09214
 975 11 73.3 136 19 AAV33218
 976 11 73.3 136 22 AAC90679
 977 11 73.3 144 23 ABV08426
 978 11 73.3 149 24 ABL75517
 979 11 73.3 150 21 AAC22340
 980 11 73.3 153 22 ABA49249
 981 11 73.3 153 22 ABA67167
 982 11 73.3 153 22 ABA34259
 983 11 73.3 153 22 AAK15609
 984 11 73.3 153 22 AAI22087
 985 11 73.3 153 22 AAI47382
 986 11 73.3 153 22 AAI07783
 987 11 73.3 153 24 ABS15349
 988 11 73.3 157 22 ABA75854
 989 11 73.3 157 22 ABA40420
 990 11 73.3 157 22 AAK24537
 991 11 73.3 157 22 AAK50526
 992 11 73.3 157 22 AAI27539
 993 11 73.3 157 22 AAI56511
 994 11 73.3 157 24 ABS24000
 995 11 73.3 158 22 ABA72255
 996 11 73.3 158 22 ABA38120
 997 11 73.3 158 22 AAK20676
 998 11 73.3 158 22 AAK46820
 999 11 73.3 158 22 AAI25754
 1000 11 73.3 158 22 AAI52660

ALIGNMENTS

RESULT 1
 ID AAH28085
 AC AAH28085;
 DT 05-SEP-2001 (first entry)
 DE Probe for human norepinephrine transporter gene A457P variant allele.
 KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
 KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
 KW amphetamine abuse; probe; ss.
 OS Homo sapiens.
 XX WO200148246-A1.
 PN 05-JUL-2001.
 PD 28-DEC-2000; 2000WO-US35491.
 PF 29-DEC-1999; 9905-0173682.
 PR 11-JAN-2000; 2000US-0175456.
 PS (UYVA-) UNIV VANDERBILT.

Human genome-deriv
 Human foetal liver
 Probe #18606 for g
 Human brain expres
 Human bone marrow
 Probe #17170 for g
 Probe #24782 used
 Human ovarian canc
 Human secreted pro
 p53 mutation exp
 p53 mutation corre
 Human secreted pro
 Human nervous syst
 Human breast canc
 Fibroblast growth
 Human FGF-13 PCR p
 Human prostate exp
 Corn tassal-deriv
 Human secreted pro
 Human breast cell
 Human foetal liver
 Probe #12725 for g
 Human brain expres
 Human bone marrow
 Probe #12020 for g
 Probe #16068 used
 Probe #7774 used t
 Human genome-deriv
 Human foetal liver
 Probe #18886 for g
 Human brain expres
 Human bone marrow
 Probe #17472 for g
 Probe #25197 used
 Human genome-deriv
 Human foetal liver
 Probe #16586 for g
 Human brain expres
 Human bone marrow
 Probe #15687 for g
 Probe #21346 used

XX Robertson D, Blakely RD;
 PI WPI; 2001-425681/45.
 XX Screening for susceptibility to sub-optimal norepinephrine transporter,
 XX particularly orthostatic intolerance in a subject by detecting a
 XX polymorphism of norepinephrine transporter gene -
 XX Claim 15; Page 69; 133pp; English.
 XX The present sequence represents a probe for the A457P variant allele of
 XX a human norepinephrine transporter gene. The specification a method
 XX for screening for susceptibility to sub-optimal norepinephrine transporter
 XX in a subject. The method comprises obtaining a biological sample from
 XX the subject and detecting a polymorphism of a norepinephrine transporter
 XX gene in the sample from the subject, the presence of the polymorphism
 XX indicating the susceptibility of the subject to sub-optimal
 XX norepinephrine transporter. The method is useful for screening for
 XX susceptibility of a subject to orthostatic intolerance. Norepinephrine
 XX transporter genes are useful for gene therapy for modulating
 XX norepinephrine transporter in a target cell and treating susceptibility
 XX to impaired norepinephrine transporter function, orthostatic intolerance
 XX or other relevant diseases in humans and animals such as mental illness,
 XX hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
 XX amphetamine abuse.
 XX Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other;
 SQ Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred No. 38;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTCTCCCTGTT 15
 Db 1 CCTTCTCCCTGTT 15
 RESULT 2
 AAC09241/c
 ID AAC09241 standard; cDNA; 352 BP.
 XX AAC09241;
 AC AAC09241;
 XX 06-OCT-2000 (first entry)
 DT Human secreted protein 5' EST, SEQ ID NO: 13316.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 KW Homo sapiens.
 OS EP1033401-A2.
 PN 06-SEP-2000.
 PD 21-FEB-2000; 2000EP-0200610.
 PF 26-FEB-1999; 9905-0122487.
 PR (GEST) GENSET.
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 PI WPI; 2000-500381/45.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 13316; 71pp + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

XX
 SQ Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;

Query Match 100.0%; Score 15; DB 21; Length 352;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGT 15
 |||||

Db 149 CCTTCTCCCGCTGT 135

RESULT 3
 ABV50337
 ID ABV50337 standard; cDNA; 445 BP.
 XX
 AC ABV50337;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 50328.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 9798; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX
 SQ Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;

Query Match 100.0%; Score 15; DB 23; Length 445;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGT 15
 |||||

Db 370 CCTTCTCCCGCTGT 384

RESULT 4
 AAS66052
 ID AAS66052 standard; cDNA; 549 BP.
 XX
 AC AAS66052;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #1856.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG01865.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 1856; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 549;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||

Db 423 CCTTCTCCCTGTT 437

RESULT 5

AAH04051/c
ID AAH04051 standard; cDNA; 827 BP.

XX AC AAH04051;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA clone (5'-primer) SEQ ID NO:886.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI; 2001-318749/34.

XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
full-length cDNAs defined in the specification, and for the detection
and/or diagnosis of the abnormality of the proteins encoded by the
full-length cDNAs -

XX PS Claim 1; SEQ ID 886; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dr primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesizing polynucleotides,
particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX SQ Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;

Query Match 100.0%; Score 15; DB 22; Length 827;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||

Db 123 CCTTCTCCCTGTT 109

RESULT 6

AAH15437/c
ID AAH15437 standard; cDNA; 1689 BP.

XX AC AAH15437;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA sequence SEQ ID NO:13660.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI; 2001-318749/34.

XX PS Claim 8; SEQ ID 13660; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dr primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesizing polynucleotides,
particularly full-length cDNAs. The primers are also useful for the

CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1689;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGTT 15
|||||

Db 123 CCTTCTCCCGCTGTT 109

RESULT 7

AAH28083
ID AAH28083 standard; cDNA; 1854 BP.

XX AC

XX AC

XX 05-SEP-2001 (first entry)

DE DNA encoding human norepinephrine transporter variant A457P.

KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.

XX Homo sapiens.

Key Location/Qualifiers
FT 1..1854
CDS /*tag= a

FT /*product= "norepinephrine transporter"

XX WO200148246-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35491.

XX 29-DEC-1999; 99US-0173682.

XX 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

XX Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

XX P-PSDB; AAB84533.

XX Screening for susceptibility to sub-optimal norepinephrine transporter,
XX particularly orthostatic intolerance in a subject by detecting a
XX polymorphism of norepinephrine transporter gene -

XX Claim 43; Page 104-108; 133pp; English.

XX The present sequence encodes a variant norepinephrine transporter. The
XX specification a method for screening for susceptibility to sub-optimal
XX norepinephrine (NE) transport in a subject. The method comprises
XX obtaining a biological sample from the subject and detecting a
XX polymorphism of a norepinephrine transporter gene in the sample from
XX the subject, the presence of the polymorphism indicating the
XX susceptibility of the subject to sub-optimal norepinephrine transporter.
XX The method is useful for screening for susceptibility of a subject to
XX orthostatic intolerance. Norepinephrine transporter genes are useful
XX for gene therapy for modulating norepinephrine transport in a target

CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.

XX Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGTT 15
|||||

Db 1362 CCTTCTCCCGCTGTT 1376

RESULT 8

AAH28087
ID AAH28087 standard; cDNA; 1854 BP.

XX AC

XX AAH28087;

XX 05-SEP-2001 (first entry)

DE DNA encoding human norepinephrine transporter variant.

KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.

XX Homo sapiens.

Key Location/Qualifiers
FT 1..1854
CDS /*tag= a

FT /*product= "norepinephrine transporter"

XX WO200148246-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35491.

XX 29-DEC-1999; 99US-0173682.

XX 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

XX Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

XX P-PSDB; AAB84533.

XX Screening for susceptibility to sub-optimal norepinephrine transporter,
XX particularly orthostatic intolerance in a subject by detecting a
XX polymorphism of norepinephrine transporter gene -

XX Claim 43; Page 119-121; 133pp; English.

XX The present sequence encodes a variant norepinephrine transporter. The
XX specification a method for screening for susceptibility to sub-optimal
XX norepinephrine (NE) transport in a subject. The method comprises
XX obtaining a biological sample from the subject and detecting a
XX polymorphism of a norepinephrine transporter gene in the sample from
XX the subject, the presence of the polymorphism indicating the
XX susceptibility of the subject to sub-optimal norepinephrine transport.
XX The method is useful for screening for susceptibility of a subject to
XX orthostatic intolerance. Norepinephrine transporter genes are useful
XX for gene therapy for modulating norepinephrine transport in a target
XX cell and treating susceptibility to impaired norepinephrine transporter
XX function, orthostatic intolerance or other relevant diseases in humans
XX and animals such as mental illness, hypertension, heart disease, psycho
XX stimulant abuse e.g. cocaine or amphetamine abuse.

```
XX SQ Sequence 1854 BP; 357 A; 554 C; 493 G; 450 T; 0 other;
Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
      |||||
Db 1362 CCTTCTCCCTGTT 1376

RESULT 9
ABK43728
ID ABK43728 standard; cDNA; 2159 BP.
XX
AC ABK43728;
XX
XX 05-JUN-2002 (first entry)
XX DNA encoding novel central nervous system protein #308.
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200155318-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-581633/65.

DR P-PSDB; AAU87398.

PT New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives -

PS Claim 1; SEQ ID No 318; 837pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (III) encoded
CC by (I), are used to treat a medical condition and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 100.0%; Score 15; DB 23; Length 2159;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
DB 1070 CCTTCTCCCCCTGTT 1084

RESULT 10

AAS83288/C

ID AAS83288 standard; cDNA; 2451 BP.

XX AAS83288;

AC AAS83288;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #19092.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG19101.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX Claim 1; SEQ ID No 19092; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 2451 BP; 670 A; 631 C; 671 G; 479 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 2451;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15

|||||

Db	164	CCTTCTCCCCCTGTT 150	
RESULT 11			
ABL90474			
ID	ABL90474	standard; cDNA; 2520 BP.	
XX	AC	ABL90474;	
XX	DT	24-MAY-2002 (first entry)	
XX	DE	Human polynucleotide SEQ ID NO 1036.	
XX	KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.	
OS	Homo sapiens.		
XX	PN	WO200190304-A2.	
XX	PD	29-NOV-2001.	
XX	PF	18-MAY-2001; 2001WO-US16450.	
XX	PR	19-MAY-2000; 2000US-205515P.	
XX	PR	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Birse CE, Rosen CA;	
XX	PI	WPI; 2002-122018/16.	
XX	DR	P-PSDB; ABB90065.	
XX	PT	Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders	
PS	Claim 4;	SEQ ID NO 1036; 208lpp + Sequence Listing; English.	
CC	The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.		
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
XX	Seq	Sequence 2520 BP; 583 A; 687 C; 623 G; 626 T; 1 other;	
Query Match 100.0%; Score 15; DB 24; Length 2520;			
Best Local Similarity 100.0%; Pred. No. 30;			
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CCTTCTCCCCCTGTT 15	
Db	1062	CCTTCTCCCCCTGTT 1076	

RESULT 12			
ABK44004/C			
ID	ABK44004	standard; cDNA; 2522 BP.	
XX	AC	ABK44004;	
XX	DT	05-JUN-2002 (first entry)	
XX	DE	DNA encoding novel central nervous system protein #584.	
XX	KW	Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.	
OS	Homo sapiens.		
XX	PN	WO200155318-A2.	
XX	PD	02-AUG-2001.	
XX	PF	17-JAN-2001; 2001WO-US01332.	
XX	PR	31-JAN-2000; 2000US-0179065.	
PR	PR	04-FEB-2000; 2000US-0180628.	
PR	PR	24-FEB-2000; 2000US-0184664.	
PR	PR	02-MAR-2000; 2000US-0186350.	
PR	PR	16-MAR-2000; 2000US-0189874.	
PR	PR	17-MAR-2000; 2000US-0190076.	
PR	PR	18-APR-2000; 2000US-0198123.	
PR	PR	19-MAY-2000; 2000US-0205515.	
PR	PR	07-JUN-2000; 2000US-0209467.	
PR	PR	28-JUN-2000; 2000US-0214886.	
PR	PR	30-JUN-2000; 2000US-0215135.	
PR	PR	07-JUL-2000; 2000US-0216647.	
PR	PR	11-JUL-2000; 2000US-0216880.	
PR	PR	11-JUL-2000; 2000US-0217487.	
PR	PR	14-JUL-2000; 2000US-0217496.	
PR	PR	26-JUL-2000; 2000US-0218290.	
PR	PR	26-JUL-2000; 2000US-0220963.	
PR	PR	14-AUG-2000; 2000US-0220964.	
PR	PR	14-AUG-2000; 2000US-0224518.	
PR	PR	14-AUG-2000; 2000US-0224519.	
PR	PR	14-AUG-2000; 2000US-0225213.	
PR	PR	14-AUG-2000; 2000US-0225214.	
PR	PR	14-AUG-2000; 2000US-0225266.	
PR	PR	14-AUG-2000; 2000US-0225267.	
PR	PR	14-AUG-2000; 2000US-0225268.	
PR	PR	14-AUG-2000; 2000US-0225270.	
PR	PR	14-AUG-2000; 2000US-0225447.	
PR	PR	14-AUG-2000; 2000US-0225757.	
PR	PR	14-AUG-2000; 2000US-0225758.	
PR	PR	18-AUG-2000; 2000US-0225759.	
PR	PR	18-AUG-2000; 2000US-0226279.	
PR	PR	22-AUG-2000; 2000US-0226681.	
PR	PR	22-AUG-2000; 2000US-0226868.	
PR	PR	22-AUG-2000; 2000US-0227182.	
PR	PR	23-AUG-2000; 2000US-0227009.	
PR	PR	30-AUG-2000; 2000US-0228924.	
PR	PR	01-SEP-2000; 2000US-0229287.	
PR	PR	01-SEP-2000; 2000US-0229343.	
PR	PR	01-SEP-2000; 2000US-0229344.	
PR	PR	01-SEP-2000; 2000US-0229345.	
PR	PR	05-SEP-2000; 2000US-0229509.	
PR	PR	05-SEP-2000; 2000US-0229513.	
PR	PR	06-SEP-2000; 2000US-0230437.	
PR	PR	06-SEP-2000; 2000US-0230438.	

PR	08-SEP-2000;	2000US-02312424.
PR	08-SEP-2000;	2000US-0231243.
PR	08-SEP-2000;	2000US-0231243.
PR	08-SEP-2000;	2000US-0231244.
PR	08-SEP-2000;	2000US-0231413.
PR	08-SEP-2000;	2000US-0231413.
PR	08-SEP-2000;	2000US-0231414.
PR	08-SEP-2000;	2000US-0232080.
PR	08-SEP-2000;	2000US-0232081.
PR	12-SEP-2000;	2000US-0231968.
PR	14-SEP-2000;	2000US-0232397.
PR	14-SEP-2000;	2000US-0232398.
PR	14-SEP-2000;	2000US-0232399.
PR	14-SEP-2000;	2000US-0232400.
PR	14-SEP-2000;	2000US-0232401.
PR	14-SEP-2000;	2000US-0233063.
PR	14-SEP-2000;	2000US-0233064.
PR	21-SEP-2000;	2000US-0233065.
PR	21-SEP-2000;	2000US-0234223.
PR	21-SEP-2000;	2000US-0234274.
PR	25-SEP-2000;	2000US-0234999.
PR	25-SEP-2000;	2000US-0234998.
PR	26-SEP-2000;	2000US-0235484.
PR	27-SEP-2000;	2000US-0235834.
PR	27-SEP-2000;	2000US-0235836.
PR	29-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	29-SEP-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	13-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	13-OCT-2000;	2000US-0239937.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0241221.
PR	20-OCT-2000;	2000US-0241182.
PR	20-OCT-2000;	2000US-0241785.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	01-NOV-2000;	2000US-0244182.
PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.

PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben	
DR	WPI; 2001-581633/65.	
DR	P-PSDB: AAU87674.	

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 594; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match	100.0%;	Score 15;	DB 23;	Length 2522;
Best Local Similarity	100.0%;	Pred. No. 30;		

Qy	1	CCTTCTCCCCCTGTT	15
Db	1460	CCTTCTCCCCCTGTT	1446

RESULT 13
 AAA16697
 ID AAA16697 standard; cDNA; 3580 BP.
 XX
 AC AAA16697;
 XX
 DT 16-JUN-2000 (first entry)

XX DE Human secreted protein clone as180_1 nucleotide sequence SEQ ID NO:159.
XX KW Human; secreted protein; immunestimulant; immunosuppressant; virucide;
KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
KW connective tissue disease; multiple sclerosis; erythematosis;
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
KW insulin dependent diabetes mellitus; graft-versus-host-disease;
KW autoimmune inflammatory eye disease; allergy; ss.
XX OS Homo sapiens.
XX KW WO200009552-A1.
XX PN 24-FEB-2000.
XX PD 13-AUG-1999; 99WO-US18298.
XX PF 14-AUG-1998; 98US-0096622.
XX PR 17-AUG-1998; 98US-0096815.
XX PR 04-SEP-1998; 98US-0099229.
XX PR 23-OCT-1998; 98US-0105368.
XX PR 08-JAN-1999; 99US-0115234.
XX PR 12-FEB-1999; 99US-0119931.
XX PR 18-FEB-1999; 99US-0120575.
XX PR 30-APR-1999; 99US-0132020.
XX PR 11-AUG-1999; 99US-0096622.
XX PA (GEMY) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Steininger RU, Spaulding V;
PI Wong GG, Clark HF, Fechtcl K;
XX WPI: 2000-205979/18.
XX P-PSDB: AAY94977.
XX New polynucleotides encoding secreted proteins, which may have e.g.
XX nutritional, chemokine, immune stimulating or suppressing,
XX hematopoiesis regulating, tissue growth, activin/inhibin
XX antiinflammatory or tumor inhibition activity
XX Claim 168; Page 613-614; 64lpp; English.
XX AAAL6618 to AAAL6697 encode the human secreted proteins given in
XX AAY94898 to AAY94980, isolated from human adult brain, adult thyroid,
XX adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,
XX adult placenta, adult testis, whole embryo, adult cartilage, kidney,
XX foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,
XX and adult bladder, cDNA libraries. The polynucleotides and proteins are
XX predicted to have biological activities which would make them suitable
XX for treating, preventing or ameliorating medical conditions in humans
XX and animals. The polynucleotides can be used as markers for tissues in
XX which the protein is preferentially expressed, as molecular weight
XX markers on Southern gels, and as chromosome markers or tags to identify
XX chromosomes or to map gene positions. The proteins can be used in the
XX treatment of immune deficiencies and disorders, such as severe combined
XX immunodeficiency (SCID), as well as viral, bacterial, fungal and other
XX infections. These infections include human immunodeficiency virus (HIV),
XX hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
XX candidiasis. The proteins can be used to treat autoimmune disorders such
XX as connective tissue disease, multiple sclerosis, systemic lupus
XX erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation,
XX Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
XX diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
XX autoimmune inflammatory eye disease. The proteins can also be used to
XX treat allergic conditions, such as asthma. AAAL6698 to AAAL6774 represent
XX probes for the human secreted proteins from the present invention.

SQ Sequence 3580 BP; 734 A; 942 C; 1024 G; 880 T; 0 other;
Query Match 100.0%; Score 15; DB 21; Length 3580;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCCCTGTT 15
Db 2528 CCTTCTCCCCCTGTT 2542
|||||
RESULT 14
ABK35630/c
ID ABK35630 standard; cDNA; 3580 BP.
XX AC ABK35630;
XX XX 08-MAY-2002 (first entry)
XX DE cDNA sequence #21 encoding novel human secreted protein.
XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
OS Homo sapiens.
XX WO200177289-A2.
XX PD 18-OCT-2001.
XX PF 29-MAR-2001; 2001WO-US10232.
XX PR 06-APR-2000; 2000US-195605P.
XX PA (GEMY) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fechtcl K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX WPI: 2002-179322/23.
XX PT Six hundred and twenty three polynucleotides derived from a variety of
XX human tissue sources which encode secreted proteins, useful for
XX treating immune deficiencies and disorders such as autoimmune disorders
XX Claim 1; Page 85-86; 393pp; English.
XX The present invention relates to the isolation of novel cDNA sequences
XX which encode human secreted proteins. The cDNA sequences have been
XX derived from a variety of human tissues. The invention also provides
XX a method for producing proteins from these polynucleotide sequences.
XX The proteins are useful for identifying compounds that modulate their
XX activity and production. The sequences of the invention are
XX useful for treating diseases such as hyperproliferative disorders
XX (e.g. cancer), immune deficiency disorders (e.g. severe combined
XX immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
XX sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
XX disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
XX allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
XX Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
XX haemophilia), and tumours. The polynucleotide sequences of the
XX invention are also useful in gene therapy. ABK35610-ABK36232 represent
XX the cDNA sequences of the invention that encode for novel human
XX secreted proteins.
SQ Sequence 3580 BP; 880 A; 1024 C; 942 G; 734 T; 0 other;
Query Match 100.0%; Score 15; DB 24; Length 3580;

Best Local Similarity 100.0%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 11, 2002, 17:09:57
Job time : 241 secs

QY 1 CCTTCTCCCGCTGTT 15
|||||

Db 1053 CCTTCTCCCGCTGTT 1039

RESULT 15

ABV22746/C

ID ABV22746 standard; cDNA; 4215 BP.

XX AC ABV22746;

XX XX

XX XX

XX 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 22737.

XX KW

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW

XX pharmacogenomic marker; gene; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200160860-A2.

XX PD

XX 23-AUG-2001.

XX PF

XX 20-FEB-2001; 2001WO-US05171.

XX PR

XX 17-FEB-2000; 2000US-183319P.

XX PR

XX 16-MAR-2000; 2000US-189862P.

XX PR

XX 25-MAY-2000; 2000US-207454P.

XX PR

XX 09-JUN-2000; 2000US-211314P.

XX PR

XX 18-JUL-2000; 2000US-219007P.

XX PR

XX 13-DEC-2000; 2000US-255281P.

XX PA

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI

XX Schlegel R, Endege WO, Monahan JE;

XX XX

XX WPI; 2001-662795/76.

XX DR

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX prostate cells and correlating with presence of prostate cancer, useful

XX for detecting presence of prostate cancer, stage of prostate cancer

XX Claim 1; Page 4005-4006; 11750pp; English.

XX PS

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX specification or its complement. (I) is useful for:

XX (a) assessing whether a patient is afflicted with prostate cancer;

XX (b) monitoring the progression of prostate cancer in a patient;

XX (c) assessing the efficacy of a test compound to inhibit prostate

XX cancer in a patient;

XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer

XX in a patient;

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX (f) assessing the prostate cell carcinogenic potential of a compound;

XX (g) determining whether prostate cancer has metastasized in a patient;

XX (h) assessing the aggressiveness or indolence of prostate cancer in a

XX patient;

XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ

XX Sequence 4215 BP; 1325 A; 808 C; 818 G; 1251 T; 13 other;

XX Query Match

XX Best Local Similarity 100.0%; Score 15; DB 23; Length 4215;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCGCTGTT 15

|||||

Db 166 CCTTCTCCCGCTGTT 152

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:59:33 : Search time 47 seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cctctcccccgttt 15

Scoring table: OLIGO_NUC

Gapop 50.0 , Gapext 50.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	86.7	776	US-09-484-970B-82	Sequence 82, Appl
2	13	86.7	1419	US-08-619-542B-29	Sequence 29, Appl
3	13	86.7	1905	US-09-295-744A-1	Sequence 1, Appl
4	13	86.7	2431	US-09-221-017B-351	Sequence 351, App
5	13	86.7	2687	US-08-149-695-8	Sequence 8, Appl
6	13	86.7	2687	US-08-377-228-8	Sequence 8, Appl
7	13	86.7	2873	US-08-149-695-1	Sequence 1, Appl
8	13	86.7	2873	US-08-377-228-1	Sequence 1, Appl
9	13	86.7	4287	US-08-244-189-1	Sequence 1, Appl
10	13	86.7	4287	US-08-306-691B-53	Sequence 53, Appl
11	13	86.7	4503	US-08-770-301A-2	Sequence 2, Appl
12	13	86.7	4503	US-09-175-581-2	Sequence 2, Appl
13	13	86.7	6032	US-09-295-744A-12	Sequence 12, Appl
14	13	86.7	55827	US-09-813-133A-3	Sequence 3, Appl
15	13	86.7	4411529	US-09-103-840A-1	Sequence 1, Appl
16	12	80.0	355	US-09-043-303-1	Sequence 1, Appl
17	12	80.0	621	US-09-328-111-414	Sequence 414, App
18	12	80.0	623	US-09-043-303-5	Sequence 5, Appl
19	12	80.0	732	US-08-145-006C-21	Sequence 8, Appl
20	12	80.0	732	US-08-145-006C-8	Sequence 21, Appl
21	12	80.0	732	US-08-145-006C-8	Sequence 8, Appl
22	12	80.0	732	US-08-145-006C-8	Sequence 22, Appl
23	12	80.0	1001	US-09-641-638-444	Sequence 444, App
24	12	80.0	1065	US-08-145-006C-11	Sequence 11, Appl
25	12	80.0	1074	US-08-975-316-54	Sequence 54, Appl
26	12	80.0	1074	US-09-615-192A-54	Sequence 54, Appl
27	12	80.0	1075	US-08-975-316-55	Sequence 55, Appl

Sequence 55, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 6, Appl
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Sequence 3, Appl
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Sequence 20, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 86, Appl
Sequence 2, Appl
Sequence 4, Appl
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Sequence 1, Appl
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Sequence 51, Appl
Sequence 18, Appl
Sequence 9, Appl
Sequence 8, Appl
Sequence 89, Appl
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Sequence 7, Appl
Sequence 7, Appl
Sequence 12, Appl
Sequence 101, App
Sequence 116, App
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
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Sequence 16, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 17, Appl
Sequence 1034, Ap
Sequence 6, Appl
Sequence 17, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 763, App
Sequence 28, Appl
Sequence 22, Appl
Sequence 230, App
Sequence 230, App
Sequence 23, Appl
Sequence 23, Appl
Sequence 167, App
Sequence 16, Appl
Sequence 55, Appl
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Sequence 174, App
Sequence 36, App
Sequence 35, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl

101	11	73.3	317	3	US-08-866-340-26	Sequence 26, Appl	c 174	11	73.3	1246	5	PCT-US93-10419-2	Sequence 2, Appli
102	11	73.3	317	4	US-09-103-875-32	Sequence 32, Appl	c 175	11	73.3	1248	5	PCT-US92-00331-2	Sequence 2, Appli
103	11	73.3	332	4	US-09-149-476-200	Sequence 200, App	176	11	73.3	1320	1	US-09-108-010B-3	Sequence 3, Appli
c 104	11	73.3	392	4	US-09-345-882-5	Sequence 5, Appli	177	11	73.3	1322	1	US-08-468-709B-5	Sequence 5, Appli
c 105	11	73.3	426	1	US-09-129-030-37	Sequence 37, Appl	178	11	73.3	1322	2	US-08-241-664B-5	Sequence 5, Appli
c 106	11	73.3	430	1	US-09-370-253-7	Sequence 7, Appli	179	11	73.3	1322	5	PCT-US93-03936-5	Sequence 5, Appli
c 107	11	73.3	439	4	US-09-397-787-308	Sequence 308, App	180	11	73.3	1323	4	US-03-651-200-9	Sequence 9, Appli
108	11	73.3	450	6	5437995-1	Patent No. 5437995	181	11	73.3	1374	4	US-08-482-746-9	Sequence 9, Appli
109	11	73.3	454	3	US-09-030-613-14	Sequence 14, Appl	182	11	73.3	1451	4	US-09-310-463-37	Sequence 37, Appl
110	11	73.3	454	3	US-09-451-905-14	Sequence 14, Appl	183	11	73.3	1498	3	US-09-173-581-14	Sequence 14, Appl
c 111	11	73.3	454	6	5175147-1	Patent No. 5175147	184	11	73.3	1498	4	US-09-420-915-14	Sequence 14, Appl
c 112	11	73.3	462	4	US-09-712-016-68	Sequence 68, Appl	185	11	73.3	1508	4	US-09-404-390-14	Sequence 14, Appl
c 113	11	73.3	463	4	US-09-132-316-52	Sequence 52, Appl	186	11	73.3	1514	1	US-08-381-433A-1	Sequence 1, Appli
c 114	11	73.3	474	4	US-09-149-476-13	Sequence 13, Appl	187	11	73.3	1539	3	US-09-058-725B-6	Sequence 6, Appli
c 115	11	73.3	499	6	5242821-2	Patent No. 5242821	188	11	73.3	1539	3	US-09-232-857-6	Sequence 13, Appl
116	11	73.3	500	4	US-09-328-111-5	Sequence 5, Appli	c 189	11	73.3	1549	4	US-09-206-344A-13	Sequence 13, Appl
117	11	73.3	501	2	US-08-483-695-2	Sequence 2, Appli	c 190	11	73.3	1560	4	US-09-453-702B-264	Sequence 264, App
118	11	73.3	501	2	US-07-965-285-2	Sequence 2, Appli	c 191	11	73.3	1572	2	US-08-933-750C-93	Sequence 93, Appl
119	11	73.3	501	2	US-08-487-231-2	Sequence 2, Appli	c 192	11	73.3	1572	3	US-09-234-613-93	Sequence 93, Appl
120	11	73.3	501	2	US-09-201-912-2	Sequence 2, Appli	c 193	11	73.3	1602	4	US-09-651-200-11	Sequence 11, Appl
c 121	11	73.3	546	4	US-09-046-479-3	Sequence 3, Appli	194	11	73.3	1626	1	US-08-381-433A-3	Sequence 3, Appli
c 122	11	73.3	546	4	US-08-822-897C-3	Sequence 3, Appli	c 195	11	73.3	1650	4	US-08-456-640-1	Sequence 1, Appli
c 123	11	73.3	550	4	US-08-991-789A-235	Sequence 235, App	c 196	11	73.3	1753	2	US-08-750-134A-8	Sequence 8, Appli
c 124	11	73.3	550	4	US-09-062-451-235	Sequence 235, App	c 197	11	73.3	1753	4	US-09-363-745-8	Sequence 8, Appli
c 125	11	73.3	550	4	US-09-598-328-235	Sequence 235, App	c 198	11	73.3	1753	3	US-09-035-706-1	Sequence 1, Appli
126	11	73.3	572	1	US-07-989-363-1	Sequence 1, Appli	c 199	11	73.3	1789	3	US-08-955-841-1	Sequence 1, Appli
127	11	73.3	572	1	US-08-264-526-1	Sequence 1, Appli	200	11	73.3	1789	3	US-09-428-219-3	Sequence 3, Appli
128	11	73.3	576	1	US-08-086-428B-2	Sequence 2, Appli	201	11	73.3	1789	4	US-09-390-425-1	Sequence 1, Appli
129	11	73.3	576	2	US-08-468-570-2	Sequence 2, Appli	202	11	73.3	1789	4	US-09-566-906-1	Sequence 1, Appli
130	11	73.3	576	2	US-08-290-665A-2	Sequence 2, Appli	203	11	73.3	1827	5	PCT-US95-05853-3	Sequence 3, Appli
131	11	73.3	576	5	PCT-US95-10398-2	Sequence 2, Appli	c 204	11	73.3	1837	5	PCT-US95-05853-3	Sequence 3, Appli
132	11	73.3	584	4	US-09-385-989-119	Sequence 119, App	c 205	11	73.3	1837	5	PCT-US95-05853-3	Sequence 3, Appli
c 133	11	73.3	600	4	US-09-462-561B-2	Sequence 2, Appli	c 206	11	73.3	1839	2	US-08-383-744-1	Sequence 1, Appli
c 134	11	73.3	638	4	US-09-098-628-3	Sequence 3, Appli	c 207	11	73.3	1839	2	US-08-399-336-1	Sequence 1, Appli
c 135	11	73.3	640	1	US-09-160-221A-1	Sequence 1, Appli	c 208	11	73.3	1839	5	PCT-US96-01427-1	Sequence 1, Appli
c 136	11	73.3	641	1	US-08-462-965A-1	Sequence 1, Appli	c 209	11	73.3	1844	4	US-09-123-912-88	Sequence 88, Appl
c 137	11	73.3	641	1	US-09-036-985A-1	Sequence 1, Appli	c 210	11	73.3	1844	4	US-09-643-597-88	Sequence 88, Appl
c 138	11	73.3	681	1	US-08-943-464-2	Sequence 2, Appli	c 211	11	73.3	1856	4	US-09-280-116-101	Sequence 101, App
c 139	11	73.3	683	1	US-08-998-416-1006	Sequence 1006, Ap	c 212	11	73.3	1870	1	US-08-592-126-86	Sequence 86, Appl
c 140	11	73.3	696	4	US-08-998-416-1006	Sequence 22, Appl	213	11	73.3	1875	3	US-09-258-373-21	Sequence 21, Appl
c 141	11	73.3	722	3	US-08-297-431B-22	Sequence 22, Appl	c 214	11	73.3	1933	3	US-08-974-380-1	Sequence 1, Appli
142	11	73.3	785	3	US-08-297-431B-21	Sequence 21, Appl	c 215	11	73.3	1950	3	US-08-685-466C-1	Sequence 1, Appli
143	11	73.3	868	3	US-08-889-502-20	Sequence 20, Appl	c 216	11	73.3	1956	1	US-08-318-831-7	Sequence 7, Appli
c 144	11	73.3	904	4	US-09-171-209-59	Sequence 59, Appl	c 217	11	73.3	1983	1	US-08-073-799C-9	Sequence 9, Appli
c 145	11	73.3	959	3	US-08-297-431B-1	Sequence 1, Appli	c 218	11	73.3	1994	3	US-08-600-982-22	Sequence 22, Appl
c 146	11	73.3	959	3	US-08-297-431B-5	Sequence 5, Appli	c 219	11	73.3	1994	5	PCT-US94-10261A-22	Sequence 22, Appl
c 147	11	73.3	959	3	US-08-297-431B-7	Sequence 7, Appli	c 220	11	73.3	2007	4	US-09-149-476-135	Sequence 135, App
c 148	11	73.3	959	3	US-08-297-431B-9	Sequence 9, Appli	c 221	11	73.3	2026	1	US-08-503-133A-1	Sequence 1, Appli
c 149	11	73.3	959	3	US-08-297-431B-13	Sequence 13, Appl	c 222	11	73.3	2026	2	US-08-576-775A-1	Sequence 1, Appli
c 150	11	73.3	959	3	US-08-297-431B-15	Sequence 15, Appl	c 223	11	73.3	2026	2	US-08-972-498-1	Sequence 1, Appli
c 151	11	73.3	959	3	US-08-297-431B-17	Sequence 17, Appl	c 224	11	73.3	2026	3	US-08-899-545-1	Sequence 1, Appli
c 152	11	73.3	959	3	US-08-297-431B-19	Sequence 19, Appl	c 225	11	73.3	2033	4	US-09-660-925B-10	Sequence 10, Appl
c 153	11	73.3	977	2	US-08-855-140-2	Sequence 2, Appli	c 226	11	73.3	2091	3	US-08-899-437-22	Sequence 22, Appl
154	11	73.3	1020	4	US-09-651-200-7	Sequence 7, Appli	c 227	11	73.3	2091	4	US-09-126-121-22	Sequence 22, Appl
155	11	73.3	1021	4	US-09-177-650-127	Sequence 127, App	c 228	11	73.3	2112	4	US-09-134-001C-178	Sequence 178, App
156	11	73.3	1024	4	US-08-806-164-78	Sequence 78, Appl	c 229	11	73.3	2118	2	US-08-619-362A-7	Sequence 7, Appli
157	11	73.3	1074	1	US-08-008-216-3	Sequence 3, Appli	c 230	11	73.3	2175	4	US-09-357-251-9	Sequence 9, Appli
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159	11	73.3	1074	1	US-08-458-831-3	Sequence 3, Appli	c 232	11	73.3	2193	1	US-08-731-716-3	Sequence 3, Appli
c 160	11	73.3	1095	1	US-08-097-828-4	Sequence 4, Appli	c 233	11	73.3	2193	1	US-08-731-716-3	Sequence 3, Appli
c 161	11	73.3	1095	1	US-08-480-756-4	Sequence 4, Appli	c 234	11	73.3	2193	1	US-08-420-235B-16	Sequence 16, Appl
c 162	11	73.3	1095	1	US-08-482-403-4	Sequence 4, Appli	c 235	11	73.3	2193	5	PCT-US95-10194-16	Sequence 16, Appl
c 163	11	73.3	1095	5	PCT-US92-00331-4	Sequence 4, Appli	c 236	11	73.3	2198	2	US-08-755-728-2	Sequence 2, Appli
c 164	11	73.3	1095	5	PCT-US93-10419-4	Sequence 4, Appli	c 237	11	73.3	2198	2	US-08-974-655-2	Sequence 2, Appli
165	11	73.3	1141	2	US-08-323-449B-1	Sequence 1, Appli	c 238	11	73.3	2198	4	US-09-283-011-2	Sequence 2, Appli
166	11	73.3	1141	2	US-08-485-981-1	Sequence 1, Appli	c 239	11	73.3	2224	4	US-08-477-347-2	Sequence 2, Appli
167	11	73.3	1141	2	US-08-867-087B-1	Sequence 1, Appli	c 240	11	73.3	2229	4	US-08-476-862-1	Sequence 1, Appli
168	11	73.3	1170	4	US-08-973-005A-9	Sequence 9, Appli	c 241	11	73.3	2238	1	US-07-841-651-1	Sequence 1, Appli
c 169	11	73.3	1192	4	US-09-142-565-1	Sequence 1, Appli	c 242	11	73.3	2267	4	US-09-660-925B-3	Sequence 3, Appli
170	11	73.3	1215	2	US-08-370-156-26	Sequence 26, Appl	c 243	11	73.3	2267	2	US-08-679-645-25	Sequence 25, Appl
c 171	11	73.3	1246	1	US-08-097-828-2	Sequence 2, Appli	c 244	11	73.3	2297	2	US-08-900-927-2	Sequence 2, Appli
c 172	11	73.3	1246	1	US-08-480-756-2	Sequence 2, Appli	c 245	11	73.3	2297	2	US-09-191-279-2	Sequence 2, Appli
c 173	11	73.3	1246	2	US-08-462-403-2	Sequence 2, Appli	c 246	11	73.3	2297	2	US-09-191-279-2	Sequence 2, Appli

c 247	11	73.3	2297	4	US-09-334-476-2	Sequence 2, Appl	320	11	73.3	4823	3	US-08-999-927-5	Sequence 5, Appl
c 248	11	73.3	2333	4	US-09-404-390-15	Sequence 15, Appl	321	11	73.3	4823	4	US-08-461-819-5	Sequence 5, Appl
c 249	11	73.3	2376	1	US-07-912-952-3	Sequence 3, Appl	322	11	73.3	4823	5	PCT-US94-08806-28	Sequence 28, Appl
c 250	11	73.3	2387	4	US-08-961-527-56	Sequence 56, Appl	323	11	73.3	4823	5	PCT-US95-01829-5	Sequence 5, Appl
c 251	11	73.3	2478	4	US-08-485-355B-47	Sequence 47, Appl	324	11	73.3	4823	5	PCT-US95-16626-5	Sequence 5, Appl
c 252	11	73.3	2478	4	US-08-485-355B-49	Sequence 49, Appl	325	11	73.3	4847	3	US-09-045-632-47	Sequence 47, Appl
c 253	11	73.3	2478	4	US-09-194-613-1	Sequence 1, Appl	326	11	73.3	4847	3	US-09-045-632-48	Sequence 48, Appl
c 254	11	73.3	2479	4	US-08-485-355B-51	Sequence 51, Appl	327	11	73.3	5100	1	US-08-164-292B-15	Sequence 15, Appl
c 255	11	73.3	2502	3	US-08-899-437-5	Sequence 5, Appl	328	11	73.3	5100	1	US-08-164-292B-17	Sequence 17, Appl
c 256	11	73.3	2502	4	US-09-126-121-5	Sequence 5, Appl	329	11	73.3	5100	1	US-08-164-292B-19	Sequence 19, Appl
c 257	11	73.3	2538	3	US-08-899-437-1	Sequence 1, Appl	330	11	73.3	5100	1	US-08-164-292B-21	Sequence 21, Appl
c 258	11	73.3	2538	4	US-09-126-121-1	Sequence 1, Appl	331	11	73.3	5100	1	US-08-164-292B-23	Sequence 23, Appl
c 259	11	73.3	2574	4	US-09-142-529-2	Sequence 2, Appl	332	11	73.3	5100	1	US-08-164-292B-25	Sequence 25, Appl
c 260	11	73.3	2580	2	US-08-887-798-1	Sequence 1, Appl	333	11	73.3	5100	3	US-08-845-623-15	Sequence 15, Appl
c 261	11	73.3	2596	4	US-09-336-447A-4	Sequence 4, Appl	334	11	73.3	5100	3	US-08-845-623-17	Sequence 17, Appl
c 262	11	73.3	2689	2	US-08-876-546A-15	Sequence 15, Appl	335	11	73.3	5100	3	US-08-845-623-19	Sequence 19, Appl
c 263	11	73.3	2889	4	US-09-412-252-15	Sequence 15, Appl	336	11	73.3	5100	3	US-08-845-623-21	Sequence 21, Appl
c 264	11	73.3	2891	4	US-09-651-200-1	Sequence 1, Appl	337	11	73.3	5100	3	US-08-845-623-23	Sequence 23, Appl
c 265	11	73.3	2763	1	US-08-176-413-1	Sequence 1, Appl	338	11	73.3	5100	3	US-08-845-623-25	Sequence 25, Appl
c 266	11	73.3	2763	2	US-08-612-542B-1	Sequence 1, Appl	339	11	73.3	5100	3	US-08-815-927-15	Sequence 15, Appl
c 267	11	73.3	2763	2	US-08-772-113-1	Sequence 1, Appl	340	11	73.3	5100	3	US-08-815-927-17	Sequence 17, Appl
c 268	11	73.3	2763	4	US-09-199-137-1	Sequence 1, Appl	341	11	73.3	5100	3	US-08-815-927-19	Sequence 19, Appl
c 269	11	73.3	2763	5	PCT-US94-14919-1	Sequence 1, Appl	342	11	73.3	5100	3	US-08-815-927-21	Sequence 21, Appl
c 270	11	73.3	2763	5	PCT-US94-14920-1	Sequence 1, Appl	343	11	73.3	5100	3	US-08-815-927-23	Sequence 23, Appl
c 271	11	73.3	2885	4	US-09-651-200-3	Sequence 3, Appl	344	11	73.3	5100	3	US-08-815-927-25	Sequence 25, Appl
c 272	11	73.3	2922	2	US-08-683-262B-74	Sequence 74, Appl	345	11	73.3	5100	4	US-09-103-330-15	Sequence 15, Appl
c 273	11	73.3	2922	4	US-09-361-707-74	Sequence 74, Appl	346	11	73.3	5100	4	US-09-103-330-17	Sequence 17, Appl
c 274	11	73.3	3000	1	US-08-393-985-3	Sequence 3, Appl	347	11	73.3	5100	4	US-09-103-330-19	Sequence 19, Appl
c 275	11	73.3	3066	1	US-08-142-439A-1	Sequence 1, Appl	348	11	73.3	5100	4	US-09-103-330-21	Sequence 21, Appl
c 276	11	73.3	3066	2	US-08-869-477-1	Sequence 1, Appl	349	11	73.3	5100	4	US-09-103-330-23	Sequence 23, Appl
c 277	11	73.3	3096	2	US-08-318-826A-6	Sequence 6, Appl	350	11	73.3	5100	4	US-09-103-330-25	Sequence 25, Appl
c 278	11	73.3	3096	2	US-08-370-156-3	Sequence 3, Appl	351	11	73.3	5100	4	US-09-435-242-15	Sequence 15, Appl
c 279	11	73.3	3129	4	US-08-814-095-3	Sequence 3, Appl	352	11	73.3	5100	4	US-09-435-242-17	Sequence 17, Appl
c 280	11	73.3	3129	4	US-09-387-695-1	Sequence 1, Appl	353	11	73.3	5100	4	US-09-435-242-19	Sequence 19, Appl
c 281	11	73.3	3507	1	US-08-315-468-3	Sequence 3, Appl	354	11	73.3	5100	4	US-09-435-242-21	Sequence 21, Appl
c 282	11	73.3	3528	1	US-08-286-889-36	Sequence 36, Appl	355	11	73.3	5100	4	US-09-435-242-23	Sequence 23, Appl
c 283	11	73.3	3528	1	US-08-485-618-36	Sequence 36, Appl	356	11	73.3	5100	4	US-09-435-242-25	Sequence 25, Appl
c 284	11	73.3	3528	1	US-08-362-652-36	Sequence 36, Appl	357	11	73.3	5152	4	US-09-690-364-10	Sequence 10, Appl
c 285	11	73.3	3528	1	US-08-605-672-36	Sequence 36, Appl	358	11	73.3	5159	2	US-08-146-930-3	Sequence 3, Appl
c 286	11	73.3	3528	2	US-08-482-293A-36	Sequence 36, Appl	359	11	73.3	5159	3	US-08-458-240-3	Sequence 3, Appl
c 287	11	73.3	3528	2	US-08-943-363-36	Sequence 36, Appl	360	11	73.3	5159	5	PCT-US93-03993-3	Sequence 3, Appl
c 288	11	73.3	3528	4	US-09-193-043-36	Sequence 36, Appl	c 361	11	73.3	5408	1	US-08-471-058-20	Sequence 20, Appl
c 289	11	73.3	3528	4	US-09-688-307A-36	Sequence 36, Appl	c 362	11	73.3	5408	3	US-08-471-057-20	Sequence 20, Appl
c 290	11	73.3	3539	4	US-08-853-948B-1	Sequence 1, Appl	c 363	11	73.3	5410	4	US-09-221-017B-70	Sequence 70, Appl
c 291	11	73.3	3597	1	US-08-485-618-54	Sequence 54, Appl	c 364	11	73.3	5470	1	US-08-441-139-12	Sequence 12, Appl
c 292	11	73.3	3597	1	US-08-362-652-54	Sequence 54, Appl	c 365	11	73.3	5470	6	5196523-5	Patent No. 5196523
c 293	11	73.3	3597	1	US-08-605-672-54	Sequence 54, Appl	c 366	11	73.3	5496	3	US-08-600-982-23	Sequence 23, Appl
c 294	11	73.3	3597	2	US-08-482-293A-54	Sequence 54, Appl	c 367	11	73.3	5496	5	PCT-US94-10261A-23	Sequence 23, Appl
c 295	11	73.3	3597	2	US-08-943-363-54	Sequence 54, Appl	c 368	11	73.3	5526	3	US-08-751-359-21	Sequence 21, Appl
c 296	11	73.3	3597	4	US-09-193-043-54	Sequence 54, Appl	c 369	11	73.3	5526	4	US-08-907-146-21	Sequence 21, Appl
c 297	11	73.3	3597	4	US-09-688-307A-54	Sequence 54, Appl	c 370	11	73.3	5746	2	US-08-637-759B-38	Sequence 38, Appl
c 298	11	73.3	3683	4	US-09-844-634-3	Sequence 3, Appl	c 371	11	73.3	5746	3	US-08-871-355A-38	Sequence 38, Appl
c 299	11	73.3	3710	4	US-07-741-453A-62	Sequence 62, Appl	c 372	11	73.3	5746	4	US-09-201-945-38	Sequence 38, Appl
c 300	11	73.3	3762	2	US-08-216-260-3	Sequence 3, Appl	c 373	11	73.3	5962	6	5386025-5	Patent No. 5386025
c 301	11	73.3	3789	1	US-08-454-455-5	Sequence 5, Appl	c 374	11	73.3	5975	1	US-08-404-354B-1	Sequence 1, Appl
c 302	11	73.3	4046	1	US-07-793-961A-1	Sequence 1, Appl	c 375	11	73.3	5975	1	US-08-314-083B-1	Sequence 1, Appl
c 303	11	73.3	4046	1	US-08-240-357-1	Sequence 1, Appl	c 376	11	73.3	5975	1	US-08-435-675B-1	Sequence 1, Appl
c 304	11	73.3	4091	4	US-08-630-915A-33	Sequence 33, Appl	c 377	11	73.3	5975	1	US-08-336-257A-3	Sequence 3, Appl
c 305	11	73.3	4112	1	US-08-340-203A-2	Sequence 2, Appl	c 378	11	73.3	5975	3	US-08-884-599-1	Sequence 1, Appl
c 306	11	73.3	4112	2	US-08-452-567-2	Sequence 2, Appl	c 379	11	73.3	6002	4	US-09-345-882-4	Sequence 4, Appl
c 307	11	73.3	4112	2	US-08-452-421-2	Sequence 2, Appl	c 380	11	73.3	6574	4	US-09-221-017B-1097	Sequence 1097, Ap
c 308	11	73.3	4112	3	US-09-085-407-2	Sequence 2, Appl	c 381	11	73.3	6709	4	US-09-285-601-3	Sequence 3, Appl
c 309	11	73.3	4294	1	US-08-152-483B-2	Sequence 2, Appl	c 382	11	73.3	6756	2	US-08-151-574-31	Sequence 31, Appl
c 310	11	73.3	4317	4	US-08-961-527-124	Sequence 124, App	c 383	11	73.3	6756	2	US-08-419-448-31	Sequence 31, Appl
c 311	11	73.3	4414	5	PCT-US95-04567-1	Sequence 1, Appl	c 384	11	73.3	6756	4	US-09-233-510-31	Sequence 31, Appl
c 312	11	73.3	4417	4	US-07-741-454A-57	Sequence 57, Appl	c 385	11	73.3	6803	3	US-08-665-259-19	Sequence 19, Appl
c 313	11	73.3	4616	2	US-08-340-203A-1	Sequence 1, Appl	c 386	11	73.3	6803	3	US-08-762-500-19	Sequence 19, Appl
c 314	11	73.3	4616	2	US-08-452-567-1	Sequence 1, Appl	c 387	11	73.3	7011	1	US-08-306-691B-42	Sequence 42, Appl
c 315	11	73.3	4616	2	US-08-452-421-1	Sequence 1, Appl	c 388	11	73.3	7301	4	US-09-816-088-3	Sequence 3, Appl
c 316	11	73.3	4616	2	US-09-085-407-1	Sequence 1, Appl	c 389	11	73.3	7319	4	US-09-221-017B-510	Sequence 510, App
c 317	11	73.3	4800	3	US-08-941-445A-4	Sequence 4, Appl	c 390	11	73.3	7571	4	US-08-961-527-16	Sequence 16, Appl
c 318	11	73.3	4823	2	US-08-457-254-5	Sequence 5, Appl	c 391	11	73.3	8411	4	US-08-961-527-16	Sequence 16, Appl
c 319	11	73.3	4823	2	US-08-484-257-20	Sequence 20, Appl	c 392	11	73.3	8501	3	US-08-793-900-1	Sequence 1, Appl

393	11	73.3	9541	4	US-08-961-527-132	Sequence 132, App	c 466	10	66.7	48	3	US-08-297-431B-26	Sequence 26, Appl
394	11	73.3	11384	4	US-08-961-527-45	Sequence 45, Appl	467	10	66.7	48	4	US-07-875-790B-4	Sequence 4, Appl
c 395	11	73.3	12284	2	US-08-876-991-1	Sequence 1, Appl	468	10	66.7	48	4	US-07-875-790B-5	Sequence 5, Appl
c 396	11	73.3	12284	2	US-09-059-853-1	Sequence 1, Appl	469	10	66.7	48	4	US-07-875-790B-6	Sequence 6, Appl
c 397	11	73.3	12732	4	US-09-060-756-1	Sequence 1, Appl	470	10	66.7	48	4	US-07-875-790B-7	Sequence 7, Appl
c 398	11	73.3	13965	4	US-09-453-702B-48	Sequence 48, Appl	471	10	66.7	48	4	US-07-875-790B-8	Sequence 8, Appl
c 399	11	73.3	14747	4	US-09-608-285A-42	Sequence 42, Appl	472	10	66.7	48	4	US-07-875-790B-9	Sequence 9, Appl
400	11	73.3	15602	4	US-09-844-634-17	Sequence 17, Appl	473	10	66.7	48	4	US-07-875-790B-9	Sequence 9, Appl
401	11	73.3	15977	4	US-09-608-285A-59	Sequence 59, Appl	c 474	10	66.7	50	3	US-08-985-162-1676	Sequence 1676, Ap
c 402	11	73.3	17606	4	US-08-943-731-4	Sequence 4, Appl	475	10	66.7	54	1	US-08-311-486C-1118	Sequence 1118, Ap
c 403	11	73.3	18627	4	US-08-961-527-113	Sequence 113, App	476	10	66.7	54	4	US-09-282-147-49	Sequence 49, Appl
c 404	11	73.3	19446	4	US-08-961-527-51	Sequence 51, Appl	c 477	10	66.7	54	4	US-08-584-040-8282	Sequence 8282, Ap
c 405	11	73.3	19446	4	US-08-961-527-51	Sequence 51, Appl	c 478	10	66.7	54	4	US-08-679-645-1150	Sequence 1150, Ap
c 406	11	73.3	20199	4	US-08-961-527-6	Sequence 6, Appl	c 479	10	66.7	60	4	US-08-538-526-3	Sequence 3, Appl
c 407	11	73.3	20303	1	US-08-370-975B-6	Sequence 6, Appl	c 480	10	66.7	64	2	US-08-205-428-24	Sequence 24, Appl
408	11	73.3	20710	1	US-08-420-235B-1	Sequence 1, Appl	c 481	10	66.7	66	2	US-08-868-162A-1	Sequence 1, Appl
409	11	73.3	20710	1	US-08-793-62A-1	Sequence 1, Appl	482	10	66.7	68	3	US-09-205-428-23	Sequence 23, Appl
410	11	73.3	20710	5	PCT-US95-10194-1	Sequence 1, Appl	483	10	66.7	81	4	US-08-477-928A-43	Sequence 43, Appl
411	11	73.3	21126	1	US-08-008-216-19	Sequence 19, Appl	484	10	66.7	84	2	US-08-426-599B-10	Sequence 10, Appl
412	11	73.3	21126	1	US-08-459-569-19	Sequence 19, Appl	485	10	66.7	90	4	US-08-943-731-10	Sequence 10, Appl
413	11	73.3	21126	1	US-08-458-831-19	Sequence 19, Appl	486	10	66.7	91	4	US-08-050-482A-19	Sequence 19, Appl
414	11	73.3	26700	1	US-08-472-217-1	Sequence 1, Appl	c 487	10	66.7	91	4	US-08-050-482A-20	Sequence 20, Appl
415	11	73.3	26700	2	US-08-488-199-5	Sequence 5, Appl	488	10	66.7	96	1	US-08-361-708-25	Sequence 25, Appl
416	11	73.3	26700	3	US-08-760-534A-1	Sequence 1, Appl	c 489	10	66.7	96	3	US-08-536-277-25	Sequence 25, Appl
c 417	11	73.3	26764	1	US-08-370-975B-1	Sequence 1, Appl	490	10	66.7	96	4	US-08-484-322-12	Sequence 12, Appl
418	11	73.3	34446	4	US-09-103-330-35	Sequence 35, Appl	491	10	66.7	97	3	US-09-342-681C-107	Sequence 107, App
419	11	73.3	35060	3	US-08-814-095-7	Sequence 7, Appl	492	10	66.7	100	4	US-09-106-638-6	Sequence 6, Appl
c 420	11	73.3	35060	3	US-08-814-095-7	Sequence 7, Appl	493	10	66.7	102	4	US-09-575-574-6	Sequence 6, Appl
421	11	73.3	35100	2	US-08-770-379-18	Sequence 18, Appl	494	10	66.7	109	1	US-08-943-731-9	Sequence 9, Appl
422	11	73.3	35100	4	US-08-757-669A-18	Sequence 18, Appl	c 495	10	66.7	110	1	US-07-640-476-3	Sequence 3, Appl
423	11	73.3	35100	4	US-09-230-370A-18	Sequence 18, Appl	496	10	66.7	110	1	US-08-487-890A-91	Sequence 91, Appl
424	11	73.3	49272	1	US-08-614-770A-1	Sequence 1, Appl	c 497	10	66.7	110	2	US-08-478-435-91	Sequence 91, Appl
c 425	11	73.3	61663	4	US-09-453-702B-62	Sequence 62, Appl	c 498	10	66.7	110	2	US-08-337-483-91	Sequence 91, Appl
c 426	11	73.3	61663	4	US-09-784-316-3	Sequence 3, Appl	c 499	10	66.7	110	2	US-08-478-373-91	Sequence 91, Appl
427	11	73.3	72928	3	US-09-009-913-1	Sequence 1, Appl	c 500	10	66.7	110	3	US-08-474-671-91	Sequence 91, Appl
c 428	11	73.3	72928	3	US-09-009-913-1	Sequence 1, Appl	c 501	10	66.7	110	3	US-08-483-577A-91	Sequence 91, Appl
c 429	11	73.3	81001	4	US-09-750-580-1	Sequence 1, Appl	c 502	10	66.7	110	4	US-09-037-990B-46	Sequence 46, Appl
c 430	11	73.3	90050	4	US-09-245-041-5	Sequence 5, Appl	c 503	10	66.7	110	4	US-09-037-990B-48	Sequence 48, Appl
c 431	11	73.3	162450	4	US-09-345-882-1	Sequence 1, Appl	c 504	10	66.7	110	4	US-08-897-438-91	Sequence 91, Appl
c 432	11	73.3	176373	3	US-09-128-155-17	Sequence 17, Appl	c 505	10	66.7	110	4	US-08-637-654-91	Sequence 91, Appl
c 433	11	73.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 506	10	66.7	116	1	US-08-649-518-91	Sequence 91, Appl
c 434	10	66.7	19	4	US-09-061-764A-3	Sequence 3, Appl	c 507	10	66.7	116	2	US-08-487-890A-89	Sequence 89, Appl
435	10	66.7	20	2	US-08-173-489C-18	Sequence 18, Appl	c 508	10	66.7	116	2	US-08-478-435-89	Sequence 89, Appl
436	10	66.7	20	4	US-08-961-810-64	Sequence 64, Appl	c 509	10	66.7	116	2	US-08-337-483-89	Sequence 89, Appl
437	10	66.7	20	4	US-08-352-902D-64	Sequence 64, Appl	c 510	10	66.7	116	3	US-08-478-373-89	Sequence 89, Appl
c 438	10	66.7	20	4	US-09-150-999-11	Sequence 11, Appl	c 511	10	66.7	116	3	US-08-474-671-89	Sequence 89, Appl
c 439	10	66.7	21	2	US-08-117-952-47	Sequence 47, Appl	c 512	10	66.7	116	4	US-08-897-438-89	Sequence 89, Appl
c 440	10	66.7	24	2	US-08-811-897A-53	Sequence 53, Appl	c 513	10	66.7	116	4	US-08-637-654-89	Sequence 89, Appl
c 441	10	66.7	24	2	US-08-855-213-53	Sequence 53, Appl	c 514	10	66.7	116	4	US-08-649-518-89	Sequence 89, Appl
c 442	10	66.7	24	4	US-09-201-47A-53	Sequence 53, Appl	c 515	10	66.7	119	1	US-08-487-890A-93	Sequence 93, Appl
c 443	10	66.7	25	1	US-08-153-848-55	Sequence 55, Appl	c 516	10	66.7	119	2	US-08-478-435-93	Sequence 93, Appl
c 444	10	66.7	25	3	US-09-299-843A-55	Sequence 55, Appl	c 517	10	66.7	119	2	US-08-337-483-93	Sequence 93, Appl
c 445	10	66.7	25	4	US-09-088-337B-55	Sequence 55, Appl	c 518	10	66.7	119	2	US-08-478-373-93	Sequence 93, Appl
c 446	10	66.7	25	5	PCT-US93-11153-55	Sequence 55, Appl	c 519	10	66.7	119	3	US-08-474-671-93	Sequence 93, Appl
447	10	66.7	26	1	US-08-379-078-554	Sequence 554, App	c 520	10	66.7	119	3	US-08-483-577A-93	Sequence 93, Appl
448	10	66.7	26	4	US-07-974-409C-177	Sequence 177, App	c 521	10	66.7	119	4	US-08-897-438-93	Sequence 93, Appl
449	10	66.7	26	5	PCT-US93-00977-177	Sequence 177, App	c 522	10	66.7	119	4	US-08-637-654-93	Sequence 93, Appl
450	10	66.7	31	3	US-08-431-0081B-9	Sequence 9, Appl	c 523	10	66.7	122	3	US-08-649-518-93	Sequence 93, Appl
451	10	66.7	31	3	US-08-608-016-9	Sequence 9, Appl	524	10	66.7	124	1	US-08-411-768B-19	Sequence 19, Appl
452	10	66.7	31	4	US-07-875-790B-16	Sequence 16, Appl	525	10	66.7	124	3	US-08-229-444B-3	Sequence 3, Appl
c 453	10	66.7	31	4	US-09-497-933A-9	Sequence 9, Appl	526	10	66.7	125	3	US-08-411-768B-17	Sequence 17, Appl
c 454	10	66.7	31	1	US-08-458-423A-8	Sequence 8, Appl	527	10	66.7	126	3	US-08-411-768B-20	Sequence 20, Appl
c 455	10	66.7	35	1	US-08-458-424B-8	Sequence 8, Appl	528	10	66.7	130	4	US-09-037-990B-18	Sequence 18, Appl
c 456	10	66.7	35	1	US-08-973-124-8	Sequence 8, Appl	529	10	66.7	131	4	US-09-037-990B-18	Sequence 18, Appl
c 457	10	66.7	35	4	PCT-US96-08014-8	Sequence 64, Appl	530	10	66.7	131	4	US-08-943-731-25	Sequence 25, Appl
458	10	66.7	38	1	US-08-049-264C-64	Sequence 64, Appl	531	10	66.7	132	2	US-08-479-577-1	Sequence 1, Appl
459	10	66.7	38	1	US-08-476-562-64	Sequence 64, Appl	532	10	66.7	132	2	US-08-756-977-1	Sequence 1, Appl
460	10	66.7	38	5	PCT-US94-04310-64	Sequence 64, Appl	533	10	66.7	132	5	PCT-US93-05331-5	Sequence 5, Appl
461	10	66.7	38	5	US-08-479-723A-64	Sequence 64, Appl	c 534	10	66.7	143	3	US-08-650-275-9	Sequence 9, Appl
462	10	66.7	39	4	US-08-961-810-103	Sequence 103, App	c 535	10	66.7	143	3	US-09-181-318-9	Sequence 9, Appl
463	10	66.7	39	4	US-08-352-902D-103	Sequence 103, App	536	10	66.7	180	4	US-09-575-574-1	Sequence 1, Appl
464	10	66.7	42	5	PCT-US92-10421-6	Sequence 6, Appl	537	10	66.7	185	4	US-08-905-223-163	Sequence 163, App
c 465	10	66.7	44	5	PCT-US92-10421-9	Sequence 9, Appl	538	10	66.7	200	1	US-07-623-953-6	Sequence 6, Appl

c 539	10	66.7	204	4	US-08-991-789A-23	Sequence 23, Appl	c 612	10	66.7	384	4	US-08-619-491-1	Sequence 1, Appl
c 540	10	66.7	204	4	US-09-062-451-23	Sequence 23, Appl	c 613	10	66.7	384	4	US-08-232-246A-14	Sequence 14, Appl
c 541	10	66.7	204	4	US-09-598-326-23	Sequence 23, Appl	c 614	10	66.7	384	4	US-08-475-815B-6	Sequence 6, Appl
c 542	10	66.7	215	4	US-09-177-650-103	Sequence 103, Appl	c 615	10	66.7	384	5	PCT-US95-07302-1	Sequence 1, Appl
c 543	10	66.7	218	4	US-08-943-731-41	Sequence 41, Appl	c 616	10	66.7	387	2	US-08-449-287-1	Sequence 1, Appl
c 544	10	66.7	240	4	US-09-116-032-28	Sequence 28, Appl	c 617	10	66.7	390	1	US-08-482-882-79	Sequence 79, Appl
c 545	10	66.7	241	4	US-09-470-191-71	Sequence 71, Appl	c 618	10	66.7	390	1	US-08-483-389-79	Sequence 79, Appl
c 546	10	66.7	246	1	US-08-165-304A-1	Sequence 1, Appl	c 619	10	66.7	390	2	US-08-487-113D-79	Sequence 79, Appl
c 547	10	66.7	249	1	US-08-439-132-1	Sequence 1, Appl	c 620	10	66.7	390	2	US-08-473-503-79	Sequence 79, Appl
c 548	10	66.7	249	6	5223407-1	Patent No. 5223407	c 621	10	66.7	390	2	US-08-483-933-79	Sequence 79, Appl
c 549	10	66.7	250	4	US-09-605-785-409	Sequence 409, App	c 622	10	66.7	390	2	US-08-720-420A-79	Sequence 79, Appl
c 550	10	66.7	250	4	US-09-439-313-409	Sequence 409, App	c 623	10	66.7	390	3	US-08-714-011-79	Sequence 79, Appl
c 551	10	66.7	250	4	US-09-352-616A-409	Sequence 409, App	c 624	10	66.7	390	3	US-08-475-680-79	Sequence 79, Appl
c 552	10	66.7	252	1	US-08-253-155A-6	Sequence 6, Appl	c 625	10	66.7	393	2	US-08-116-778B-39	Sequence 39, Appl
c 553	10	66.7	254	3	US-08-866-340-31	Sequence 31, Appl	c 626	10	66.7	393	2	US-08-438-562-39	Sequence 39, Appl
c 554	10	66.7	254	4	US-09-103-875-37	Sequence 37, Appl	c 627	10	66.7	393	2	US-08-483-528B-2	Sequence 2, Appl
c 555	10	66.7	284	4	US-08-905-223-219	Sequence 219, App	c 628	10	66.7	393	3	US-08-673-739C-2	Sequence 2, Appl
c 556	10	66.7	286	2	US-08-332-766A-6	Sequence 6, Appl	c 629	10	66.7	393	4	US-09-393-739B-2	Sequence 2, Appl
c 557	10	66.7	287	2	US-08-332-766A-27	Sequence 27, Appl	c 630	10	66.7	396	4	US-09-199-637A-396	Sequence 396, App
c 558	10	66.7	287	3	US-08-881-037-55	Sequence 55, Appl	c 631	10	66.7	400	1	US-08-301-718-1	Sequence 1, Appl
c 559	10	66.7	290	4	US-08-896-164-18	Sequence 18, Appl	c 632	10	66.7	401	4	US-09-221-298-38	Sequence 38, Appl
c 560	10	66.7	292	2	US-08-308-494A-12	Sequence 12, Appl	c 633	10	66.7	405	4	US-08-905-223-93	Sequence 38, Appl
c 561	10	66.7	292	4	US-09-280-028-3	Sequence 3, Appl	c 634	10	66.7	413	4	US-09-657-453A-23	Sequence 23, Appl
c 562	10	66.7	297	4	US-09-042-353-93	Sequence 93, Appl	c 635	10	66.7	415	4	US-09-615-192A-177	Sequence 177, App
c 563	10	66.7	297	4	US-08-758-417A-357	Sequence 357, App	c 636	10	66.7	416	1	US-07-653-091A-12	Sequence 12, Appl
c 564	10	66.7	300	2	US-08-308-494A-20	Sequence 20, Appl	c 637	10	66.7	416	1	US-08-485-068-12	Sequence 12, Appl
c 565	10	66.7	300	3	US-08-881-037-27	Sequence 27, Appl	c 638	10	66.7	416	1	US-08-481-598-12	Sequence 12, Appl
c 566	10	66.7	300	3	US-08-881-037-30	Sequence 30, Appl	c 639	10	66.7	416	2	US-08-483-353-12	Sequence 12, Appl
c 567	10	66.7	301	4	US-09-222-575-8	Sequence 8, Appl	c 640	10	66.7	416	2	US-08-473-702-12	Sequence 12, Appl
c 568	10	66.7	309	1	US-08-467-393-3	Sequence 3, Appl	c 641	10	66.7	420	1	US-08-470-179-108	Sequence 108, App
c 569	10	66.7	311	2	US-08-611-757-23	Sequence 23, Appl	c 642	10	66.7	420	2	US-08-726-306A-46	Sequence 46, Appl
c 570	10	66.7	311	5	PCT-US95-05980-23	Sequence 23, Appl	c 643	10	66.7	423	4	US-09-199-637A-394	Sequence 394, App
c 571	10	66.7	315	1	US-08-459-310-3	Sequence 3, Appl	c 644	10	66.7	434	2	US-08-997-080-50	Sequence 50, Appl
c 572	10	66.7	318	3	US-08-783-853A-104	Sequence 104, App	c 645	10	66.7	434	2	US-08-997-362-50	Sequence 50, Appl
c 573	10	66.7	318	4	US-09-344-050-104	Sequence 104, App	c 646	10	66.7	434	3	US-08-873-970-50	Sequence 50, Appl
c 574	10	66.7	321	3	US-08-783-853A-6	Sequence 6, Appl	c 647	10	66.7	434	4	US-09-095-855-50	Sequence 50, Appl
c 575	10	66.7	321	4	US-09-344-050-6	Sequence 6, Appl	c 648	10	66.7	434	4	US-08-705-347A-50	Sequence 50, Appl
c 576	10	66.7	322	3	US-08-434-000A-11	Sequence 11, Appl	c 649	10	66.7	434	4	US-09-324-543-50	Sequence 50, Appl
c 577	10	66.7	322	4	US-09-312-157-11	Sequence 11, Appl	c 650	10	66.7	434	4	US-09-205-426-50	Sequence 50, Appl
c 578	10	66.7	324	3	US-08-483-749A-7	Sequence 7, Appl	c 651	10	66.7	434	4	US-09-200-643-50	Sequence 50, Appl
c 579	10	66.7	324	3	US-08-881-037-56	Sequence 56, Appl	c 652	10	66.7	435	4	US-09-641-638-534	Sequence 534, App
c 580	10	66.7	330	1	US-08-207-996-28	Sequence 28, Appl	c 653	10	66.7	435	4	US-09-641-638-535	Sequence 535, App
c 581	10	66.7	330	2	US-08-760-840A-29	Sequence 29, Appl	c 654	10	66.7	435	4	US-09-641-638-536	Sequence 536, App
c 582	10	66.7	332	3	US-08-760-840A-31	Sequence 31, Appl	c 655	10	66.7	435	4	US-09-641-638-537	Sequence 537, App
c 583	10	66.7	330	3	US-09-266-119-29	Sequence 29, Appl	c 656	10	66.7	435	4	US-09-641-638-538	Sequence 538, App
c 584	10	66.7	330	3	US-09-266-119-31	Sequence 31, Appl	c 657	10	66.7	435	4	US-09-641-638-539	Sequence 539, App
c 585	10	66.7	330	4	US-09-602-709-29	Sequence 29, Appl	c 658	10	66.7	441	1	US-07-781-254A-8	Sequence 8, Appl
c 586	10	66.7	330	4	US-09-602-709-31	Sequence 31, Appl	c 659	10	66.7	441	1	US-08-149-091-4	Sequence 4, Appl
c 587	10	66.7	331	3	US-08-836-561-32	Sequence 32, Appl	c 660	10	66.7	441	2	US-08-637-761-4	Sequence 4, Appl
c 588	10	66.7	334	3	US-08-581-918A-24	Sequence 24, Appl	c 661	10	66.7	441	5	PCT-US94-12672-4	Sequence 4, Appl
c 589	10	66.7	334	4	US-08-346-147B-24	Sequence 24, Appl	c 662	10	66.7	442	4	US-09-397-787-325	Sequence 325, App
c 590	10	66.7	334	4	US-08-497-214D-24	Sequence 24, Appl	c 663	10	66.7	443	4	US-09-397-787-202	Sequence 202, App
c 591	10	66.7	334	4	US-09-311-625B-41	Sequence 41, Appl	c 664	10	66.7	443	4	US-09-397-787-281	Sequence 281, App
c 592	10	66.7	335	3	US-08-783-853A-102	Sequence 102, App	c 665	10	66.7	449	4	US-09-397-787-175	Sequence 175, App
c 593	10	66.7	335	4	US-09-344-050-102	Sequence 102, App	c 666	10	66.7	456	4	US-09-040-984-79	Sequence 79, Appl
c 594	10	66.7	344	2	US-08-875-972-17	Sequence 17, Appl	c 667	10	66.7	456	4	US-09-123-912-79	Sequence 79, Appl
c 595	10	66.7	347	4	US-09-397-787-309	Sequence 309, App	c 668	10	66.7	456	4	US-09-643-597-79	Sequence 79, Appl
c 596	10	66.7	357	4	US-09-171-945-8	Sequence 8, Appl	c 669	10	66.7	456	4	US-09-920-672-11	Sequence 11, Appl
c 597	10	66.7	359	3	US-09-184-658-6	Sequence 6, Appl	c 670	10	66.7	458	1	US-08-751-782-1	Sequence 1, Appl
c 598	10	66.7	366	4	US-09-380-190A-3	Sequence 3, Appl	c 671	10	66.7	458	2	US-08-925-171-1	Sequence 1, Appl
c 599	10	66.7	377	4	US-09-453-702B-139	Sequence 139, App	c 672	10	66.7	458	4	US-08-961-810-16	Sequence 16, Appl
c 600	10	66.7	380	4	US-09-037-990B-4	Sequence 4, Appl	c 673	10	66.7	458	4	US-08-352-902D-16	Sequence 16, Appl
c 601	10	66.7	381	4	US-09-037-990B-3	Sequence 3, Appl	c 674	10	66.7	461	1	US-08-454-720A-37	Sequence 37, Appl
c 602	10	66.7	384	1	US-07-634-278-30	Sequence 30, Appl	c 675	10	66.7	462	1	US-07-946-421-25	Sequence 25, Appl
c 603	10	66.7	384	1	US-08-477-728-30	Sequence 30, Appl	c 676	10	66.7	462	4	US-09-227-357-124	Sequence 124, App
c 604	10	66.7	384	1	US-08-474-040-30	Sequence 30, Appl	c 677	10	66.7	470	4	US-09-615-192A-149	Sequence 149, App
c 605	10	66.7	384	1	US-08-487-200-30	Sequence 30, Appl	c 678	10	66.7	474	1	US-07-730-853-2	Sequence 2, Appl
c 606	10	66.7	384	1	US-08-149-099C-6	Sequence 6, Appl	c 679	10	66.7	474	1	US-08-280-041-2	Sequence 2, Appl
c 607	10	66.7	384	1	US-08-476-275-3	Sequence 3, Appl	c 680	10	66.7	478	4	US-09-227-357-50	Sequence 50, Appl
c 608	10	66.7	384	2	US-08-656-586-1	Sequence 1, Appl	c 681	10	66.7	484	4	US-09-056-556-224	Sequence 224, App
c 609	10	66.7	384	2	US-08-478-967A-6	Sequence 6, Appl	c 682	10	66.7	484	4	US-09-072-596-219	Sequence 219, App
c 610	10	66.7	384	3	US-08-444-644-14	Sequence 14, Appl	c 683	10	66.7	487	4	US-09-380-190A-2	Sequence 2, Appl
c 611	10	66.7	384	4	US-08-484-537-30	Sequence 30, Appl	c 684	10	66.7	492	3	US-08-729-416C-12	Sequence 12, Appl

c 685	10	66.7	494	4	US-09-404-879A-196	Sequence 196, App	c 758	10	66.7	726	2	US-08-553-497A-27	Sequence 27, Appl
c 686	10	66.7	497	4	US-09-328-111-114	Sequence 114, App	c 759	10	66.7	726	4	US-09-134-001C-2656	Sequence 2656, Ap
c 687	10	66.7	500	4	US-09-575-57A-2	Sequence 2, Appl	c 760	10	66.7	732	4	US-08-553-497A-19	Sequence 19, Appl
c 688	10	66.7	500	4	US-09-370-838-269	Sequence 269, App	c 761	10	66.7	732	2	US-08-553-497A-21	Sequence 21, Appl
c 689	10	66.7	504	4	US-09-328-111-340	Sequence 340, App	c 762	10	66.7	732	2	US-08-860-882A-26	Sequence 26, Appl
c 690	10	66.7	504	4	US-09-328-111-104	Sequence 104, App	c 763	10	66.7	732	4	US-09-423-439-57	Sequence 57, Appl
c 691	10	66.7	517	4	US-09-052-469-4	Sequence 4, Appl1	c 764	10	66.7	732	4	US-08-965-087-1	Sequence 1, Appl1
c 692	10	66.7	531	4	US-08-991-789A-220	Sequence 220, App	c 765	10	66.7	732	4	US-09-011-769A-22	Sequence 22, Appl
c 693	10	66.7	531	4	US-09-062-451-220	Sequence 220, App	c 766	10	66.7	735	1	US-08-466-033-118	Sequence 118, App
c 694	10	66.7	531	4	US-09-598-326-220	Sequence 220, App	c 767	10	66.7	735	1	US-08-444-733-118	Sequence 118, App
c 695	10	66.7	535	4	US-09-603-785-596	Sequence 596, App	c 768	10	66.7	735	2	US-08-464-134-118	Sequence 118, App
c 696	10	66.7	552	1	US-08-149-091-3	Sequence 3, Appl1	c 769	10	66.7	735	2	US-08-461-361-118	Sequence 118, App
c 697	10	66.7	552	1	US-08-637-761-3	Sequence 3, Appl1	c 770	10	66.7	735	2	US-08-485-910-118	Sequence 118, App
c 698	10	66.7	552	5	PTC-US94-12672-3	Sequence 3, Appl1	c 771	10	66.7	735	4	US-09-502-653-11	Sequence 11, Appl
c 699	10	66.7	555	4	US-08-479-089A-4	Sequence 4, Appl1	c 772	10	66.7	738	2	US-08-553-497A-23	Sequence 23, Appl
c 700	10	66.7	561	4	US-09-392-184-28	Sequence 28, Appl	c 773	10	66.7	755	4	US-09-484-970B-158	Sequence 158, App
c 701	10	66.7	562	5	PTC-US92-03993-6	Sequence 6, Appl1	c 774	10	66.7	758	3	US-08-279-772A-5	Sequence 5, Appl1
c 702	10	66.7	564	3	US-08-545-809A-8	Sequence 8, Appl1	c 775	10	66.7	759	3	US-08-902-486-8	Sequence 8, Appl1
c 703	10	66.7	568	4	US-09-247-155-136	Sequence 136, App	c 776	10	66.7	765	4	US-08-861-774E-57	Sequence 57, Appl
c 704	10	66.7	569	4	US-09-276-531-69	Sequence 69, App	c 777	10	66.7	769	4	US-09-404-879A-320	Sequence 320, App
c 705	10	66.7	578	4	US-09-328-111-744	Sequence 744, App	c 778	10	66.7	778	3	US-09-188-930-27	Sequence 27, Appl
c 706	10	66.7	581	4	US-09-643-597-133	Sequence 133, App	c 779	10	66.7	778	3	US-09-188-930-202	Sequence 202, App
c 707	10	66.7	588	4	US-09-473-316A-105	Sequence 105, App	c 780	10	66.7	785	4	US-09-812-484-9	Sequence 9, Appl1
c 708	10	66.7	590	2	US-08-600-999-1	Sequence 1, Appl1	c 781	10	66.7	786	4	US-08-635-928-31	Sequence 31, Appl
c 709	10	66.7	591	2	US-08-481-814A-4	Sequence 4, Appl1	c 782	10	66.7	788	4	US-09-142-623-10	Sequence 10, Appl
c 710	10	66.7	591	4	US-09-385-982-77	Sequence 77, App	c 783	10	66.7	790	1	US-08-393-985-22	Sequence 22, Appl
c 711	10	66.7	591	4	US-09-602-877A-99	Sequence 89, Appl	c 784	10	66.7	795	2	US-08-967-101-119	Sequence 119, App
c 712	10	66.7	593	2	US-08-443-639-12	Sequence 12, Appl	c 785	10	66.7	796	2	US-08-592-541-119	Sequence 119, App
c 713	10	66.7	593	3	US-08-577-483-12	Sequence 12, Appl	c 786	10	66.7	796	3	US-09-124-698-119	Sequence 119, App
c 714	10	66.7	596	4	US-09-385-982-304	Sequence 304, App	c 787	10	66.7	796	4	US-09-127-480-119	Sequence 119, App
c 715	10	66.7	598	4	US-09-385-982-267	Sequence 267, App	c 788	10	66.7	796	4	US-08-496-841C-119	Sequence 119, App
c 716	10	66.7	602	4	US-09-385-982-369	Sequence 369, App	c 789	10	66.7	796	4	US-09-124-523-119	Sequence 119, App
c 717	10	66.7	603	2	US-08-924-838-6	Sequence 6, Appl1	c 790	10	66.7	801	4	US-09-276-531-111	Sequence 111, App
c 718	10	66.7	611	4	US-08-642-274D-16	Sequence 16, Appl	c 791	10	66.7	803	4	US-09-221-017B-684	Sequence 684, App
c 719	10	66.7	611	4	US-08-952-014C-16	Sequence 16, Appl	c 792	10	66.7	810	2	US-08-632-507-1	Sequence 1, Appl1
c 720	10	66.7	612	4	US-09-385-982-506	Sequence 506, App	c 793	10	66.7	811	3	US-08-961-083-63	Sequence 63, Appl
c 721	10	66.7	612	4	US-09-222-575-56	Sequence 56, Appl	c 794	10	66.7	815	4	US-08-998-416-441	Sequence 441, App
c 722	10	66.7	614	4	US-09-920-672-3	Sequence 3, Appl1	c 795	10	66.7	820	4	US-08-988-416-343	Sequence 343, App
c 723	10	66.7	616	4	US-09-289-349-5	Sequence 5, Appl1	c 796	10	66.7	825	2	US-08-486-148B-1	Sequence 1, Appl1
c 724	10	66.7	616	4	US-09-292-097-7	Sequence 7, Appl1	c 797	10	66.7	829	4	US-08-998-416-495	Sequence 495, App
c 725	10	66.7	617	4	US-09-328-111-138	Sequence 158, App	c 798	10	66.7	843	4	US-09-423-439-43	Sequence 43, Appl
c 726	10	66.7	624	2	US-08-426-599B-3	Sequence 3, Appl1	c 799	10	66.7	845	4	US-09-105-390-14	Sequence 14, Appl
c 727	10	66.7	625	4	US-09-328-111-734	Sequence 734, App	c 800	10	66.7	850	4	US-08-998-416-314	Sequence 314, App
c 728	10	66.7	631	4	US-09-385-982-322	Sequence 322, App	c 801	10	66.7	851	3	US-09-126-646-3	Sequence 3, Appl1
c 729	10	66.7	640	4	US-09-385-982-2	Sequence 2, Appl1	c 802	10	66.7	851	4	US-09-421-491-3	Sequence 3, Appl1
c 730	10	66.7	646	2	US-08-737-129A-3	Sequence 3, Appl1	c 803	10	66.7	853	2	US-08-179-557-19	Sequence 19, Appl
c 731	10	66.7	646	4	US-09-438-906-5	Sequence 5, Appl1	c 804	10	66.7	864	1	US-08-396-650-2	Sequence 2, Appl1
c 732	10	66.7	650	4	US-08-961-527-286	Sequence 286, App	c 805	10	66.7	864	1	US-08-768-626-2	Sequence 2, Appl1
c 733	10	66.7	663	1	US-08-555-394-18	Sequence 18, App	c 806	10	66.7	864	4	US-09-199-637A-392	Sequence 392, App
c 734	10	66.7	663	3	US-08-745-892-18	Sequence 18, App	c 807	10	66.7	866	4	US-09-257-583-6	Sequence 6, Appl1
c 735	10	66.7	672	2	US-08-190-199A-62	Sequence 62, Appl	c 808	10	66.7	872	3	US-08-581-148C-5	Sequence 5, Appl1
c 736	10	66.7	678	1	US-08-149-091-5	Sequence 5, Appl1	c 809	10	66.7	872	3	US-08-581-148C-6	Sequence 6, Appl1
c 737	10	66.7	678	2	US-08-637-761-5	Sequence 5, Appl1	c 810	10	66.7	874	3	US-08-462-436-1	Sequence 1, Appl1
c 738	10	66.7	678	5	PTC-US94-12672-5	Sequence 5, Appl1	c 811	10	66.7	874	3	US-08-465-275-1	Sequence 1, Appl1
c 739	10	66.7	680	4	US-09-056-285A-5	Sequence 5, Appl1	c 812	10	66.7	874	4	US-08-640-877-1	Sequence 1, Appl1
c 740	10	66.7	687	4	US-09-328-111-115	Sequence 115, App	c 813	10	66.7	879	4	US-09-605-785-531	Sequence 531, App
c 741	10	66.7	695	4	US-09-328-111-67	Sequence 67, App	c 814	10	66.7	879	4	US-09-439-313-531	Sequence 531, App
c 742	10	66.7	697	2	US-08-401-638-1	Sequence 1, Appl1	c 815	10	66.7	883	3	US-09-184-658-7	Sequence 7, Appl1
c 743	10	66.7	697	2	US-08-411-920-1	Sequence 1, Appl1	c 816	10	66.7	900	4	US-09-105-058C-3	Sequence 3, Appl1
c 744	10	66.7	704	3	US-09-048-889-7	Sequence 7, Appl1	c 817	10	66.7	909	4	US-09-228-986-67	Sequence 67, App
c 745	10	66.7	705	4	US-08-998-416-1080	Sequence 1080, Ap	c 818	10	66.7	910	4	US-09-221-017B-969	Sequence 969, App
c 746	10	66.7	705	4	US-09-171-945-16	Sequence 16, Appl	c 819	10	66.7	921	1	US-08-396-650-3	Sequence 3, Appl1
c 747	10	66.7	705	4	US-09-423-439-17	Sequence 17, Appl	c 820	10	66.7	921	1	US-08-396-650-4	Sequence 4, Appl1
c 748	10	66.7	711	1	US-08-061-092A-1	Sequence 1, Appl1	c 821	10	66.7	921	1	US-08-270-985-11	Sequence 11, Appl
c 749	10	66.7	711	2	US-08-190-199A-64	Sequence 64, Appl	c 822	10	66.7	921	1	US-08-768-626-3	Sequence 3, Appl1
c 750	10	66.7	711	2	US-08-468-252-4	Sequence 4, Appl1	c 823	10	66.7	921	1	US-08-768-626-4	Sequence 4, Appl1
c 751	10	66.7	711	3	US-08-668-706B-4	Sequence 4, Appl1	c 824	10	66.7	924	2	US-08-478-208-19	Sequence 19, Appl
c 752	10	66.7	711	5	PTC-US95-10740-4	Sequence 4, Appl1	c 825	10	66.7	924	3	US-08-860-174A-9	Sequence 9, Appl1
c 753	10	66.7	717	4	US-09-142-974B-1	Sequence 1, Appl1	c 826	10	66.7	930	4	US-09-171-025-26	Sequence 26, Appl
c 754	10	66.7	719	3	US-08-279-772A-7	Sequence 7, Appl1	c 827	10	66.7	934	4	US-09-171-025-3	Sequence 3, Appl1
c 755	10	66.7	720	3	US-08-902-486-10	Sequence 10, Appl	c 828	10	66.7	933	4	US-09-347-803-21	Sequence 21, Appl
c 756	10	66.7	720	4	US-08-913-014A-4	Sequence 4, Appl1	c 829	10	66.7	943	2	US-08-303-569B-4	Sequence 4, Appl1
c 757	10	66.7	726	2	US-08-553-497A-25	Sequence 25, Appl	c 830	10	66.7	943	2	US-08-116-247-4	Sequence 4, Appl1

c 831	10	66.7	951	1	US-08-221-750A-12	Sequence 12, Appl	c 904	10	66.7	1256	4	US-09-553-498-7	Sequence 7, Appl
c 832	10	66.7	952	4	US-08-943-731-87	Sequence 87, Appl	c 905	10	66.7	1256	4	US-09-618-869-7	Sequence 7, Appl
c 833	10	66.7	959	3	US-08-297-431B-11	Sequence 11, Appl	c 906	10	66.7	1257	4	US-08-791-115B-8	Sequence 8, Appl
c 834	10	66.7	969	4	US-08-346-147B-23	Sequence 23, Appl	c 907	10	66.7	1277	2	US-08-555-568B-18	Sequence 18, Appl
c 835	10	66.7	975	2	US-08-637-761-7	Sequence 7, Appl	c 908	10	66.7	1277	4	US-09-519-223-18	Sequence 18, Appl
c 836	10	66.7	975	5	PCT-US94-12672-7	Sequence 7, Appl	c 909	10	66.7	1281	3	US-09-063-893A-1	Sequence 1, Appl
c 837	10	66.7	980	4	US-09-171-209-8	Sequence 8, Appl	c 910	10	66.7	1281	4	US-09-082-092-7	Sequence 7, Appl
c 838	10	66.7	987	4	US-08-910-722-1	Sequence 1, Appl	c 911	10	66.7	1281	4	US-09-082-092-8	Sequence 8, Appl
c 839	10	66.7	987	4	US-09-457-568-27	Sequence 27, Appl	c 912	10	66.7	1288	2	US-09-172-977-2	Sequence 2, Appl
c 840	10	66.7	987	4	US-09-457-646-27	Sequence 27, Appl	c 913	10	66.7	1290	4	US-09-149-476-176	Sequence 176, App
c 841	10	66.7	987	4	US-09-370-838-289	Sequence 289, App	c 914	10	66.7	1302	3	US-08-932-823A-1	Sequence 1, Appl
c 842	10	66.7	994	2	US-08-627-610-1	Sequence 1, Appl	c 915	10	66.7	1314	4	US-09-242-737-1	Sequence 1, Appl
c 843	10	66.7	994	2	US-08-306-511A-1	Sequence 1, Appl	c 916	10	66.7	1320	4	US-09-210-748A-1	Sequence 1, Appl
c 844	10	66.7	994	2	US-08-993-274-1	Sequence 1, Appl	c 917	10	66.7	1322	4	US-09-128-450-27	Sequence 27, Appl
c 845	10	66.7	994	3	US-08-581-918A-1	Sequence 1, Appl	c 918	10	66.7	1322	4	US-09-823-494-27	Sequence 27, Appl
c 846	10	66.7	994	4	US-08-346-147B-1	Sequence 1, Appl	c 919	10	66.7	1329	3	US-09-296-284-23	Sequence 23, Appl
c 847	10	66.7	994	4	US-08-822-936-1	Sequence 1, Appl	c 920	10	66.7	1340	3	US-09-184-658-8	Sequence 8, Appl
c 848	10	66.7	994	4	US-08-497-214D-1	Sequence 1, Appl	c 921	10	66.7	1341	4	US-09-018-633-30	Sequence 30, Appl
c 849	10	66.7	994	5	PCT-US95-04636-1	Sequence 1, Appl	c 922	10	66.7	1345	1	US-08-592-214A-7	Sequence 7, Appl
c 850	10	66.7	999	2	US-08-860-174A-6	Sequence 6, Appl	c 923	10	66.7	1345	3	US-08-659-188-7	Sequence 7, Appl
c 851	10	66.7	999	4	US-09-171-025-25	Sequence 25, Appl	c 924	10	66.7	1345	3	US-08-655-227-7	Sequence 7, Appl
c 852	10	66.7	1000	4	US-09-128-450-25	Sequence 25, Appl	c 925	10	66.7	1345	3	US-08-655-241-7	Sequence 7, Appl
c 853	10	66.7	1000	4	US-09-823-494-25	Sequence 25, Appl	c 926	10	66.7	1345	3	US-09-149-976-7	Sequence 7, Appl
c 854	10	66.7	1001	4	US-09-641-638-320	Sequence 320, App	c 927	10	66.7	1345	4	US-09-386-328-5	Sequence 5, Appl
c 855	10	66.7	1011	4	US-09-134-001C-1342	Sequence 1342, App	c 928	10	66.7	1351	1	US-07-816-283-5	Sequence 5, Appl
c 856	10	66.7	1024	3	US-08-934-494-3	Sequence 3, Appl	c 929	10	66.7	1351	1	US-08-417-103-5	Sequence 5, Appl
c 857	10	66.7	1024	3	US-09-143-068-3	Sequence 3, Appl	c 930	10	66.7	1353	4	US-08-913-014A-6	Sequence 6, Appl
c 858	10	66.7	1024	4	US-09-143-707-3	Sequence 3, Appl	c 931	10	66.7	1357	4	US-09-448-176-9	Sequence 9, Appl
c 859	10	66.7	1024	4	US-09-202-089-3	Sequence 3, Appl	c 932	10	66.7	1357	4	US-09-448-176-10	Sequence 10, Appl
c 860	10	66.7	1024	4	US-09-511-133-3	Sequence 3, Appl	c 933	10	66.7	1357	4	US-09-448-176-11	Sequence 11, Appl
c 861	10	66.7	1024	4	US-09-690-169-3	Sequence 3, Appl	c 934	10	66.7	1359	1	US-08-275-488A-1	Sequence 1, Appl
c 862	10	66.7	1024	4	US-09-511-631-3	Sequence 3, Appl	c 935	10	66.7	1359	1	US-08-275-490-1	Sequence 1, Appl
c 863	10	66.7	1035	1	US-07-601-094-30	Sequence 30, Appl	c 936	10	66.7	1359	1	US-08-446-380-1	Sequence 1, Appl
c 864	10	66.7	1035	1	US-08-012-735-30	Sequence 30, Appl	c 937	10	66.7	1359	1	US-08-446-374-1	Sequence 1, Appl
c 865	10	66.7	1053	5	PCT-US91-06418-2	Sequence 2, Appl	c 938	10	66.7	1359	1	US-08-446-382-1	Sequence 1, Appl
c 866	10	66.7	1075	4	US-09-276-531-95	Sequence 95, Appl	c 939	10	66.7	1359	1	US-08-445-801-1	Sequence 1, Appl
c 867	10	66.7	1092	4	US-09-134-001C-1382	Sequence 1382, Ap	c 940	10	66.7	1359	1	US-08-275-487-1	Sequence 1, Appl
c 868	10	66.7	1094	2	US-08-902-294-1	Sequence 1, Appl	c 941	10	66.7	1359	3	US-08-227-496C-17	Sequence 17, Appl
c 869	10	66.7	1094	3	US-09-178-637-1	Sequence 1, Appl	c 942	10	66.7	1359	5	PCT-US95-08919-1	Sequence 1, Appl
c 870	10	66.7	1098	4	US-09-221-017B-928	Sequence 928, App	c 943	10	66.7	1362	1	US-08-275-488A-11	Sequence 11, Appl
c 871	10	66.7	1100	2	US-08-481-814A-5	Sequence 5, Appl	c 944	10	66.7	1362	1	US-08-275-490-11	Sequence 11, Appl
c 872	10	66.7	1102	4	US-09-641-638-586	Sequence 586, App	c 945	10	66.7	1362	1	US-08-446-380-11	Sequence 11, Appl
c 873	10	66.7	1108	5	PCT-US93-03035-1	Sequence 1, Appl	c 946	10	66.7	1362	1	US-08-446-374-11	Sequence 11, Appl
c 874	10	66.7	1111	4	US-09-221-017B-56	Sequence 56, Appl	c 947	10	66.7	1362	1	US-08-446-382-11	Sequence 11, Appl
c 875	10	66.7	1114	3	US-09-048-889-10	Sequence 10, Appl	c 948	10	66.7	1362	1	US-08-445-801-11	Sequence 11, Appl
c 876	10	66.7	1116	4	US-09-221-017B-125	Sequence 125, App	c 949	10	66.7	1362	1	US-08-275-487-11	Sequence 11, Appl
c 877	10	66.7	1128	1	US-07-872-678A-11	Sequence 11, Appl	c 950	10	66.7	1362	5	PCT-US95-08919-11	Sequence 11, Appl
c 878	10	66.7	1138	3	US-08-913-842-8	Sequence 8, Appl	c 951	10	66.7	1362	6	5290690-8	Patent No. 5290690
c 879	10	66.7	1147	1	US-08-417-103-15	Sequence 15, Appl	c 952	10	66.7	1365	1	US-08-114-072-1	Sequence 1, Appl
c 880	10	66.7	1168	4	US-09-149-476-79	Sequence 79, Appl	c 953	10	66.7	1365	5	PCT-US94-09361-1	Sequence 1, Appl
c 881	10	66.7	1170	2	US-08-933-750C-76	Sequence 76, Appl	c 954	10	66.7	1371	4	US-09-134-001C-517	Sequence 517, App
c 882	10	66.7	1170	3	US-09-234-613-76	Sequence 76, Appl	c 955	10	66.7	1386	4	US-09-433-248A-1	Sequence 1, Appl
c 883	10	66.7	1173	4	US-09-232-200-50	Sequence 50, Appl	c 956	10	66.7	1401	1	US-07-843-948A-3	Sequence 3, Appl
c 884	10	66.7	1173	4	US-09-232-197-50	Sequence 50, Appl	c 957	10	66.7	1401	2	US-08-218-978-3	Sequence 3, Appl
c 885	10	66.7	1173	4	US-09-232-201-50	Sequence 50, Appl	c 958	10	66.7	1407	1	US-08-278-630A-7	Sequence 7, Appl
c 886	10	66.7	1176	4	US-09-142-974B-3	Sequence 3, Appl	c 959	10	66.7	1407	2	US-08-879-260-1	Sequence 1, Appl
c 887	10	66.7	1188	1	US-08-048-700-1	Sequence 1, Appl	c 960	10	66.7	1409	6	5242798-6	Patent No. 5242798
c 888	10	66.7	1188	3	US-08-839-711-5	Sequence 5, Appl	c 961	10	66.7	1410	3	US-08-147-592A-1	Sequence 1, Appl
c 889	10	66.7	1191	2	US-08-968-751-5	Sequence 5, Appl	c 962	10	66.7	1410	4	US-08-292-694A-1	Sequence 1, Appl
c 890	10	66.7	1196	1	US-08-167-939A-5	Sequence 5, Appl	c 963	10	66.7	1416	1	US-08-236-311-3	Sequence 3, Appl
c 891	10	66.7	1196	1	US-08-567-538-5	Sequence 5, Appl	c 964	10	66.7	1416	3	US-08-457-918-3	Sequence 3, Appl
c 892	10	66.7	1204	4	US-08-861-774B-87	Sequence 87, Appl	c 965	10	66.7	1419	2	US-08-194-981E-4	Sequence 4, Appl
c 893	10	66.7	1213	4	US-08-976-259-7	Sequence 7, Appl	c 966	10	66.7	1419	4	US-09-276-531-1	Sequence 1, Appl
c 894	10	66.7	1215	1	US-08-696-139-1	Sequence 1, Appl	c 967	10	66.7	1425	3	US-08-729-416C-10	Sequence 10, Appl
c 895	10	66.7	1217	4	US-09-610-040-4	Sequence 4, Appl	c 968	10	66.7	1437	4	US-09-296-284-2	Sequence 2, Appl
c 896	10	66.7	1217	4	US-09-610-040-10	Sequence 10, Appl	c 969	10	66.7	1438	4	US-08-821-827C-1	Sequence 1, Appl
c 897	10	66.7	1225	2	US-08-674-149A-1	Sequence 1, Appl	c 970	10	66.7	1438	4	US-09-290-202B-1	Sequence 1, Appl
c 898	10	66.7	1233	4	US-09-276-531-7	Sequence 7, Appl	c 971	10	66.7	1443	1	US-08-443-965B-10	Sequence 10, Appl
c 899	10	66.7	1235	3	US-09-004-171-1	Sequence 1, Appl	c 972	10	66.7	1443	2	US-08-425-989B-10	Sequence 10, Appl
c 900	10	66.7	1245	1	US-07-887-072B-1	Sequence 1, Appl	c 973	10	66.7	1443	2	US-08-443-966B-10	Sequence 10, Appl
c 901	10	66.7	1245	1	US-08-466-444-1	Sequence 1, Appl	c 974	10	66.7	1446	2	US-08-484-126-2	Sequence 2, Appl
c 902	10	66.7	1246	1	US-09-302-769-22	Sequence 22, Appl	c 975	10	66.7	1451	1	US-08-161-286-2	Sequence 2, Appl
c 903	10	66.7	1251	4	US-09-105-537-38	Sequence 38, Appl	c 976	10	66.7	1452	4	US-09-039-982A-36	Sequence 36, Appl

c 977 10 66.7 1452 4 US-09-039-641-36 Sequence 36, Appl
c 978 10 66.7 1452 4 US-09-039-762A-36 Sequence 36, Appl
c 979 10 66.7 1452 4 US-09-042-492D-36 Sequence 36, Appl
c 980 10 66.7 1452 4 US-08-913-612A-36 Sequence 36, Appl
c 981 10 66.7 1455 1 US-08-446-803-5 Sequence 5, Appl
c 982 10 66.7 1455 2 US-08-861-837-5 Sequence 5, Appl
c 983 10 66.7 1455 3 US-08-600-650-5 Sequence 5, Appl
c 984 10 66.7 1455 4 US-09-170-670-10 Sequence 10, Appl
c 985 10 66.7 1455 4 US-09-170-670-15 Sequence 15, Appl
c 986 10 66.7 1455 4 US-09-193-068-10 Sequence 10, Appl
c 987 10 66.7 1455 4 US-09-193-068-14 Sequence 14, Appl
c 988 10 66.7 1455 4 US-09-183-412-10 Sequence 10, Appl
c 989 10 66.7 1455 4 US-09-183-412-14 Sequence 14, Appl
c 990 10 66.7 1455 4 US-09-354-191A-5 Sequence 5, Appl
c 991 10 66.7 1455 4 US-09-290-734-10 Sequence 10, Appl
c 992 10 66.7 1455 4 US-09-290-734-15 Sequence 15, Appl
c 993 10 66.7 1457 1 US-08-460-512-1 Sequence 1, Appl
c 994 10 66.7 1462 1 US-08-552-142A-16 Sequence 16, Appl
c 995 10 66.7 1470 4 US-09-099-041A-27 Sequence 27, Appl
c 996 10 66.7 1470 4 US-09-245-281-27 Sequence 27, Appl
c 997 10 66.7 1470 4 US-09-207-359B-27 Sequence 27, Appl
c 998 10 66.7 1479 1 US-08-644-271-31 Sequence 31, Appl
c 999 10 66.7 1479 4 US-09-077-955-35 Sequence 35, Appl
1000 10 66.7 1482 3 US-09-032-365A-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-484-970B-82
; Sequence 82, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmutch, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484, 970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 82
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 199069.2CB1
US-09-484-970B-82

Query Match 86.7%; Score 13; DB 4; Length 776;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTGT 15
| | | | |
DB 638 TTCTCCCTGTGT 650

RESULT 2
US-08-619-542B-29/c
; Sequence 29, Application US/08619542B
; Patent No. 5830662
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City
; APPLICANT: of New York
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
; TITLE OF INVENTION: CDNA LIBRARIES
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,542B
FILING DATE: June 21, 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 1419 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-08-619-542B-29

Query Match 86.7%; Score 13; DB 2; Length 1419;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 13

DB 1020 CCTTCTCCCTGT 1008

RESULT 3

US-09-295-744A-1

; Sequence 1, Application US/09295744A

; Patent No. 6355228

; GENERAL INFORMATION:

APPLICANT: Fuglsang, Claus Crone

TITLE OF INVENTION: An Oral Care Product Comprising A Mutan

Binding Domain

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6355228o No. 6355228disk of No. 6355228th America, Inc.

STREET: 405 Lexington Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/295,744A

FILING DATE: 20-Apr-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Rozek, Carol

REGISTRATION NUMBER: 36,993

REFERENCE/DOCKET NUMBER: 4735.204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Trichoderma harzianum CBS 243.71
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..120
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-295-744A-1

Query Match 86.7%; Score 13; DB 4; Length 1905;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCTGTT 14
|||||
DB 1568 CTTCTCCCTGTT 1580

RESULT 4
US-09-221-017B-351/c
Sequence 351, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA: PP1546
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: PP2911
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA: PCT/AU98/01023
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...2431
US-09-221-017B-351

Query Match 86.7%; Score 13; DB 4; Length 2431;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
|||||
DB 655 TTCTCCCTGTT 643

RESULT 5
US-08-149-695-8
Sequence 8, Application US/08149695
Patent No. 5412085
GENERAL INFORMATION:
APPLICANT: Allen, Rebecca L.

TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held and Malloy
STREET: 500 W. Madison, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,695
FILING DATE:

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/911,532
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:

NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32167
REFERENCE/DOCKET NUMBER: 92 P139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)707-8889
TELEFAX: (312)707-9155
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
STRAIN: Line W22
US-08-149-695-8

Query Match 86.7%; Score 13; DB 1; Length 2687;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15

Db 477 TTCTCCCCCTGTT 489

RESULT 6

US-08-377-228-8
; Sequence 8, Application US/08377228
; Patent No. 5545546
; GENERAL INFORMATION:
; APPLICANT: ALLEN, Rebecca L.
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,228
; FILING DATE: 24-JAN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,695
; FILING DATE: 09-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,532
; FILING DATE: 09-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/290/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2687 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-377-228-8

Query Match 86.7%; Score 13; DB 1; Length 2687;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCCCTGTT 15
Db 477 TTCTCCCCCTGTT 489

RESULT 7

US-08-149-695-1
; Sequence 1, Application US/08149695
; Patent No. 5412085
; GENERAL INFORMATION:
; APPLICANT: Allen, Rebecca L.
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held and Malloy
; STREET: 500 W. Madison, 34th Floor
; CITY: Chicago

; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,695
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/911,532
; FILING DATE: 09-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32167
; REFERENCE/DOCKET NUMBER: 92 P139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)707-8889
; TELEFAX: (312)707-9155
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: Line W22
; TISSUE TYPE: Pollen
US-08-149-695-1

Query Match 86.7%; Score 13; DB 1; Length 2873;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCCCTGTT 15
Db 663 TTCTCCCCCTGTT 675

RESULT 8

US-08-377-228-1
; Sequence 1, Application US/08377228
; Patent No. 5545546
; GENERAL INFORMATION:
; APPLICANT: ALLEN, Rebecca L.
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,228
; FILING DATE: 24-JAN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,695

;
; FILING DATE: 09-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,532
; FILING DATE: 09-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/290/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-377-228-1

Query Match 86.7%; Score 13; DB 1; Length 2873;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
|||||
Db 663 TTCTCCCTGTT 675

RESULT 9
US-08-244-189-1/c
; Sequence 1, Application US/08244189
; Patent No. 5580727
; GENERAL INFORMATION:
; APPLICANT: Ohki, Misao
; APPLICANT: Kikuchi, Kimiko
; APPLICANT: Miyoshi, Hiroyuki
; APPLICANT: Kozu, Tomoko
; TITLE OF INVENTION: No. 5580727el DNAs, Polypeptides Encoded Thereby
; TITLE OF INVENTION: and Methods for Detecting the DNAs and Polypeptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,189
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 760-183P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

;
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1579..3834
; US-08-244-189-1

Query Match 86.7%; Score 13; DB 1; Length 4287;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
|||||
Db 298 TTCTCCCTGTT 286

RESULT 10
US-08-306-691B-53/c
; Sequence 53, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-306-691B-53

Query Match 86.7%; Score 13; DB 1; Length 4287;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
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Db 298 TTCTCCCTGTT 286

RESULT 11
US-08-770-301A-2/c

; Sequence 2, Application US/08770301A
; Patent No. 5948637
; GENERAL INFORMATION:
; APPLICANT: IKEDA, JUN
; APPLICANT: KANEDA, SUMIKO
; APPLICANT: YANAGI, HIDEKI
; APPLICANT: MATSUMOTO, MASAYASU
; APPLICANT: YURA, TAKASHI
; TITLE OF INVENTION: NOVEL STRESS PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,301A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1422-287
; TELEPHONE: (703)-205-8000
; TELEFAX: (703)-205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4503 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; IDENTIFICATION METHOD: E
US-08-770-301A-2
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2923 CCTTCTCCCCCTG 2911
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; Sequence 2, Application US/09175581
; Patent No. 6034232
; GENERAL INFORMATION:
; APPLICANT: IKEDA, JUN
; APPLICANT: KANEDA, SUMIKO
; APPLICANT: YANAGI, HIDEKI
; APPLICANT: MATSUMOTO, MASAYASU
; APPLICANT: YURA, TAKASHI
; TITLE OF INVENTION: NOVEL STRESS PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/175,581
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,301
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1422-287
; TELEPHONE: (703)-205-8000
; TELEFAX: (703)-205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4503 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; IDENTIFICATION METHOD: E
US-09-175-581-2
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 12, Application US/09295744A
; Patent No. 6355228
; GENERAL INFORMATION:
; APPLICANT: Fudlsang, Claus Crone
; TITLE OF INVENTION: An Oral Care Product Comprising A Mutan
; Binding Domain
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6355228o No. 6355228disk of No. 6355228th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/295,744A
; FILING DATE: 20-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4735.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 6032 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Trichoderma harzianum CBS 243.71
FEATURE:
NAME/KEY: CDS
LOCATION: 3188..5092
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-295-744A-12

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Best Local Similarity 100.0%; Pred. No. 36;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-09-813-133A-3/c
; Sequence 3, Application US/09813133A
; Patent No. 6455294

; GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001173

; CURRENT APPLICATION NUMBER: US/09/813,133A

; CURRENT FILING DATE: 2001-06-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 55827

; TYPE: DNA

; ORGANISM: Human

US-09-813-133A-3

Query Match

Best Local Similarity 86.7%; Score 13; DB 4; Length 55827;

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RESULT 15

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37RV

US-09-103-840A-1

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Best Local Similarity 100.0%; Pred. No. 27;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	14	93.3	594	10	US-09-864-761-13104
6	14	93.3	8894	10	US-09-764-864-1692
7	14	93.3	8894	10	US-09-764-877-3063
8	14	93.3	16877	10	US-09-764-877-3349
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11	13	86.7	210	10	US-09-833-263-616
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16	13	86.7	383	10	US-09-880-107-1077
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c 93	12	80.0	635	10	US-09-878-574-4564	Sequence 4564, Ap	c 166	11	73.3	166	10	US-09-878-574-8838	Sequence 8838, Ap
c 94	12	80.0	686	10	US-09-764-870-189	Sequence 189, App	167	11	73.3	171	10	US-09-864-761-18715	Sequence 18715, A
c 95	12	80.0	787	10	US-09-853-386-122	Sequence 122, App	168	11	73.3	174	10	US-09-864-761-31719	Sequence 31719, A
c 96	12	80.0	791	10	US-09-861-893-36	Sequence 36, Appl	169	11	73.3	180	10	US-09-864-761-17125	Sequence 17125, A
c 97	12	80.0	899	10	US-09-920-345-9	Sequence 9, Appl	c 170	11	73.3	195	10	US-09-998-598-1826	Sequence 1826, Ap
c 98	12	80.0	936	10	US-09-974-300-836	Sequence 836, App	171	11	73.3	195	12	US-10-033-528-1847	Sequence 1847, Ap
c 99	12	80.0	970	10	US-09-974-300-1871	Sequence 1871, Ap	172	11	73.3	209	10	US-09-864-761-21470	Sequence 21470, A
c 100	12	80.0	987	10	US-09-738-396-41	Sequence 41, Appl	173	11	73.3	216	10	US-09-974-300-7574	Sequence 7574, Ap
c 101	12	80.0	1012	10	US-09-864-761-17503	Sequence 17503, A	174	11	73.3	233	10	US-09-752-639-3	Sequence 3, Appl
c 102	12	80.0	1101	10	US-09-801-368-253	Sequence 253, App	175	11	73.3	233	10	US-09-984-198-3	Sequence 3, Appl
c 103	12	80.0	1274	9	US-09-981-876-72	Sequence 72, Appl	c 176	11	73.3	234	10	US-09-815-343-84	Sequence 84, Appl
c 104	12	80.0	1296	9	US-09-981-876-126	Sequence 126, App	c 177	11	73.3	235	10	US-09-783-590-2146	Sequence 2146, Ap
c 105	12	80.0	1343	10	US-09-925-300-779	Sequence 779, App	178	11	73.3	235	10	US-09-867-701-8842	Sequence 8842, Ap
c 106	12	80.0	1346	10	US-09-728-952-77	Sequence 77, Appl	179	11	73.3	236	10	US-09-923-876-2115	Sequence 2115, Ap
c 107	12	80.0	1486	10	US-09-925-302-247	Sequence 247, App	180	11	73.3	236	10	US-09-843-856-24	Sequence 24, Appl
c 108	12	80.0	1584	10	US-09-974-300-231	Sequence 231, App	181	11	73.3	240	10	US-09-923-876-5718	Sequence 5718, Ap
c 109	12	80.0	1622	10	US-09-864-864-303	Sequence 303, App	182	11	73.3	242	10	US-09-920-345-23	Sequence 23, Appl
c 110	12	80.0	1652	10	US-09-938-803-23	Sequence 23, Appl	183	11	73.3	254	10	US-09-908-711-44	Sequence 44, Appl
c 111	12	80.0	1657	10	US-09-764-870-28	Sequence 28, Appl	184	11	73.3	254	10	US-09-867-701-8876	Sequence 8876, Ap
c 112	12	80.0	1715	10	US-09-917-800A-1631	Sequence 1631, Ap	185	11	73.3	256	10	US-09-923-876-656	Sequence 656, App
c 113	12	80.0	1756	10	US-09-925-297-221	Sequence 221, App	186	11	73.3	258	10	US-09-923-876-2314	Sequence 2314, Ap
c 114	12	80.0	2100	10	US-09-799-777-94	Sequence 94, Appl	187	11	73.3	260	10	US-09-783-590-2807	Sequence 2807, Ap
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c 117	12	80.0	2590	10	US-09-908-988B-3	Sequence 3, Appl	190	11	73.3	261	9	US-09-902-941-405	Sequence 405, App
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c 119	12	80.0	2680	10	US-09-782-378A-20	Sequence 20, Appl	192	11	73.3	261	9	US-09-867-701-7801	Sequence 7801, Ap
c 120	12	80.0	2770	10	US-09-977-269-5	Sequence 5, Appl	193	11	73.3	264	10	US-09-878-574-6353	Sequence 6353, Ap
c 121	12	80.0	3394	10	US-09-880-107-2178	Sequence 5, Appl	194	11	73.3	265	10	US-09-867-701-1171	Sequence 1171, Ap
c 122	12	80.0	3622	12	US-10-002-600-5	Sequence 5, Appl	195	11	73.3	285	10	US-09-983-965-3168	Sequence 3168, Ap
c 123	12	80.0	4152	10	US-10-044-090-493	Sequence 493, App	196	11	73.3	287	10	US-09-878-574-7886	Sequence 7886, Ap
c 124	12	80.0	4620	10	US-09-925-300-359	Sequence 359, App	197	11	73.3	268	10	US-09-878-574-7148	Sequence 7148, Ap
c 125	12	80.0	5230	10	US-09-880-253A-60	Sequence 60, Appl	198	11	73.3	276	10	US-09-815-343-800	Sequence 800, App
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c 137	12	80.0	19345	10	US-09-962-832-222	Sequence 222, App	210	11	73.3	302	10	US-09-974-300-3463	Sequence 3463, Ap
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c 139	12	80.0	30013	10	US-09-962-832-222	Sequence 222, App	212	11	73.3	310	10	US-09-833-381-317	Sequence 317, App
c 140	12	80.0	30352	10	US-09-764-877-3297	Sequence 3297, App	213	11	73.3	316	10	US-09-878-574-13656	Sequence 13656, A
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c 142	12	80.0	30568	10	US-09-764-877-3851	Sequence 3851, Ap	215	11	73.3	322	10	US-09-783-590-6936	Sequence 6936, Ap
c 143	12	80.0	32189	10	US-09-764-878-379	Sequence 379, App	216	11	73.3	325	10	US-09-867-701-4951	Sequence 4951, Ap
c 144	12	80.0	32221	10	US-09-764-878-377	Sequence 377, App	217	11	73.3	326	10	US-09-728-445-78	Sequence 78, Appl
c 145	12	80.0	33332	10	US-09-801-861-3	Sequence 3, Appl	218	11	73.3	334	10	US-09-925-299-422	Sequence 422, App
c 146	12	80.0	53542	10	US-09-801-574-61	Sequence 61, Appl	219	11	73.3	335	9	US-10-040-739-749	Sequence 749, App
c 147	12	80.0	63000	10	US-09-780-172-18	Sequence 18, Appl	220	11	73.3	335	9	US-09-864-761-22350	Sequence 22350, A
c 148	12	80.0	65608	9	US-09-954-531-180	Sequence 180, App	221	11	73.3	337	10	US-09-099-823-3	Sequence 3, Appl
c 149	12	80.0	65608	10	US-09-962-436-292	Sequence 292, App	222	11	73.3	339	10	US-09-867-701-9248	Sequence 9248, Ap
c 150	12	80.0	65608	10	US-09-962-832-119	Sequence 119, App	223	11	73.3	345	10	US-09-983-965-4371	Sequence 4371, Ap
c 151	12	80.0	111282	12	US-10-094-989-3	Sequence 3, Appl	224	11	73.3	348	10	US-09-867-701-3917	Sequence 3917, Ap
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c 153	12	80.0	173808	12	US-10-003-806-10	Sequence 10, Appl	226	11	73.3	351	9	US-09-974-300-3758	Sequence 3758, Ap
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c 156	11	73.3	24	10	US-09-885-441-40	Sequence 40, Appl	229	11	73.3	359	10	US-09-878-574-3336	Sequence 3336, Ap
c 157	11	73.3	29	10	US-09-989-441-17	Sequence 17, Appl	230	11	73.3	361	10	US-09-954-456-216	Sequence 216, App
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c 160	11	73.3	115	10	US-09-867-701-1787	Sequence 1787, Ap	233	11	73.3	367	10	US-09-867-701-6005	Sequence 6005, App
c 161	11	73.3	149	10	US-09-904-093B-4891	Sequence 4891, Ap	234	11	73.3	370	10	US-09-960-352-4081	Sequence 4081, Ap
c 162	11	73.3	149	10	US-09-923-876-3663	Sequence 3663, Ap	235	11	73.3	378	9	US-09-954-531-57	Sequence 57, Appl
c 163	11	73.3	153	10	US-09-864-761-19579	Sequence 19579, A	236	11	73.3	378	9	US-09-954-531-236	Sequence 236, App
c 164	11	73.3	157	10	US-09-864-761-25740	Sequence 25740, A	237	11	73.3				
c 165	11	73.3	158	10	US-09-864-761-23440	Sequence 23440, A	238	11	73.3				

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c 240	11	73.3	381	10	US-09-216-393-44	Sequence 44, Appl	c 313	11	73.3	502	10	US-09-783-590-4163	Sequence 4163, App
c 241	11	73.3	387	10	US-09-878-574-875	Sequence 875, App	c 314	11	73.3	504	10	US-09-864-761-22567	Sequence 22567, A
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c 243	11	73.3	393	10	US-09-783-590-6945	Sequence 6945, App	c 316	11	73.3	509	10	US-09-783-590-3787	Sequence 3787, App
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c 247	11	73.3	408	10	US-09-764-877-3004	Sequence 3004, App	c 320	11	73.3	526	10	US-09-917-800A-1156	Sequence 1156, App
c 248	11	73.3	410	10	US-09-864-761-10520	Sequence 10520, A	c 321	11	73.3	529	9	US-09-764-868-126	Sequence 126, App
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c 250	11	73.3	411	10	US-09-783-590-3737	Sequence 3737, App	c 323	11	73.3	529	10	US-09-864-761-16389	Sequence 16389, A
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c 254	11	73.3	418	10	US-09-960-352-7989	Sequence 7989, App	c 327	11	73.3	539	10	US-09-216-393-52	Sequence 52, Appl
c 255	11	73.3	418	10	US-09-960-352-9491	Sequence 9491, App	c 328	11	73.3	539	10	US-09-864-761-12409	Sequence 12409, A
c 256	11	73.3	419	9	US-09-954-531-332	Sequence 332, App	c 329	11	73.3	540	10	US-09-962-436-7	Sequence 7, Appl
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c 258	11	73.3	419	10	US-09-864-761-309	Sequence 309, App	c 331	11	73.3	544	10	US-09-864-761-28521	Sequence 28521, A
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c 293	11	73.3	471	10	US-09-864-761-6481	Sequence 6481, App	c 366	11	73.3	632	10	US-09-749-225-4	Sequence 4, Appl
c 294	11	73.3	472	10	US-09-864-761-72	Sequence 72, Appl	c 367	11	73.3	640	9	US-10-035-895-1	Sequence 1, Appl
c 295	11	73.3	474	10	US-09-998-598-1749	Sequence 1749, App	c 368	11	73.3	641	10	US-09-764-877-918	Sequence 918, App
c 296	11	73.3	475	10	US-09-864-761-1361	Sequence 1361, App	c 369	11	73.3	642	10	US-09-216-393-42	Sequence 42, Appl
c 297	11	73.3	478	10	US-09-864-761-1368	Sequence 1368, App	c 370	11	73.3	673	10	US-09-917-800A-1258	Sequence 1258, App
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c 299	11	73.3	479	10	US-09-864-761-33103	Sequence 33103, A	c 372	11	73.3	692	10	US-09-099-823-5	Sequence 5, Appl
c 300	11	73.3	481	10	US-09-864-761-1151	Sequence 1151, App	c 373	11	73.3	700	10	US-09-864-761-17529	Sequence 17529, A
c 301	11	73.3	485	10	US-09-864-761-5987	Sequence 5987, App	c 374	11	73.3	738	10	US-09-974-300-1621	Sequence 1621, App
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c 303	11	73.3	486	10	US-09-764-869-2144	Sequence 2144, App	c 376	11	73.3	742	10	US-09-772-134B-96	Sequence 96, Appl
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c 387	11	73.3	858	10	US-09-764-869-1984	Sequence 1984, Ap	c 460	11	73.3	1636	10	US-09-967-552A-1	Sequence 1, Appli
c 388	11	73.3	871	10	US-09-770-445-560	Sequence 560, App	c 461	11	73.3	1660	9	US-09-764-868-244	Sequence 244, App
c 389	11	73.3	900	10	US-09-974-300-2377	Sequence 2377, Ap	c 462	11	73.3	1682	10	US-09-925-297-129	Sequence 129, App
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c 394	11	73.3	959	10	US-09-917-800A-1381	Sequence 1381, Ap	c 467	11	73.3	1802	10	US-09-967-552A-25	Sequence 32, Appl
c 395	11	73.3	970	10	US-09-925-299-232	Sequence 232, App	c 468	11	73.3	1842	10	US-09-822-830A-52	Sequence 52, Appl
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c 443	11	73.3	1364	10	US-09-822-830A-363	Sequence 363, App	c 516	11	73.3	2284	10	US-09-944-449-82	Sequence 82, Appl
c 444	11	73.3	1365	10	US-09-815-242-9347	Sequence 9347, Ap	c 517	11	73.3	2284	10	US-09-989-731-514	Sequence 514, App
c 445	11	73.3	1367	9	US-09-764-884-21	Sequence 21, Appl	c 518	11	73.3	2284	10	US-09-944-457-82	Sequence 82, Appl
c 446	11	73.3	1367	10	US-09-925-299-53	Sequence 53, Appl	c 519	11	73.3	2284	10	US-09-989-732-514	Sequence 514, App
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c 448	11	73.3	1391	9	US-09-938-842A-4490	Sequence 4490, Ap	c 521	11	73.3	2284	10	US-09-945-587-82	Sequence 82, Appl
c 449	11	73.3	1441	9	US-10-001-887-24	Sequence 24, Appl	c 522	11	73.3	2284	10	US-09-990-442-514	Sequence 514, App
c 450	11	73.3	1444	10	US-09-801-574-37	Sequence 37, Appl	c 523	11	73.3	2284	10	US-09-991-163-514	Sequence 514, App
c 451	11	73.3	1494	10	US-09-728-952-80	Sequence 80, Appl	c 524	11	73.3	2284	10	US-09-945-015-82	Sequence 82, Appl
c 452	11	73.3	1498	10	US-09-870-962-14	Sequence 14, Appl	c 525	11	73.3	2284	10	US-09-944-396-82	Sequence 82, Appl
c 453	11	73.3	1514	10	US-09-881-401-1	Sequence 1, Appli	c 526	11	73.3	2284	10	US-09-944-097-82	Sequence 82, Appl
c 454	11	73.3	1545	10	US-09-925-301-392	Sequence 392, App	c 527	11	73.3	2284	10	US-09-993-604-514	Sequence 514, App
c 455	11	73.3	1545	10	US-09-900-700-1	Sequence 1, Appli	c 528	11	73.3	2284	10	US-09-990-456-514	Sequence 514, App
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c 457	11	73.3	1575	10	US-09-735-169A-4	Sequence 4, Appli	c 530	11	73.3	2284	10	US-09-943-762-82	Sequence 82, Appl

c 531	11	73.3	2284	10	US-09-944-654-82	Sequence 82, Appl	604	11	73.3	3402	10	US-09-989-723-118	Sequence 118, App
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c 534	11	73.3	2297	10	US-09-934-332-1	Sequence 1, Appli	607	11	73.3	3402	10	US-09-989-731-118	Sequence 118, App
c 535	11	73.3	2311	10	US-09-764-870-583	Sequence 583, App	608	11	73.3	3402	10	US-09-989-732-118	Sequence 118, App
c 536	11	73.3	2311	10	US-09-764-853-865	Sequence 865, App	609	11	73.3	3402	10	US-09-991-073-118	Sequence 118, App
c 537	11	73.3	2314	10	US-09-764-870-584	Sequence 584, App	610	11	73.3	3402	10	US-09-990-442-118	Sequence 118, App
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c 541	11	73.3	2333	10	US-09-726-643-33	Sequence 33, Appl	614	11	73.3	3402	10	US-09-989-721-118	Sequence 118, App
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c 543	11	73.3	2391	10	US-09-801-368-29	Sequence 29, Appl	c 616	11	73.3	3413	10	US-09-796-858-3	Sequence 3, Appli
c 544	11	73.3	2434	10	US-09-764-877-3336	Sequence 3336, Ap	617	11	73.3	3436	10	US-09-789-561-12	Sequence 12, Appl
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c 547	11	73.3	2502	9	US-10-136-573A-5	Sequence 5, Appli	c 620	11	73.3	3497	10	US-09-764-887-425	Sequence 425, App
c 548	11	73.3	2502	9	US-09-877-665-5	Sequence 5, Appli	c 621	11	73.3	3500	10	US-09-764-887-426	Sequence 426, App
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c 550	11	73.3	2533	10	US-09-764-869-1656	Sequence 1656, Ap	c 623	11	73.3	3528	10	US-09-350-259-36	Sequence 36, Appl
c 551	11	73.3	2535	10	US-09-925-302-147	Sequence 147, App	c 624	11	73.3	3597	10	US-09-350-259-54	Sequence 54, Appl
c 552	11	73.3	2538	9	US-10-136-573A-1	Sequence 1, Appli	c 625	11	73.3	3613	10	US-09-764-847-1746	Sequence 1746, Ap
c 553	11	73.3	2538	9	US-09-877-665-1	Sequence 1, Appli	c 626	11	73.3	3683	10	US-09-954-456-1187	Sequence 1187, Ap
c 554	11	73.3	2538	10	US-09-817-647-1	Sequence 1, Appli	c 627	11	73.3	3731	10	US-09-925-299-114	Sequence 114, App
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c 556	11	73.3	2547	10	US-09-765-298A-9	Sequence 9, Appli	c 629	11	73.3	3945	10	US-09-747-835A-30	Sequence 30, Appl
c 557	11	73.3	2569	10	US-09-925-300-769	Sequence 769, App	c 630	11	73.3	3996	10	US-09-747-835A-28	Sequence 28, Appl
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c 560	11	73.3	2599	10	US-09-822-849A-416	Sequence 416, App	c 633	11	73.3	4152	10	US-09-925-300-359	Sequence 359, App
c 561	11	73.3	2617	10	US-09-853-386-123	Sequence 123, App	c 634	11	73.3	4160	10	US-09-920-552-19	Sequence 19, Appl
c 562	11	73.3	2694	12	US-10-002-600-102	Sequence 102, App	c 635	11	73.3	4166	10	US-09-764-870-625	Sequence 625, App
c 563	11	73.3	2791	10	US-09-729-674-51	Sequence 51, Appl	c 636	11	73.3	4188	10	US-09-920-552-20	Sequence 20, Appl
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c 566	11	73.3	2824	10	US-09-905-983-3	Sequence 3, Appli	c 639	11	73.3	4376	10	US-09-875-124-1	Sequence 1, Appli
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c 570	11	73.3	2901	12	US-10-044-090-528	Sequence 528, App	c 643	11	73.3	4600	9	US-09-736-457-1797	Sequence 1797, Ap
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c 572	11	73.3	2935	9	US-09-764-868-242	Sequence 242, App	c 645	11	73.3	4735	10	US-09-967-552A-71	Sequence 71, Appl
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c 574	11	73.3	3033	9	US-09-992-598-5	Sequence 5, Appli	c 647	11	73.3	4859	10	US-09-880-107-1647	Sequence 1647, App
c 575	11	73.3	3033	9	US-09-989-293A-5	Sequence 5, Appli	c 648	11	73.3	4901	10	US-09-764-864-1710	Sequence 1710, Ap
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c 577	11	73.3	3033	10	US-09-989-723-5	Sequence 5, Appli	c 650	11	73.3	4961	10	US-09-920-552-18	Sequence 18, Appl
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c 579	11	73.3	3033	10	US-09-989-727-5	Sequence 5, Appli	c 652	11	73.3	5025	10	US-09-960-253-176	Sequence 176, App
c 580	11	73.3	3033	10	US-09-989-731-5	Sequence 5, Appli	c 653	11	73.3	5080	10	US-09-764-847-1197	Sequence 1197, Ap
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c 584	11	73.3	3033	10	US-09-991-163-5	Sequence 5, Appli	c 657	11	73.3	5444	10	US-09-931-071-1	Sequence 1, Appli
c 585	11	73.3	3033	10	US-09-993-604-5	Sequence 5, Appli	c 658	11	73.3	5450	12	US-10-044-090-504	Sequence 504, App
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c 588	11	73.3	3080	10	US-09-815-108-18	Sequence 18, Appl	c 661	11	73.3	5511	12	US-10-044-090-285	Sequence 285, App
c 589	11	73.3	3112	10	US-09-758-386-1	Sequence 1, Appli	c 662	11	73.3	5551	10	US-09-905-129-17	Sequence 17, Appl
c 590	11	73.3	3112	10	US-09-815-108-16	Sequence 16, Appl	c 663	11	73.3	5551	10	US-09-991-630-17	Sequence 17, Appl
c 591	11	73.3	3129	10	US-09-815-242-9247	Sequence 9247, Ap	c 664	11	73.3	5551	10	US-09-991-630-17	Sequence 17, Appl
c 592	11	73.3	3129	10	US-09-925-697-1	Sequence 1, Appli	c 665	11	73.3	5557	10	US-09-764-869-1473	Sequence 1473, Ap
c 593	11	73.3	3129	9	US-09-925-697-1	Sequence 1, Appli	c 666	11	73.3	5557	10	US-09-764-869-2252	Sequence 2252, Ap
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c 595	11	73.3	3160	9	US-09-860-670-287	Sequence 287, App	c 668	11	73.3	5763	12	US-10-002-600-79	Sequence 79, Appl
c 596	11	73.3	3197	10	US-09-875-338-6	Sequence 6, Appli	c 669	11	73.3	6065	10	US-09-764-877-3627	Sequence 3627, Ap
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681	11	73.3	7303	10	US-09-764-887-415	Sequence 415, App	754	11	73.3	176373	9	US-10-095-407-17	Sequence 17, Appli
682	11	73.3	7703	10	US-09-764-887-456	Sequence 456, App	755	11	73.3	249487	9	US-10-026-188-3	Sequence 3, Appli
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685	11	73.3	7934	9	US-09-764-868-1390	Sequence 1390, App	758	11	73.3	326014	10	US-09-931-231A-3	Sequence 3, Appli
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687	11	73.3	9121	10	US-09-070-927A-221	Sequence 221, App	c 760	11	73.3	455237	10	US-09-933-267A-1	Sequence 1, Appli
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689	11	73.3	9914	10	US-09-764-847-1558	Sequence 1558, App	762	11	73.3	684973	10	US-09-263-959-1	Sequence 1, Appli
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717	11	73.3	26668	10	US-09-962-832-222	Sequence 222, App	790	10	66.7	117	10	US-09-764-877-2721	Sequence 2721, App
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ALIGNMENTS

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RESULT 1
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; Sequence 1704, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764.864
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 15857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1704

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Query Match      100.0%; Score 15; DB 10; Length 15857;
Best Local Similarity 100.0%; Pred. No. 3.7;
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RESULT 2
US-09-954-456-1577/c
; Sequence 1577, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets

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; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954.456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1577
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: n-a,t,g or c
US-09-954-456-1577

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Query Match      93.3%; Score 14; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CCTTCTCCCTCTGT 14
        |||||
Db      296 CCTTCTCCCTCTGT 283

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RESULT 3
US-09-880-107-3234/c
; Sequence 3234, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3234
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 T84491
; NAME/KEY: unsure
; LOCATION: (1)..(389)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3234

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Query Match 93.3%; Score 14; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

DB 296 CCTTCTCCCCCTGT 283

RESULT 4

US-10-001-835-84/c
; Sequence 84, Application US/10001835
; Patent No. US20020160387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Caifkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,997
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-835-84

Query Match 93.3%; Score 14; DB 9; Length 482;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCTCCCCCTGT 15
|||||

DB 188 CTCTCTCCCCCTGT 175

RESULT 5

US-09-864-761-13104
; Sequence 13104, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13104
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL36968.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
US-09-864-761-13104

Query Match 93.3%; Score 14; DB 10; Length 594;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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DB 192 CCTTCTCCCCCTGT 205

RESULT 6

US-09-764-864-1692/c
; Sequence 1692, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1692
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1692

Query Match 93.3%; Score 14; DB 10; Length 8894;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

DB 4843 CCTTCTCCCCCTGT 4830

RESULT 7

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US-09-764-877-3063
; Sequence 3063, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3063
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3063

Query Match      93.3%; Score 14; DB 10; Length 8894;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
| | | | | | | | | | | | | | | |
Db 4052 CCTTCTCCCCCTGT 4065

RESULT 8
US-09-764-877-3349/c
; Sequence 3349, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3349

Query Match      93.3%; Score 14; DB 10; Length 16877;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
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Db 1269 CCTTCTCCCCCTGT 1256

RESULT 9
US-09-864-761-25357
; Sequence 25357, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 864
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-761-25357

Query Match      86.7%; Score 13; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCCCCCTGT 14
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Db 41 CTTCTCCCCCTGT 53

RESULT 10
US-09-922-217-616/c
; Sequence 616, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Mesgher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
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; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25357
; LENGTH: 209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC018506.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EST HUMAN HIT: BE540550.1, EVALUATE 1.00e-107
; OTHER INFORMATION: NT HIT: gill420735, EVALUATE 1.20e-01
US-09-864-761-25357

Query Match      86.7%; Score 13; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCCCCCTGT 14
| | | | | | | | | | | | | | | |
Db 41 CTTCTCCCCCTGT 53

RESULT 10
US-09-922-217-616/c
; Sequence 616, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Mesgher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
```

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 156, 181, 194
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-616

Query Match 86.7%; Score 13; DB 10; Length 210;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13
Db 173 CCTTCTCCCCCTG 161

RESULT 11

US-09-833-263-616/c
; Sequence 616, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833.263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 616
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-616

Query Match 86.7%; Score 13; DB 10; Length 210;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13
Db 173 CCTTCTCCCCCTG 161

RESULT 12

US-09-867-701-4769/c
; Sequence 4769, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert

; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867.701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4769
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-867-701-4769

Query Match 86.7%; Score 13; DB 10; Length 285;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13
Db 23 CCTTCTCCCCCTG 11

RESULT 13

US-09-712-363-96/c
; Sequence 96, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712.363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-96

Query Match 86.7%; Score 13; DB 9; Length 315;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13
Db 106 CCTTCTCCCCCTG 94

RESULT 14

US-09-867-701-10110/c

; Sequence 10110, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10110
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(337)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10110

Query Match 86.7%; Score 13; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCCCTGTT 15
|||||
Db 130 TTCTCCCCCTGTT 118

RESULT 15

US-09-954-456-892/c
; Sequence 892, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 892
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-892

Query Match 86.7%; Score 13; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 52;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCCCTG 13
|||||
Db 287 CCTTCTCCCCCTG 275

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Job time : 75.5 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:56:23 ; Search time 1655.5 Seconds
(without alignments)
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Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 cctctcccccgttt 15

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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2: em_esthum:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 3	15	100.0	247 9	AL708655
c 4	15	100.0	297 9	AV067076
5	15	100.0	378 14	F07213
6	15	100.0	393 14	T08889

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c 86	15	100.0	935	10	BE250545	600943221	159	14	93.3	378	12	BF803021	CM1-CI009
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c 90	15	100.0	992	17	CNS037BW	AL231125	163	14	93.3	382	14	T81121	yq24303.r1
c 91	15	100.0	1024	17	CNS04QEC	AL302493	164	14	93.3	383	9	AI243920	qn7e08.x
c 92	15	100.0	1042	10	BE250477	600943221	c 165	14	93.3	384	12	BF805833	CM1-CI001
c 93	15	100.0	1045	14	BM803241	AGENCOURT	166	14	93.3	385	12	BF805832	CM1-CI001
c 94	15	100.0	1056	17	CNS05F31	AL334486	167	14	93.3	386	12	BF805864	CM1-CI009
c 95	15	100.0	1075	12	BF676401	602084592	168	14	93.3	388	12	BF847001	CM0-EN004
c 96	15	100.0	1083	17	CNS05F32	AL334487	169	14	93.3	388	12	BF087456	QV2-HT054
c 97	15	100.0	1099	17	AG052686	Pan trogl	170	14	93.3	388	12	BF372412	QV3-FT003
c 98	15	100.0	1101	17	CNS05D5A	AL331975	171	14	93.3	389	9	AI918458	ts31c06.x
c 99	15	100.0	1105	12	BG776955	602664152	c 172	14	93.3	389	14	T84491	yd47g10.s1
c 100	15	100.0	1152	14	BM925445	AGENCOURT	173	14	93.3	391	12	BF803010	CM1-CI009
c 101	15	100.0	1360	12	BE729544	601564633	174	14	93.3	392	14	H19733	yn60f08.r1
c 102	15	100.0	1530	14	BM921681	BM921581	175	14	93.3	393	12	BF802019	CM1-CI009
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c 104	15	100.0	4427	11	BC034038	BC034038	177	14	93.3	395	12	BF805843	CM1-CI001
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c 107	14	93.3	174	9	AA212165	mu43d02.r	180	14	93.3	398	12	BF846988	CM0-EN004
c 108	14	93.3	193	12	BF512918	UI-H-BI3-	c 181	14	93.3	398	17	AZ711196	RPC1-24-8
c 109	14	93.3	217	12	BF950238	CM3-NN118	c 182	14	93.3	399	12	BF845770	CM0-EN004
c 110	14	93.3	224	10	BF950256	CM3-NN118	183	14	93.3	399	13	BE769449	QV3-FT003
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c 112	14	93.3	228	10	BF149305	BB149305	c 185	14	93.3	400	12	BF805842	CM1-CI001
c 113	14	93.3	232	12	BF950328	CM3-NN118	c 186	14	93.3	400	12	BF850712	CM0-EN004
c 114	14	93.3	235	12	BF950252	CM3-NN118	c 187	14	93.3	404	12	BF848311	CM0-EN004
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c 116	14	93.3	236	10	AV380926	AV380926	c 189	14	93.3	408	12	BF802043	CM1-CI009
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c 122	14	93.3	254	12	BF950239	CM3-NN118	c 195	14	93.3	412	12	BF801583	CM1-CI009
c 123	14	93.3	256	12	BF950264	CM3-NN118	c 196	14	93.3	412	12	BF801592	CM1-CI009
c 124	14	93.3	257	12	BF950303	CM3-NN118	c 197	14	93.3	412	12	BF848303	CM0-EN004
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c 128	14	93.3	262	12	BF950261	CM3-NN118	c 201	14	93.3	414	12	BF803014	CM1-CI009
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c 135	14	93.3	288	10	AW377774	AW377774	c 208	14	93.3	418	12	BF850710	CM0-EN004
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c 140	14	93.3	308	10	BB215312	BB215312	c 213	14	93.3	423	10	AW822429	uq0f12.x
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c 143	14	93.3	316	10	BE507362	BE507362	c 216	14	93.3	425	12	BF846991	CM0-EN004
c 144	14	93.3	327	14	H41711	H41711	c 217	14	93.3	425	14	BU022123	QHE5P19.y
c 145	14	93.3	333	12	BF845771	BF845771	c 218	14	93.3	425	17	AQ113334	CITP-HSP-2
c 146	14	93.3	340	14	H23897	Yn71H10.r1	c 219	14	93.3	426	12	BF802002	CM1-CI009
c 147	14	93.3	355	12	BF848315	BF848315	c 220	14	93.3	426	14	BQ340311	QV2-NN200
c 148	14	93.3	357	12	BF805845	CM1-CI001	c 221	14	93.3	427	10	AW751856	QV2-CT012
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c 150	14	93.3	365	12	BF808577	CM1-CI009	c 223	14	93.3	428	9	AI124748	am61e12.x
c 151	14	93.3	365	12	BF808575	CM1-CI009	c 224	14	93.3	428	12	BF801995	CM1-CI009
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226	14	93.3	430	12	BF802018	BF802018	CM1-CI009	299	14	93.3	586	10	AW365203	AW365203	MRO-HT006
227	14	93.3	430	12	BF802024	BF802024	CM1-CI009	300	14	93.3	587	10	AW177882	AW177882	IL3-HT005
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229	14	93.3	430	12	BF848298	BF848298	CM0-EN004	302	14	93.3	588	10	BE614114	BE614114	601503857
230	14	93.3	431	12	BF808544	BF808544	CM1-CI009	303	14	93.3	588	10	BQ182579	BQ182579	UI-H-EU0-
231	14	93.3	432	12	BF803013	BF803013	CM1-CI009	c 304	14	93.3	595	13	B1908590	B1908590	603069993
232	14	93.3	432	12	BF808581	BF808581	CM1-CI009	305	14	93.3	599	10	AW177833	AW177833	IL3-HT005
233	14	93.3	434	12	BF846978	BF846978	CM0-EN004	306	14	93.3	599	10	AW177833	AW177833	IL3-HT005
234	14	93.3	434	12	BG897595	BG897595	HOA15-1-G	307	14	93.3	599	10	AW177881	AW177881	IL3-HT005
235	14	93.3	434	17	BH169414	BH169414	SALK_0013	308	14	93.3	599	10	AW177881	AW177881	IL3-HT005
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237	14	93.3	436	12	BF931083	BF931083	CM1-NF027	c 310	14	93.3	600	13	B1986645	B1986645	3174-44 M
238	14	93.3	437	12	BF803008	BF803008	CM1-CI009	311	14	93.3	601	12	BE747858	BE747858	601578641
239	14	93.3	437	12	BF848312	BF848312	CM0-EN004	312	14	93.3	602	14	BQ180978	BQ180978	UI-H-EU0-
240	14	93.3	439	12	BF801998	BF801998	CM1-CI009	c 313	14	93.3	602	13	BQ181939	BQ181939	UI-H-EU0-
241	14	93.3	440	9	AI744681	AI744681	wg02g02.x	c 314	14	93.3	603	13	BG924790	BG924790	HNC36-1-G
242	14	93.3	440	12	BF802020	BF802020	CM1-CI009	c 315	14	93.3	605	17	B16174	B16174	347C19-TP C
243	14	93.3	440	12	BF802069	BF802069	CM1-CI009	316	14	93.3	605	17	AQ525566	AQ525566	HS-5227-B
244	14	93.3	441	12	BF802256	BF802256	CM1-CI009	317	14	93.3	609	14	BQ396664	BQ396664	NISC_mq15
245	14	93.3	442	12	BF802010	BF802010	CM1-CI009	318	14	93.3	610	14	AL646235	AL646235	NISC_ng22
246	14	93.3	443	12	BF808572	BF808572	CM1-CI009	c 319	14	93.3	612	9	AL646235	AL646235	AL646235
247	14	93.3	444	12	BF846989	BF846989	CM0-EN004	c 320	14	93.3	612	17	BH083105	BH083105	RPCI-24-3
248	14	93.3	445	13	BG927815	BG927815	HNC45-1-B	c 321	14	93.3	614	14	BQ183139	BQ183139	UI-H-EU0-
249	14	93.3	445	14	BQ329284	BQ329284	CM0-EN004	c 322	14	93.3	615	12	BG988807	BG988807	HOA4-1-C-
250	14	93.3	446	12	BF847000	BF847000	CM0-EN004	c 323	14	93.3	615	12	BF031013	BF031013	601558879
251	14	93.3	447	12	BF848316	BF848316	CM0-EN004	c 324	14	93.3	617	10	BE542024	BE542024	601066932
252	14	93.3	447	12	BF850711	BF850711	CM0-EN004	325	14	93.3	623	9	AJ398773	AJ398773	AJ398773
253	14	93.3	449	9	AA670642	AA670642	v107a05.r	c 326	14	93.3	628	14	BQ392790	BQ392790	NISC_mq26
254	14	93.3	449	12	BF801585	BF801585	CM1-CI009	327	14	93.3	630	10	BH657487	BH657487	BB657487
255	14	93.3	450	10	AW403106	AW403106	UI-HF-BK0	328	14	93.3	634	14	BQ181814	BQ181814	UI-H-EU0-
256	14	93.3	450	12	BF847003	BF847003	CM0-EN004	329	14	93.3	634	14	BQ183943	BQ183943	UI-H-EU0-
257	14	93.3	451	17	AZ883987	AZ883987	RPCI-23-1	330	14	93.3	638	14	BQ182672	BQ182672	UI-H-EU0-
258	14	93.3	453	12	BF802265	BF802265	CM1-CI009	c 331	14	93.3	639	13	BM120815	BM120815	L0944D12-
259	14	93.3	453	12	BF850717	BF850717	CM0-EN004	c 332	14	93.3	642	17	AG050166	AG050166	Pan trogl
260	14	93.3	453	17	AZ816990	AZ816990	CM1-CI009	c 333	14	93.3	649	9	AL659701	AL659701	AL659701
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262	14	93.3	456	12	BF801999	BF801999	CM1-CI009	c 335	14	93.3	651	10	BQ004619	BQ004619	UI-H-EI0-
263	14	93.3	460	14	R94700	R94700	Yq43c03.s1	c 336	14	93.3	653	10	AW365204	AW365204	MRO-HT006
264	14	93.3	461	17	BH212045	BH212045	SALK_0070	337	14	93.3	653	12	BG789292	BG789292	SEAUMC009
265	14	93.3	470	12	BF802021	BF802021	CM1-CI009	c 338	14	93.3	656	17	AZ753211	AZ753211	RPCI-24-8
266	14	93.3	471	13	BM254581	BM254581	nbe0071A	c 339	14	93.3	660	10	BE514784	BE514784	601316712
267	14	93.3	474	17	AA043101	AA043101	zk55d09.s	340	14	93.3	662	12	BQ324914	BQ324914	602423553
268	14	93.3	476	9	AA043101	AA043101	zk55d09.s	341	14	93.3	662	14	BQ446761	BQ446761	UI-H-EU0-
269	14	93.3	478	14	BQ339938	BQ339938	QV2-NN004	342	14	93.3	664	14	BQ004652	BQ004652	UI-H-EI0-
270	14	93.3	481	13	BM308641	BM308641	sak48f11	343	14	93.3	664	14	BQ0181085	BQ0181085	UI-H-EU0-
271	14	93.3	489	12	BF953694	BF953694	RC4-NN117	c 344	14	93.3	674	17	BH335850	BH335850	CH230-169
272	14	93.3	500	12	BF019465	BF019465	uxi0e10.y	c 345	14	93.3	677	13	BG975859	BG975859	602842179
273	14	93.3	503	14	BQ557334	BQ557334	H4045D12-	346	14	93.3	677	14	BQ405396	BQ405396	GA_Ed008
274	14	93.3	504	12	BE705850	BE705850	IL3-HT005	347	14	93.3	680	14	BQ044975	BQ044975	UI-H-EU0-
275	14	93.3	505	14	T84490	T84490	Yd47g10.r1	c 348	14	93.3	685	10	AW604437	AW604437	RC3-CT025
276	14	93.3	513	10	BE584979	BE584979	2-6B-20 P	c 349	14	93.3	688	13	BG928689	BG928689	HNC72-1-G
277	14	93.3	519	13	BF791283	BF791283	id04b01.y	c 350	14	93.3	688	13	BM041978	BM041978	603615856
278	14	93.3	519	17	AZ654173	AZ654173	IM0528009	351	14	93.3	688	14	BQ405399	BQ405399	GA_Ed008
279	14	93.3	523	17	AZ650845	AZ650845	IM0520M22	c 352	14	93.3	691	12	BG680572	BG680572	602629006
280	14	93.3	525	14	BQ074021	BQ074021	fz34c12.x	353	14	93.3	693	17	AG077385	AG077385	Pan trogl
281	14	93.3	533	13	BI465317	BI465317	603206638	c 354	14	93.3	695	12	BE747221	BE747221	601580938
282	14	93.3	535	9	AI949103	AI949103	wq19e09.x	c 355	14	93.3	701	12	BG428158	BG428158	602498808
283	14	93.3	536	12	BE705855	BE705855	IL3-HT005	c 356	14	93.3	712	14	BM726822	BM726822	UI-E-EJ0-
284	14	93.3	536	14	R21046	R21046	Yg52a04.r1	357	14	93.3	721	17	AG122350	AG122350	Pan trogl
285	14	93.3	542	12	BG980084	BG980084	HOA38-1-F	c 358	14	93.3	723	17	CNS034JM	CNS034JM	AL227515
286	14	93.3	553	10	AW365206	AW365206	MRO-HT006	c 359	14	93.3	727	12	BG472445	BG472445	602514136
287	14	93.3	555	17	AZ818736	AZ818736	2M0088M19	360	14	93.3	729	14	BQ183753	BQ183753	UI-H-EU0-
288	14	93.3	556	10	AV702592	AV702592	AV702592	c 361	14	93.3	732	14	BQ182050	BQ182050	UI-H-EU0-
289	14	93.3	556	13	BT035372	BT035372	EJ035372	c 362	14	93.3	733	12	BG473938	BG473938	602516428
290	14	93.3	560	12	BF792066	BF792066	602252473	c 363	14	93.3	739	13	BE741013	BE741013	601595387
291	14	93.3	567	14	BQ182258	BQ182258	UI-H-EU0-	364	14	93.3	739	13	BI684772	BI684772	603307140
292	14	93.3	567	14	BQ334034	BQ334034	MRO-MT015	c 365	14	93.3	743	13	BI890095	BI890095	2F637-2-0
293	14	93.3	568	12	BE705849	BE705849	IL3-HT005	c 366	14	93.3	746	17	AQ368213	AQ368213	tox00001N
294	14	93.3	577	17	AZ344936	AZ344936	IM0079D16	c 367	14	93.3	751	12	BG327445	BG327445	602426427
295	14	93.3	583	14	BQ419281	BQ419281	faa36h04.	c 368	14	93.3	752	14	BQ007885	BQ007885	UI-H-EI0-
296	14	93.3	584	14	BQ004253	BQ004253	UI-H-EI0-	369	14	93.3	755	10	BE130672	BE130672	L48-873T3
297	14	93.3	585	10	AV764095	AV764095	AV764095	370	14	93.3	758	14	BQ181926	BQ181926	UI-H-EU0-
298	14	93.3	585	14	BQ285725	BQ285725	faa29b10.	c 371	14	93.3	762	12	BG860360	BG860360	1024070A0

372	14	93.3	762	17	AG180802	Pan trogl	c 445	13	86.7	114	17	BH607467	BH607467
373	14	93.3	779	12	BG548733	602576352	446	13	86.7	122	17	BH639659	BH639659
374	14	93.3	779	14	BM718964	UI-E-E01-	c 447	13	86.7	126	17	AZ342525	1M007507
375	14	93.3	786	17	BH588802	BOHT002TR	c 448	13	86.7	144	10	AW391528	MR3-ST021
376	14	93.3	798	13	BI143705	602307352	449	13	86.7	148	9	AL714822	AL714822
377	14	93.3	797	13	BI868694	603392022	450	13	86.7	150	14	H48109	H48109
378	14	93.3	801	17	BI9622	BF19622	c 451	13	86.7	151	9	AV130769	AV130769
379	14	93.3	804	12	BF974470	602243566	c 452	13	86.7	151	9	AO267724	RPCI11-74
380	14	93.3	814	12	BG583044	EST484786	453	13	86.7	151	17	FR0024607	FR0024607
381	14	93.3	825	12	BF248204	601821203	454	13	86.7	151	17	AZ716683	RPCI-24-8
382	14	93.3	827	13	BI079126	602873417	c 455	13	86.7	157	17	AZ716683	RPCI-24-8
383	14	93.3	839	17	AQ741331	HS_5570_B	c 456	13	86.7	158	9	AI071619	UI-R-C2-m
384	14	93.3	850	12	BF029076	601764573	c 457	13	86.7	161	17	AZ737405	RPCI-24-1
385	14	93.3	854	12	BG853922	1024038E0	c 458	13	86.7	161	17	AZ746018	RPCI-24-1
386	14	93.3	855	17	AQ329452	nbxb0045C	459	13	86.7	164	12	BF805837	CM1-C1001
387	14	93.3	862	14	BQ224734	AGENCOURT	460	13	86.7	175	9	AI213318	zla03a1.f
388	14	93.3	865	12	BF246979	601954369	c 461	13	86.7	178	10	AW779636	hn97h01.x
389	14	93.3	869	12	BF979683	602288532	c 462	13	86.7	183	17	AZ019037	RPCI-23-2
390	14	93.3	872	14	BQ898530	AGENCOURT	c 463	13	86.7	189	9	AL079975	DKEF2586M
391	14	93.3	878	14	BQ215741	AGENCOURT	c 464	13	86.7	190	10	AW815589	QVO-ST021
392	14	93.3	881	12	BF036952	601459183	c 465	13	86.7	190	14	C01728	HUMG000349
393	14	93.3	890	12	BF668633	602123688	c 466	13	86.7	194	17	BH777251	fzmb013f0
394	14	93.3	894	12	BF672581	602152157	467	13	86.7	194	17	BH889400	3526_1_10
395	14	93.3	895	17	CNS01TLD	Tetraodon	468	13	86.7	202	17	AZ6522917	hw05f03.x
396	14	93.3	906	13	BM008669	603618339	469	13	86.7	213	9	AV097028	AV097028
397	14	93.3	915	9	AI524687	th12a07.x	470	13	86.7	213	10	BE011550	CM4-BM022
398	14	93.3	929	12	BF182768	601809275	471	13	86.7	214	9	AI906075	RC-BT105
399	14	93.3	940	14	BQ691486	AGENCOURT	472	13	86.7	214	9	AI906075	RC-BT105
400	14	93.3	948	17	AQ091536	HS_3233_B	c 473	13	86.7	214	9	AV152676	AV152676
401	14	93.3	959	12	BQ24674	602275481	c 474	13	86.7	214	10	BB429038	BB429038
402	14	93.3	964	14	BQ711308	AGENCOURT	475	13	86.7	215	10	BB269976	BB269976
403	14	93.3	965	14	BQ958755	AGENCOURT	c 476	13	86.7	216	12	BE700178	MRO-NN008
404	14	93.3	972	17	CNS055QD	Tetraodon	c 477	13	86.7	216	17	BM762670	K-EST0043
405	14	93.3	976	17	AQ743771	HS_5501_A	c 478	13	86.7	217	17	BH642291	1008031B0
406	14	93.3	978	12	BG257353	602377878	c 479	13	86.7	218	10	BB591677	BB591677
407	14	93.3	984	17	CNS055VJ	Tetraodon	c 480	13	86.7	218	10	BB600484	BB600484
408	14	93.3	987	17	CNS042VD	Tetraodon	c 481	13	86.7	218	10	BE326565	hw05f03.x
409	14	93.3	992	12	BF308416	601890733	482	13	86.7	219	10	BB435389	BB435389
410	14	93.3	1001	17	CNS04VKF	AGENCOURT	c 483	13	86.7	220	10	BB162320	BB162320
411	14	93.3	1010	13	BM044425	603621780	484	13	86.7	220	10	BB435937	BB435937
412	14	93.3	1027	14	BQ059568	AGENCOURT	485	13	86.7	221	9	AV096817	AV096817
413	14	93.3	1041	17	CNS03DDE	Tetraodon	c 486	13	86.7	223	9	AA277728	AA277728
414	14	93.3	1047	13	BI255744	602977157	487	13	86.7	224	9	AI986006	wu43a10.x
415	14	93.3	1052	12	BE745033	601576127	488	13	86.7	224	10	BB573977	BB573977
416	14	93.3	1067	14	BQ052391	AGENCOURT	c 489	13	86.7	224	14	BQ761694	Ehem10_SQ
417	14	93.3	1074	14	BM917151	AGENCOURT	490	13	86.7	224	17	AZ759964	1M0553E16
418	14	93.3	1098	17	CNS04WE	Tetraodon	491	13	86.7	228	10	BB431706	BB431706
419	14	93.3	1106	12	BE962757	601656153	492	13	86.7	229	17	BH780156	BH780156
420	14	93.3	1111	13	BM551502	AGENCOURT	493	13	86.7	232	10	BB010620	BB010620
421	14	93.3	1119	14	BQ051343	AGENCOURT	c 494	13	86.7	232	12	BG816697	BG816697
422	14	93.3	1120	13	BM477118	AGENCOURT	c 495	13	86.7	233	10	BB581505	BB581505
423	14	93.3	1122	13	BM454475	AGENCOURT	496	13	86.7	235	17	BH771436	BH771436
424	14	93.3	1123	12	BF143187	601788085	497	13	86.7	236	9	AB030425	AB030425
425	14	93.3	1128	12	BG831422	602766345	498	13	86.7	236	10	AW320415	AW320415
426	14	93.3	1129	14	BM805290	AGENCOURT	c 499	13	86.7	236	17	AZ426618	AZ426618
427	14	93.3	1196	14	BQ948502	AGENCOURT	500	13	86.7	237	9	AI471025	tf89f07.x
428	14	93.3	1203	12	BG845061	1024008F0	501	13	86.7	237	10	BB112151	BB112151
429	14	93.3	1212	14	BQ650647	AGENCOURT	502	13	86.7	237	10	BB558253	BB558253
430	14	93.3	1232	13	BM461098	AGENCOURT	503	13	86.7	237	17	BH110722	RPCI-24-3
431	14	93.3	1247	17	AG073214	Pan trogl	c 504	13	86.7	238	9	AV054336	AV054336
432	14	93.3	1277	12	BG843851	1024004C1	505	13	86.7	238	13	BI035026	BI035026
433	14	93.3	1350	12	BE747035	601580783	506	13	86.7	238	14	BQ244667	BQ244667
434	14	93.3	1484	12	BG111620	602282659	507	13	86.7	239	9	AV277865	AV277865
435	14	93.3	1501	12	BE964757	602080846	508	13	86.7	239	13	BI027975	BI027975
436	14	93.3	1541	12	BE964119	601657803	509	13	86.7	240	9	AA016724	AA016724
437	14	93.3	1626	14	BG171210	602321410	510	13	86.7	240	10	BB029874	BB029874
438	14	93.3	1739	14	BM924739	AGENCOURT	511	13	86.7	240	10	BB208957	BB208957
439	14	93.3	1806	12	BF163541	601809843	c 512	13	86.7	241	9	AI688865	AI688865
440	14	93.3	1998	11	AK018387	Mus muscu	513	13	86.7	242	17	BH771488	BH771488
441	14	93.3	6320	11	AF161390	Homo sapi	514	13	86.7	243	10	AV364197	AV364197
442	13	86.7	39	17	AZ405991	1M0175L05	515	13	86.7	243	17	BH620099	BH620099
443	13	86.7	87	9	AI869477	tw41f12.x	516	13	86.7	244	10	BB318509	BB318509
444	13	86.7	113	12	BG274355	WHE2227_F	517	13	86.7	245	9	AV028813	AV028813

c 518	13	86.7	246	9	AI683289	AT1683289	tw50b04.x	591	13	86.7	289	17	BH873402	BH873402	hp44g05.b
519	13	86.7	246	10	BF3398012	BF3398012	BF3398012	592	13	86.7	290	10	BB053804	BB053804	BB053804
520	13	86.7	246	12	BF332977	BF332977	MR1-BT079	c 593	13	86.7	290	10	BB070371	BB070371	BB070371
c 521	13	86.7	246	17	AG019279	AG019279	Homo sapi	594	13	86.7	290	10	BB163034	BB163034	BB163034
522	13	86.7	248	9	AI695589	AI695589	we51f08.x	595	13	86.7	290	10	BB163469	BB163469	BB163469
523	13	86.7	248	13	BI803042	BI803042	H098F07.E	596	13	86.7	290	10	BB338926	BB338926	BB338926
c 524	13	86.7	248	13	BM544141	BM544141	AGENCOURT	c 597	13	86.7	290	14	BQ750100	SnEST4a68	BQ750100
c 525	13	86.7	249	9	AI963337	AI963337	wt61h04.x	c 598	13	86.7	290	14	T32268	EST45993.Hu	T32268
c 526	13	86.7	249	9	AA491947	AA491947	ng16f10.s	c 599	13	86.7	291	9	AA482059	zv41f12.r	AA482059
527	13	86.7	251	9	AA481877	AA481877	zv41f12.s	600	13	86.7	291	9	AA481877	BB481877	AA481877
528	13	86.7	253	9	AT000537	AT000537	AT000537	601	13	86.7	292	9	AI006401	ua71f05.f	AI006401
529	13	86.7	254	10	BB051872	BB051872	BB051872	602	13	86.7	292	9	AV150532	AV150532	AV150532
c 530	13	86.7	254	12	BG320136	BG320136	Zm03.04c1	603	13	86.7	292	13	BM279763	zah5425.z	BM279763
531	13	86.7	254	17	AQ845288	AQ845288	an31f01.J	604	13	86.7	294	10	BB359045	BB359045	BB359045
532	13	86.7	255	9	AA464195	AA464195	zx83h03.s	605	13	86.7	295	10	BB351351	BB351351	BB351351
533	13	86.7	255	10	BB226299	BB226299	BB226299	606	13	86.7	295	10	BB472827	BB472827	BB472827
534	13	86.7	256	17	AQ065580	AQ065580	HS_2238_A	607	13	86.7	295	10	BE489813	WHE1071-1	BE489813
535	13	86.7	257	12	BF804130	BF804130	CM2-C1013	608	13	86.7	296	9	AA252217	zrf63g09.s	AA252217
536	13	86.7	259	9	AV289511	AV289511	AV289511	609	13	86.7	296	10	BB361168	BB361168	BB361168
537	13	86.7	260	9	AI417259	AI417259	tg76g02.x	610	13	86.7	296	10	BB504125	BB504125	BB504125
538	13	86.7	261	10	BB049278	BB049278	BB049278	611	13	86.7	297	9	AA087682	nm27e09.r	AA087682
539	13	86.7	261	9	AA989734	AA989734	am71h08.s	612	13	86.7	297	10	BB082200	BB082200	BB082200
540	13	86.7	261	9	AA989735	AA989735	am71h09.s	c 613	13	86.7	297	13	BM444856	EBem09_SO	BM444856
c 541	13	86.7	262	10	BB281028	BB281028	BB281028	614	13	86.7	298	10	BB566497	BB566497	BB566497
c 542	13	86.7	263	9	AU275477	AU275477	AU275477	615	13	86.7	299	10	BB870221	hm58e06.g	BB870221
c 543	13	86.7	263	10	BB600421	BB600421	BB600421	616	13	86.7	299	10	BB393284	BB393284	BB393284
c 544	13	86.7	264	9	AV041290	AV041290	AV041290	c 617	13	86.7	299	13	BI544220	EST000014	BI544220
545	13	86.7	266	9	AI220015	AI220015	qg78f03.x	618	13	86.7	299	13	BM055337	le93e08.y	BM055337
546	13	86.7	266	10	BB410916	BB410916	BB410916	619	13	86.7	300	9	AA577082	nm68e03.s	AA577082
547	13	86.7	266	17	BH780001	BH780001	fzmb014f0	c 620	13	86.7	301	9	AU055940	AU055940	AU055940
548	13	86.7	268	10	BB394149	BB394149	BB394149	621	13	86.7	302	10	BB082086	BB082086	BB082086
c 549	13	86.7	268	10	BB595252	BB595252	BB595252	622	13	86.7	304	10	BB090072	BB090072	BB090072
550	13	86.7	268	14	H95951	H95951	yv89g09.sl	c 623	13	86.7	304	14	F20768	HSD005172.H	F20768
551	13	86.7	268	17	BH771664	BH771664	hg35h02.g	624	13	86.7	305	10	BH111799	BH111799	BH111799
552	13	86.7	269	12	BF435251	BF435251	nab37a08.f	625	13	86.7	305	10	BB395564	BB395564	BB395564
553	13	86.7	269	12	BF435865	BF435865	nab42h08.f	626	13	86.7	306	9	AA591585	vk49b03.f	AA591585
554	13	86.7	269	13	BM286435	BM286435	BM286435	c 627	13	86.7	306	10	AA261976	xg29g03.x	AA261976
555	13	86.7	270	9	AI537021	AI537021	to15a12.x	c 628	13	86.7	307	9	AI174421	an46a08.s	AI174421
556	13	86.7	271	9	AV267711	AV267711	AV267711	629	13	86.7	307	9	AI125316	qg88c12.x	AI125316
c 557	13	86.7	271	10	BB372040	BB372040	BB372040	630	13	86.7	308	10	BB122255	BB122255	BB122255
558	13	86.7	272	10	BB455651	BB455651	BB455651	c 631	13	86.7	309	9	AI836417	UI-M-AIO-	AI836417
559	13	86.7	273	9	AA809722	AA809722	nk96h07.s	c 632	13	86.7	313	9	AA252216	zrf63g09.f	AA252216
560	13	86.7	274	10	AV372754	AV372754	AV372754	633	13	86.7	313	10	BB492349	BB492349	BB492349
561	13	86.7	274	10	BB329366	BB329366	BB329366	634	13	86.7	314	10	AW121317	UI-M-BH2	AW121317
c 562	13	86.7	274	10	BB561701	BB561701	BB561701	635	13	86.7	314	10	BB255595	BB255595	BB255595
563	13	86.7	275	9	AI476509	AI476509	tm22d03.x	636	13	86.7	315	9	AA809592	nj43f04.s	AA809592
c 564	13	86.7	275	9	AA464790	AA464790	zx83h03.f	637	13	86.7	315	9	AV101685	AV101685	AV101685
565	13	86.7	275	10	BB534668	BB534668	BB534668	638	13	86.7	315	9	AA371837	EST83720	AA371837
c 566	13	86.7	276	12	BF928076	BF928076	IL5-NT022	639	13	86.7	315	12	BF843172	MR2-HT104	BF843172
c 567	13	86.7	277	12	BF509374	BF509374	UI-H-BI4-	640	13	86.7	315	14	F13867	ATTS4789.Ve	F13867
568	13	86.7	278	10	BB409191	BB409191	BB409191	c 641	13	86.7	316	12	BG788712	SEAUMC008	BG788712
569	13	86.7	279	14	R48778	R48778	yj69c06.sl	c 642	13	86.7	317	9	AA678615	an03c09.s	AA678615
570	13	86.7	280	17	BH780065	BH780065	fzmb014f0	643	13	86.7	317	10	BB095270	BB095270	BB095270
571	13	86.7	281	14	R50555	R50555	yj57g04.sl	644	13	86.7	317	13	BM030039	BM030039	BM030039
c 572	13	86.7	282	10	AW654109	AW654109	103368.MA	645	13	86.7	317	14	T95069	ye39e08.sl	T95069
c 573	13	86.7	282	12	BE862910	BE862910	UI-M-BG1-	646	13	86.7	318	9	AV211282	AV211282	AV211282
c 574	13	86.7	283	9	AI797864	AI797864	we83e07.x	647	13	86.7	319	9	AV102122	AV102122	AV102122
575	13	86.7	283	10	BB005412	BB005412	BB005412	c 648	13	86.7	319	10	BB105083	BB105083	BB105083
576	13	86.7	286	10	BB400252	BB400252	BB400252	649	13	86.7	319	14	T23821	seq1081.b4H	T23821
577	13	86.7	286	10	BB439644	BB439644	BB439644	650	13	86.7	320	10	AV538193	AV538193	AV538193
c 578	13	86.7	286	12	BG607089	BG607089	WHE2489_C	651	13	86.7	320	17	BH778661	fzmb013f0	BH778661
579	13	86.7	287	13	BB361253	BB361253	BB361253	652	13	86.7	321	10	BB206435	BB206435	BB206435
c 580	13	86.7	287	17	A2727252	A2727252	RPC1-24-1	653	13	86.7	322	14	BQ005821	UI-H-ED0-	BQ005821
581	13	86.7	286	9	AA428416	AA428416	zr32d05.f	c 654	13	86.7	322	9	AI875363	uk31c06.y	AI875363
c 582	13	86.7	286	9	AI874407	AI874407	tz65c12.x	655	13	86.7	323	9	AI875363	uk31c06.y	AI875363
583	13	86.7	286	10	BB330111	BB330111	BB330111	656	13	86.7	324	10	BB459722	BB459722	BB459722
c 584	13	86.7	286	10	BB439644	BB439644	BB439644	657	13	86.7	324	10	BB093093	BB093093	BB093093
c 585	13	86.7	287	13	BI440693	BI440693	lb93g03.x	c 658	13	86.7	324	17	BH77593	hr39c10.g	BH77593
c 586	13	86.7	287	9	AA429183	AA429183	zv49f06.f	659	13	86.7	325	10	AA559093	nj33p06.s	AA559093
c 587	13	86.7	287	10	BB382737	BB382737	BB382737	660	13	86.7	325	10	AW739687	BRI00200	AW739687
c 588	13	86.7	287	10	BB550230	BB550230	BB550230	661	13	86.7	325	10	BB138611	BB138611	BB138611
c 589	13	86.7	287	14	WI0844	WI0844	ma47d05.r1	c 662	13	86.7	325	14	BQ161052	WHE1077.E	BQ161052
c 590	13	86.7	287	17	BH128332	BH128332	G-3b16.f	c 663	13	86.7	326	12	BF890915	PM2-MT010	BF890915
591	13	86.7	289	10	BB113081	BB113081	BB113081								

c 664	13	86.7	326	12	BE995814	BE995814	UI-M-BZ1-	737	13	86.7	359	10	BB847677	BB847677	BB847677	BB847677
c 665	13	86.7	326	12	BF197918	BF197918	7p86e09.x	c 738	13	86.7	360	9	AI422524	AI422524	AI422524	AI422524
c 666	13	86.7	327	14	BM709300	BM709300	UI-E-CQ1-	739	13	86.7	360	9	AJ473628	AJ473628	AJ473628	AJ473628
c 667	13	86.7	328	10	AI033641	AI033641	ow14d10.x	c 740	13	86.7	361	17	BH782688	BH782688	fzmb011f0	fzmb011f0
c 668	13	86.7	328	10	BE489020	BE489020	WHE1061.E	c 741	13	86.7	361	12	BF022915	BF022915	uw58g11.x	uw58g11.x
c 669	13	86.7	328	17	AQ001238	AQ001238	CIT-HSP-2	c 742	13	86.7	361	13	BI315305	BI315305	dan97h10.	dan97h10.
c 670	13	86.7	329	12	BE765167	BE765167	IL2-NT009	c 743	13	86.7	362	9	AI415262	AI415262	md19d04.x	md19d04.x
c 671	13	86.7	330	9	AI168814	AI168814	AI68814	c 744	13	86.7	362	10	AV740084	AV740084	AV740084	AV740084
c 672	13	86.7	330	10	BB760094	BB760094	BB760094	745	13	86.7	362	12	BF987482	BF987482	MR3-GN015	MR3-GN015
c 673	13	86.7	330	14	W87797	W87797	zh66a06.s1	746	13	86.7	362	14	W70497	W70497	me17a04.r1	me17a04.r1
c 674	13	86.7	331	9	AI152630	AI152630	ud93a03.r	747	13	86.7	363	17	AQ0908392	AQ0908392	GSSTC0515	GSSTC0515
c 675	13	86.7	332	10	BB453211	BB453211	BB453211	c 748	13	86.7	363	17	AZ033969	AZ033969	RPCI-23-3	RPCI-23-3
c 676	13	86.7	332	12	BF988105	BF988105	CM0-GN016	c 749	13	86.7	364	9	AI376555	AI376555	te64f02.x	te64f02.x
c 677	13	86.7	332	14	BQ027478	BQ027478	UI-H-COO-	c 750	13	86.7	364	12	BF458128	BF458128	UI-M-BZ1-	UI-M-BZ1-
c 678	13	86.7	332	14	BQ662007	BQ662007	HR01C24u	c 751	13	86.7	364	12	BF511472	BF511472	UI-H-B14-	UI-H-B14-
c 679	13	86.7	332	17	AQ002729	AQ002729	CIT978SK-	c 752	13	86.7	365	12	BF760803	BF760803	RC4-CT062	RC4-CT062
c 680	13	86.7	333	10	BB470027	BB470027	BB470027	c 753	13	86.7	365	13	BM661180	BM661180	952044H07	952044H07
c 681	13	86.7	333	14	BQ173952	BQ173952	UI-N-DJ2-	c 754	13	86.7	366	10	AW123992	AW123992	UI-M-BH2.	UI-M-BH2.
c 682	13	86.7	334	9	AI040367	AI040367	ox16b02.x	c 755	13	86.7	369	12	BF525271	BF525271	UI-R-GO-u	UI-R-GO-u
c 683	13	86.7	334	14	R75256	R75256	MD81263 Mou	c 756	13	86.7	370	12	BB841297	BB841297	BB841297	BB841297
c 684	13	86.7	335	9	AA621224	AA621224	zu81g03.s	c 757	13	86.7	370	12	BG878712	BG878712	ib70f02.x	ib70f02.x
c 685	13	86.7	335	10	BB105498	BB105498	BB105498	c 758	13	86.7	370	13	BI351446	BI351446	IPL1-71.G0	IPL1-71.G0
c 686	13	86.7	335	17	A2932917	A2932917	zb50g08.J	c 759	13	86.7	370	17	BH866687	BH866687	hg83c06.x	hg83c06.x
c 687	13	86.7	337	9	AA111310	AA111310	mp10g02.r	c 760	13	86.7	372	10	AW338489	AW338489	xw71c09.x	xw71c09.x
c 688	13	86.7	337	9	AI521408	AI521408	th60c01.x	c 761	13	86.7	373	13	BI316733	BI316733	saf72f06.	saf72f06.
c 689	13	86.7	337	9	AA396436	AA396436	vb27d01.r	c 762	13	86.7	373	17	BH772592	BH772592	tf10g07.b	tf10g07.b
c 690	13	86.7	338	9	AA931006	AA931006	vy81b12.r	c 763	13	86.7	373	17	BH867654	BH867654	hk18h08.x	hk18h08.x
c 691	13	86.7	338	10	AV688484	AV688484	AV688484	c 764	13	86.7	374	9	AU020189	AU020189	AU020189	AU020189
c 692	13	86.7	338	10	BB846949	BB846949	BB846949	c 765	13	86.7	374	10	AW469469	AW469469	hc84g11.x	hc84g11.x
c 693	13	86.7	338	12	BE765001	BE765001	IL2-NT009	c 766	13	86.7	377	10	AW665237	AW665237	AV665237	AV665237
c 694	13	86.7	338	14	BQ344404	BQ344404	MR2-NT013	c 767	13	86.7	377	10	AW439937	AW439937	hal1e03.x	hal1e03.x
c 695	13	86.7	339	9	AI935919	AI935919	wo07h04.x	c 768	13	86.7	377	10	BE018552	BE018552	bb81h11.y	bb81h11.y
c 696	13	86.7	339	9	AV170184	AV170184	AV170184	c 769	13	86.7	377	14	BM692744	BM692744	UI-E-CK1-	UI-E-CK1-
c 697	13	86.7	339	9	AA513326	AA513326	nh85e12.s	c 770	13	86.7	377	14	BM716110	BM716110	UI-E-CK1-	UI-E-CK1-
c 698	13	86.7	340	9	AA856126	AA856126	vw83c08.r	c 771	13	86.7	378	10	BB809329	BB809329	BB809329	BB809329
c 699	13	86.7	340	14	BM717792	BM717792	UI-E-E30-	c 772	13	86.7	378	12	BF591931	BF591931	7o22a06.x	7o22a06.x
c 700	13	86.7	340	14	C95515	C95515	Citr	c 773	13	86.7	378	17	AQ011970	AQ011970	HS-2190.A	HS-2190.A
c 701	13	86.7	342	10	AW167626	AW167626	xn49g07.x	c 774	13	86.7	379	10	BB844236	BB844236	BB844236	BB844236
c 702	13	86.7	343	9	AV207859	AV207859	AV207859	c 775	13	86.7	380	17	AQ827195	AQ827195	HS-5255.A	HS-5255.A
c 703	13	86.7	343	10	AW656179	AW656179	108286.MA	c 776	13	86.7	382	9	AI138567	AI138567	qd85a09.x	qd85a09.x
c 704	13	86.7	343	10	BB271907	BB271907	BB271907	c 777	13	86.7	382	12	BF706002	BF706002	280129.MA	280129.MA
c 705	13	86.7	343	10	BB869774	BB869774	BB869774	c 778	13	86.7	383	9	AA443585	AA443585	zw35a11.s	zw35a11.s
c 706	13	86.7	343	17	AZ453786	AZ453786	qb21f05.x	c 779	13	86.7	383	9	AA461424	AA461424	zx63g12.r	zx63g12.r
c 707	13	86.7	344	9	AA309669	AA309669	EST18057	c 780	13	86.7	383	12	BF735563	BF735563	CM1-AN008	CM1-AN008
c 708	13	86.7	344	14	BM679812	BM679812	UI-E-E30-	c 781	13	86.7	384	13	BM106462	BM106462	510201.MA	510201.MA
c 709	13	86.7	344	17	BH049025	BH049025	RPCI-24-2	c 782	13	86.7	385	9	AI007102	AI007102	ua71g01.r	ua71g01.r
c 710	13	86.7	345	10	BB868274	BB868274	BB868274	c 783	13	86.7	386	13	BI333717	BI333717	AV089B12P	AV089B12P
c 711	13	86.7	346	13	BI321044	BI321044	sa724h09.	c 784	13	86.7	387	10	AV815957	AV815957	AV815957	AV815957
c 712	13	86.7	346	13	BI321044	BI321044	sa724h09.	c 785	13	86.7	387	12	BF442623	BF442623	259522.MA	259522.MA
c 713	13	86.7	347	9	AA524736	AA524736	ng42f10.s	c 786	13	86.7	387	14	D81224	D81224	HUM139B05B	HUM139B05B
c 714	13	86.7	347	12	BF455276	BF455276	UI-M-BZ1-	c 787	13	86.7	388	9	AA926636	AA926636	om28a08.S	om28a08.S
c 715	13	86.7	347	12	BF974052	BF974052	602243236	c 788	13	86.7	388	10	AW044694	AW044694	wy74c07.x	wy74c07.x
c 716	13	86.7	347	17	BH779644	BH779644	fzmb014f0	c 789	13	86.7	388	12	BF122891	BF122891	601760234	601760234
c 717	13	86.7	349	13	BM545596	BM545596	AGENCOURT	c 790	13	86.7	389	12	BF655157	BF655157	279563.MA	279563.MA
c 718	13	86.7	350	10	BE239963	BE239963	EST404012	c 791	13	86.7	389	14	BM987540	BM987540	UI-H-COO-	UI-H-COO-
c 719	13	86.7	350	14	W53624	W53624	md56g04.r1	c 792	13	86.7	390	9	AI767790	AI767790	w196f03.x	w196f03.x
c 720	13	86.7	350	17	BH867767	BH867767	hk19h11.x	c 793	13	86.7	390	10	BB372536	BB372536	BB372536	BB372536
c 721	13	86.7	351	9	AI826583	AI826583	wk16d02.x	c 794	13	86.7	391	14	BM673680	BM673680	UI-E-CR1-	UI-E-CR1-
c 722	13	86.7	351	10	AW662668	AW662668	hi34f11.x	c 795	13	86.7	392	17	AZ081527	AZ081527	pl02E11#9	pl02E11#9
c 723	13	86.7	351	12	BF891691	BF891691	PM2-MT010	c 796	13	86.7	393	14	C97650	C97650	c97650.Rice	c97650.Rice
c 724	13	86.7	351	13	BI977204	BI977204	486592.MA	c 797	13	86.7	394	9	AA579788	AA579788	nk43d02.S	nk43d02.S
c 725	13	86.7	351	14	W78359	W78359	me88d08.r1	c 798	13	86.7	394	14	B54661	B54661	md02c10.r1	md02c10.r1
c 726	13	86.7	352	9	AA639101	AA639101	ns03d02.r	c 799	13	86.7	395	14	BQ102373	BQ102373	ij70g02.x	ij70g02.x
c 727	13	86.7	353	9	AA007911	AA007911	mg76c08.r	c 800	13	86.7	396	13	BI070611	BI070611	C040P66U	C040P66U
c 728	13	86.7	353	10	AA356726	AA356726	39283.MAR	c 801	13	86.7	397	9	AI014664	AI014664	ov34g04.x	ov34g04.x
c 729	13	86.7	354	14	R45332	R45332	Y946H05.s1	c 802	13	86.7	397	9	AI753292	AI753292	cr08b02.x	cr08b02.x
c 730	13	86.7	354	14	T35373	T35373	EST83721.Hu	c 803	13	86.7	397	17	BB813203	BB813203	BB813203	BB813203
c 731	13	86.7	355	10	BE646787	BE646787	UI-M-BH1-	c 804	13	86.7	397	17	BH788847	BH788847	fzmb021f0	fzmb021f0
c 732	13	86.7	355	17	BH781844	BH781844	fzmb021f0	c 805	13	86.7	398	9	AI250924	AI250924	qi37f04.x	qi37f04.x
c 733	13	86.7	356	9	AI032641	AI032641	ow17h08.x	c 806	13	86.7	399	10	AW476210	AW476210	uq81b11.x	uq81b11.x
c 734	13	86.7	357	10	BB791064	BB791064	BB791064	c 807	13	86.7	399	12	BE758785	BE758785	an_3030.A	an_3030.A
c 735	13	86.7	358	9	AI025462	AI025462	ov67a03.x	c 808	13	86.7	399	14	R44022	R44022	yg21c10.s1	yg21c10.s1
c 736	13	86.7	358	9	AI569435	AI569435	tn86g08.x	c 809	13	86.7	399	17	AQ908014	AQ908014	GSSTC0539	GSSTC0539

810	13	86.7	399	17	BH881185	BH881185 hv23g10.b	883	13	86.7	430	9	AA584277	AA584277 nn75g06.s
811	13	86.7	400	9	AA962442	AA962442 om81b06.s	884	13	86.7	430	10	BB864334	BB864334 BB864334
812	13	86.7	400	9	AL360883	AL360883 AL360883	885	13	86.7	430	12	BF476704	BF476704 nae43c02
813	13	86.7	400	14	BQ567225	BQ567225 g183c06.y	886	13	86.7	430	17	AQ727176	AQ727176 HS_5436.B
814	13	86.7	400	17	BH871284	BH871284 hm72c10.g	887	13	86.7	430	17	BH328201	BH328201 CH230-93N
815	13	86.7	401	10	AW298895	AW298895 146 MARC	888	13	86.7	430	17	AI496901	AI496901 fb63g01.x
816	13	86.7	402	17	R05796	R05796 ye93d06.s1	889	13	86.7	431	9	AI529848	AI529848 u183b09.y
817	13	86.7	402	17	BH875706	BH875706 hr26e08.g	890	13	86.7	431	9	BB845857	BB845857 BB845857
818	13	86.7	403	9	AA890247	AA890247 aj92c04.s	891	13	86.7	431	12	BG408305	BG408305 qc9q012.y
819	13	86.7	403	12	BE992411	BE992411 UI-M-BZ1-	892	13	86.7	431	12	BE814752	BE814752 PM3-BN008
820	13	86.7	403	17	B71800	B71800 RPC111-1004	893	13	86.7	431	12	BH255985	BH255985 RDH10BAM0
821	13	86.7	404	9	AI086544	AI086544 oz27b07.x	894	13	86.7	431	17	BH784110	BH784110 fzm0013f0
822	13	86.7	404	9	AA551617	AA551617 nj57c01.s	895	13	86.7	432	9	AI240297	AI240297 q114a03.x
823	13	86.7	404	17	AZ778546	AZ778546 2M0013M03	896	13	86.7	432	9	AI963396	AI963396 w62f08.x
824	13	86.7	405	17	BH881683	BH881683 hv27d06.b	897	13	86.7	432	9	BB774535	BB774535 BB774535
825	13	86.7	407	9	AA548655	AA548655 nj17f09.s	898	13	86.7	432	17	AQ035689	AQ035689 CIT-HSP-2
826	13	86.7	407	14	H24597	H24597 y14h08.s1	899	13	86.7	434	10	AV689988	AV689988 AV689988
827	13	86.7	407	17	BH127109	BH127109 G-10h7.f	900	13	86.7	435	9	AA725177	AA725177 a115d12.s
828	13	86.7	408	10	AW575812	AW575812 UI-HF-BN0	901	13	86.7	435	9	AI367006	AI367006 qz23f02.x
829	13	86.7	408	10	AW673006	AW673006 ba61c08.x	902	13	86.7	435	12	BE946309	BE946309 UI-M-BZ0-
830	13	86.7	408	14	BM958820	BM958820 PLATE.18	903	13	86.7	435	14	N31678	N31678 yx69d07.r1
831	13	86.7	408	14	BQ640275	BQ640275 he26d07.y	904	13	86.7	435	17	BH780566	BH780566 fzm0020f0
832	13	86.7	409	9	AI991978	AI991978 ws43d02.x	905	13	86.7	436	9	AI012202	AI012202 EST206653
833	13	86.7	409	10	AV689509	AV689509 AV689509	906	13	86.7	436	10	AV688845	AV688845 AV688845
834	13	86.7	409	12	BG801437	BG801437 0103-91 M	907	13	86.7	436	13	BI735392	BI735392 603356879
835	13	86.7	409	14	T15835	T15835 IB1965 Infa	908	13	86.7	437	10	AW483775	AW483775 56394 MAR
836	13	86.7	409	17	AG019551	AG019551 Homo sapi	909	13	86.7	438	9	AI161177	AI161177 qb50f09.x
837	13	86.7	410	9	AI090391	AI090391 oy18f06.s	910	13	86.7	438	10	AV594520	AV594520 AV594520
838	13	86.7	410	17	BH778436	BH778436 fzm0013f0	911	13	86.7	438	10	BB847418	BB847418 BB847418
839	13	86.7	411	9	AI853865	AI853865 UI-M-BH0-	912	13	86.7	438	12	BF072706	BF072706 NCSM4B87
840	13	86.7	412	9	AA601639	AA601639 no01b10.s	913	13	86.7	438	17	BH774709	BH774709 fzm0001f0
841	13	86.7	412	10	BB788314	BB788314 BB788314	914	13	86.7	439	14	W74185	W74185 zd75f07.s1
842	13	86.7	412	12	BG092933	BG092933 mac21d01.	915	13	86.7	440	9	AA127951	AA127951 z113e06.s
843	13	86.7	412	12	BE754204	BE754204 207644 MA	916	13	86.7	440	12	BE695584	BE695584 MRI-BT079
844	13	86.7	413	9	AA274572	AA274572 vb05c07.r	917	13	86.7	441	10	AW351507	AW351507 IL2-CT003
845	13	86.7	413	17	AQ705660	AQ705660 HS_5543.A	918	13	86.7	441	10	BB750305	BB750305 BR2-50305
846	13	86.7	413	17	BH358434	BH358434 CH230-176	919	13	86.7	441	12	BE716060	BE716060 MR2-HT075
847	13	86.7	416	9	AA813568	AA813568 al67h06.s	920	13	86.7	441	12	BE809015	BE809015 214353 MA
848	13	86.7	416	9	AI624144	AI624144 ts26d10.x	921	13	86.7	441	12	BF072745	BF072745 NCSM4D97
849	13	86.7	416	10	AW144717	AW144717 EST290643	922	13	86.7	441	13	BM236172	BM236172 K0431C12-
850	13	86.7	416	12	BG345227	BG345227 gdc39b12.	923	13	86.7	441	17	BQ086285	BQ086285 lj20g02.y
851	13	86.7	416	14	R44643	R44643 yg29b11.s1	924	13	86.7	441	17	BH748735	BH748735 SALK_0466
852	13	86.7	416	17	BH127411	BH127411 G-1c3.f M	925	13	86.7	441	17	BH876189	BH876189 hr29e09.b
853	13	86.7	418	9	AA724315	AA724315 ah99c12.s	926	13	86.7	442	9	AI385287	AI385287 UI-R-C2-m
854	13	86.7	418	12	BE947281	BE947281 UI-M-BH3-	927	13	86.7	442	13	BM106305	BM106305 510007 MA
855	13	86.7	419	13	B1287651	B1287651 UI-R-CW0S	928	13	86.7	442	14	R51120	R51120 yg71a03.r1
856	13	86.7	419	13	BM303974	BM303974 SNEST4a46	929	13	86.7	443	9	AU171605	AU171605 AU171605
857	13	86.7	419	14	W97620	W97620 mg01h05.r1	930	13	86.7	443	12	BE750911	BE750911 202583 MA
858	13	86.7	420	10	BE049539	BE049539 xw88f11.x	931	13	86.7	444	9	AA461891	AA461891 vf94g12.r
859	13	86.7	420	17	AQ444133	AQ444133 GSSTC0996	932	13	86.7	444	14	BQ490255	BQ490255 33-59436-
860	13	86.7	421	14	BM716007	BM716007 UI-E-EJ0-	933	13	86.7	445	9	AI786501	AI786501 uf15g02.y
861	13	86.7	422	9	AI911472	AI911472 wd25e04.x	934	13	86.7	445	9	AI786501	AI786501 ui-M-BH1-
862	13	86.7	422	17	AZ289156	AZ289156 RPCI-23-1	935	13	86.7	445	10	AW045639	AW045639 UI-M-BH1-
863	13	86.7	423	9	AI925801	AI925801 wo35h02.x	936	13	86.7	445	10	AW483773	AW483773 56386 MAR
864	13	86.7	423	10	BB789324	BB789324 BB789324	937	13	86.7	445	10	BB858735	BB858735 BB858735
865	13	86.7	423	17	AZ444275	AZ444275 1M0239114	938	13	86.7	445	12	BG274755	BG274755 WHE223.F
866	13	86.7	425	10	AW762669	AW762669 ur58b10.y	939	13	86.7	446	9	AA895769	AA895769 vy14h04.r
867	13	86.7	425	12	BF444227	BF444227 262018 MA	940	13	86.7	446	9	AI955593	AI955593 wt58f08.x
868	13	86.7	425	17	B34167	B34167 HS-1024-A1-	941	13	86.7	446	17	BH788624	BH788624 fzm0020f0
869	13	86.7	426	9	AA843487	AA843487 aj17b02.s	942	13	86.7	446	17	AQ645383	AQ645383 RPC193-Dp
870	13	86.7	426	10	AW048205	AW048205 UI-M-BH1-	943	13	86.7	447	12	BF602136	BF602136 267295 MA
871	13	86.7	426	17	BH873766	BH873766 hp46f08.b	944	13	86.7	447	12	BG372987	BG372987 UI-R-CV1-
872	13	86.7	427	9	AA096944	AA096944 mol5h03.r	945	13	86.7	447	17	AQ276450	AQ276450 IM0561A04
873	13	86.7	427	9	AI825921	AI825921 tg92c09.x	946	13	86.7	447	17	AQ359885	AQ359885 HS_5032.B
874	13	86.7	427	10	BH847997	BH847997 BB847997	947	13	86.7	448	14	W79856	W79856 zd75f07.r1
875	13	86.7	427	17	AQ763977	AQ763977 HS_2174_B	948	13	86.7	448	17	BH881107	BH881107 hv23c10.b
876	13	86.7	427	17	BH779502	BH779502 fzm0014f0	949	13	86.7	449	10	AW446622	AW446622 UI-H-B13-
877	13	86.7	428	9	AA466584	AA466584 ve20d09.r	950	13	86.7	449	12	BE716058	BE716058 BB771750
878	13	86.7	428	17	BH867655	BH867655 hk18h08.y	951	13	86.7	449	12	BE716058	BE716058 MR2-HT075
879	13	86.7	429	13	BM288529	BM288529 529819 MA	952	13	86.7	449	14	W71661	W71661 me17f04.r1
880	13	86.7	429	17	AZ759667	AZ759667 1M0552K04	953	13	86.7	450	9	AI690276	AI690276 tx33f10.x
881	13	86.7	429	17	BH255980	BH255980 RDH10BAM0	954	13	86.7	450	17	BH771938	BH771938 hg85d08.b
882	13	86.7	429	17	BH772096	BH772096 hg88d03.b	955	13	86.7	450	17	BH771939	BH771939 hg85d08.g

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c 956      13      86.7      450      17      BH876695      hr32g07.b
c 957      13      86.7      451      10      BB840417
c 958      13      86.7      451      14      R50904      yg70f04.r1
c 959      13      86.7      452      9      AI384036
c 960      13      86.7      452      14      B0787218
c 961      13      86.7      453      9      AI922046
c 962      13      86.7      453      12      BF365993
c 963      13      86.7      453      17      BF365993      PM2-NT007
c 964      13      86.7      454      9      AA102916
c 965      13      86.7      454      10      AW463201
c 966      13      86.7      454      10      AW764260
c 967      13      86.7      454      12      BE810059
c 968      13      86.7      454      17      AQ426561
c 969      13      86.7      455      9      AU155693
c 970      13      86.7      455      10      BH831127
c 971      13      86.7      455      13      BJ275006
c 972      13      86.7      456      9      AA871195
c 973      13      86.7      456      12      BF344323
c 974      13      86.7      456      14      T90046
c 975      13      86.7      457      10      BB861945
c 976      13      86.7      458      9      AA811285
c 977      13      86.7      459      9      AA595097
c 978      13      86.7      459      17      BH129015
c 979      13      86.7      460      9      AI264033
c 980      13      86.7      460      9      AL650989
c 981      13      86.7      460      10      AW230991
c 982      13      86.7      460      10      BE303796
c 983      13      86.7      460      12      BG231740
c 984      13      86.7      460      17      BH098427
c 985      13      86.7      460      17      BH873765
c 986      13      86.7      461      9      AI660101
c 987      13      86.7      461      12      BG002754
c 988      13      86.7      461      12      BE810065
c 989      13      86.7      461      13      BM102770
c 990      13      86.7      461      17      BH837196
c 991      13      86.7      462      9      AI073428
c 992      13      86.7      462      9      AI798852
c 993      13      86.7      462      10      AW296329
c 994      13      86.7      462      10      BB836778
c 995      13      86.7      462      12      BF291788
c 996      13      86.7      462      14      C22356
c 997      13      86.7      462      17      BH785148
c 998      13      86.7      463      9      AI424915
c 999      13      86.7      463      10      AV668547
c 1000     13      86.7      463      14      W23819

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ALIGNMENTS

```

RESULT 1
AZ284882      181 bp      DNA      linear      GSS      27-JUL-2000
LOCUS      RPCI-23-442E20.TV      RPCI-23      Mus musculus      genomic clone      RPCI-23-442E20
DEFINITION      , DNA sequence.
ACCESSION      AZ284882
VERSION      AZ284882.1      GI:9526668
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 181)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Kroi,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-442E20.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

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Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.Org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
Plate: 442      row: E      column: 20
Seq primer: T7
Class: BAC ends.

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FEATURES

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source
Location/Qualifiers
1..181
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-442E20"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site.1:
EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      54 a      54 c      26 g      47 t
ORIGIN
Query Match      100.0%; Score 15; DB 17; Length 181;
Best Local Similarity      100.0%; Pred. No. 5.5e+02;
Matches      15; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
QY      1      CCTTCTCCCTGTT      15
|||||
Db      165      CCTTCTCCCTGTT      179

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RESULT 2
AV335397
LOCUS      AV335397      226 bp      mRNA      linear      EST      11-NOV-1999
DEFINITION      AV335397      RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 630571M18 3' similar to AF006196 Mus
musculus metallopeptidase-disintegrin MDC15 mRNA, mRNA sequence.
ACCESSION      AV335397
VERSION      AV335397.1      GI:6375449
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 226)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
,C., Kawai,J., Kikuchi,N., Kojima,Y., Koyama,S., Kusakabe,M.,
Masuyama,T., Miki,K., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
Suzuki,H., Takahashi,F., Tateno,M., Tomimaga,N., Tsunoda,Y.,
Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

```

Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999).
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES

source
 Location/Qualifiers
 1..226
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="633057IM18"
 /clone_lib="RIKEN full-length enriched, adult male medulla
 oblongata"
 /sex="male"
 /tissue.type="medulla oblongata"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGAGAGAGAGAGAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATTCGAGTAAATTAATCCCGCCCGCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
 BamHI"

BASE COUNT 55 a 51 c 63 g 56 t 1 others
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 226;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTCTCCCCCTGTT 15
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 Db 77 CCTTCTCCCCCTGTT 91

RESULT 3
 AL708655/c
 LOCUS AL708655 246 bp mRNA linear EST 22-MAR-2002
 DEFINITION DKFZp686J0853_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DKFZp686J0853 5', mRNA sequence.

ACCESSION AL708655
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 246)
 Wambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.

TITLE

JOURNAL Unpublished (1999)
 COMMENT Contact: Wambutt R
 MIPS
 Am Klopferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 No sl sequence available.

This clone (DKFZp686J0853) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
 Location/Qualifiers
 1..246
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZp686J0853"
 /clone_lib="686 (synonym: hlcc3)"
 /tissue.type="human skeletal muscle"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiIB;
 cDNA-collection"

BASE COUNT 71 a 47 c 88 g 40 t
 ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 246;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
 |||||||||||||
 Db 176 CCTTCTCCCCCTGTT 162

RESULT 4
 AV067076/c
 LOCUS AV067076 297 bp mRNA linear EST 24-JUN-1999
 DEFINITION AV067076 Mus musculus small intestine C57BL/6J adult Mus musculus
 cDNA clone 2010200P09, mRNA sequence.

ACCESSION AV067076
 VERSION AV067076.1 GI:5186904
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 297)
 Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
 Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara,
 A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
 Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C.,
 Sato, K., Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara,
 Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomimaga, N.,
 Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
 Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermotabilization and thermoactivation of thermostable enzymes by
 trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for


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ACCESSION      AJ449549
VERSION        AJ449549.1  GI:20216770
KEYWORDS       EST.
SOURCE         chicken.
ORGANISM       Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
               Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 399)
AUTHORS        Buerstedde,J.M.
TITLE          Gallus gallus bursal lymphocyte EST
JOURNAL        Unpublished (2002)
COMMENT        Contact: Buerstedde JM
               Cellular Immunology
               Heinrich-Pette-Institute
               Martinistr. 52, 20251 Hamburg, Germany
               Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
               Location/Qualifiers
               1..399
               /organism="Gallus gallus"
               /db_xref="taxon:9031"
               /clone="22g1lrl"
               /clone_lib="rikeni"
               /cell_type="bursal lymphocyte"
               /dev_stage="2-3 weeks old"
               /note="CB inbred strain"

BASE COUNT    120 a 78 c 103 g 97 t 1 others
ORIGIN

Query Match      100.0%; Score 15; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||
DB 107 CCTTCTCCCCCTGTT 93

RESULT 8
TABE07P
LOCUS          TABE07P
DEFINITION    T. brucei sheared genomic DNA clone 8e07, forward sequence, genomic
               survey sequence.
ACCESSION     AL452614.1  GI:11861158
VERSION       AL452614
KEYWORDS      GSS.
SOURCE        Trypanosoma brucei.
ORGANISM      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE     1 (bases 1 to 401)
AUTHORS       Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
               Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
               Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE         Direct Submission
JOURNAL       Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
COMMENT       Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/projects/T_brucei/.
               Location/Qualifiers
               1....401

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/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="8e07"

BASE COUNT    81 a 91 c 118 g 111 t
ORIGIN

Query Match      100.0%; Score 15; DB 17; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||
DB 67 CCTTCTCCCCCTGTT 81

RESULT 9
BI706542/c
LOCUS          BI706542
DEFINITION    fq07c03.y1 Zebrafish adult retina cDNA Danio rerio cDNA clone
               4790765 5', similar to TR:Q9UH03 Q9UH03 BK250D10.3 ;, mRNA sequence.
ACCESSION     BI706542
VERSION       BI706542.1  GI:15682237
KEYWORDS      EST.
SOURCE        zebrafish.
ORGANISM      Danio rerio
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
               ; Cyprinidae; Danio.
REFERENCE     1 (bases 1 to 403)
AUTHORS       Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
               ,K., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
               ,K., Stepcoe,M., Thelsing,B., Allen,M., Bowers,T., Person,B.,
               Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
               Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
               and Willson,R.
TITLE         WashU Zebrafish EST Project 1998
JOURNAL       Unpublished (1998)
COMMENT       Contact: Stephen L. Johnson
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: zbrafish@watson.wustl.edu
               Library constructed by: Chandra Tucker and Gregory Niemi DNA
               Sequencing by: Washington University Genome Sequencing Center Clone
               distribution: RessourcenzentrumPrimarDatenbank, Berlin, Germany
               (web address: www.rzpd.de)
               Seq primer: T3 ET from Amersham
               High quality sequence stop: 396.
               Location/Qualifiers
               1..403
               /organism="Danio rerio"
               /strain="wild-type"
               /db_xref="taxon:7955"
               /clone="4790765"
               /clone_lib="Zebrafish adult retina cDNA"
               /sex="mixed"
               /dev_stage="1-2 years"
               /lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
               /note="vector: Lambda ZAP II (pBluescript SK-); Site_1:
               EcoRI; Site_2: SalI; This Zebrafish library was
               constructed by Dr. Susan E. Brockerhoff (email:
               sbrocker@u.washington.edu) RZPD library number: 760"

BASE COUNT    105 a 89 c 116 g 93 t
ORIGIN

Query Match      100.0%; Score 15; DB 13; Length 403;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||

```

```

Db 114 CCTTCTCCCCCTGTT 100
      TAG_SEQ=AATGC"
      110 a 124 c 91 g 85 t

RESULT 10
AW139708/c
LOCUS
DEFINITION
  UI-H-B11-aeb-a-03-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
  IMAGE:2718605 3', mRNA sequence.
ACCESSION
  AW139708
VERSION
  EST.
KEYWORDS
  human.
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 410)
  NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  Oligo-dT track not found. Not 1 site shown in beginning of sequence
  is likely internal to the message. cDNA Library Preparation: M.B.
  Soares Lab Clone distribution: NCI_CGAP clone distribution
  information can be found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html The following repetitive
  elements were found in this cDNA sequence: 151-216, >(GGGA
  )n$Simple.repeat
  Seq primer: M13 Forward
  POLYA-No.

FEATURES
      source
      1..410
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:2718605"
      /clone_lib="NCI_CGAP_Sub3"
      /lab_host="DH10B (Life Technologies)"
      /note="Vector: pT7T3-Pac (Pharmacia) with a modified
      polylinker. Site.1: Not 1; Site.2: Eco RI; The
      NCI_CGAP_Sub3 library is a subtracted library derived from
      the NCI_CGAP_Sub1 library, which is a subtracted library
      derived from B1. B1 constitutes a mixture of 21
      normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
      , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
      NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
      NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
      NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_C11L1, NCI_CGAP_Le12,
      NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
      NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
      NCI_CGAP_Brn25. These 21 libraries were pooled and a
      single-stranded DNA preparation of the resulting mixture
      was used as a tracer in a subtractive hybridization with
      a driver whose composition is detailed below:
      NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
      3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775
      , 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342
      , 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831,
      1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
      LLAM 3375-3582, 3851-3854 (IMAGE Clonoids 1141920-1417991,
      1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
      3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,
      1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
      LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids
      985608-986759, 1101192-1101959, 1217928-1220615);
      NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
      Clonoids 1057416-1061255, 1144584-1145351). Subtraction
      was performed as previously described [Bonaldo, Lennon &
      Soares (1996): Normalization and Subtraction: Two
      Approaches To Facilitate Gene Discovery. Genome Research
      6, 791-806.
      TAG_LIB=NCI_CGAP_Kid3
      TAG_TISSUE=Kidney

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```

BASE COUNT 110 a 124 c 91 g 85 t
ORIGIN
  Query Match 100.0%; Score 15; DB 10; Length 410;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
  |||||
Db 396 CCTTCTCCCCCTGTT 382
  |||||

RESULT 11
AW504644/c
LOCUS
DEFINITION
  UI-HF-BN0-alk-h-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
  IMAGE:3079943 5', mRNA sequence.
ACCESSION
  AW504644
VERSION
  EST.
KEYWORDS
  human.
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 420)
  NIH-MGC http://imgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  Eco RI site shown at the beginning of the sequence.
  Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
  cDNA Library Preparation: M.B. Soares Lab
  cDNA Library Arrayed by: M.B. Soares Lab
  DNA Sequencing by: M.B. Soares Lab
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Seq primer: M13 Forward.

FEATURES
      source
      1..420
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:3079943"
      /clone_lib="NIH_MGC_50"
      /tissue_type="lymph"
      /cell_type="germinal center B cells"
      /cell_line="MGC85"
      /lab_host="DH10B (LTI)"
      /note="Vector: pT7T3-Pac; Site.1: Not1; Site.2: Eco RI;
      Constructed from size fractionated cytoplasmic mRNA
      (3.5-4.4Kb). Directionally cloned. Cells provided by
      Louis M. Staudt, Ph.D. Library preparation by Maria de
      Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
      124 a 72 c 126 g 98 t

BASE COUNT 124 a 72 c 126 g 98 t
ORIGIN
  Query Match 100.0%; Score 15; DB 10; Length 420;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
  |||||
Db 159 CCTTCTCCCCCTGTT 145
  |||||

RESULT 12
BF514910/c
LOCUS
DEFINITION
  UI-H-BM1-app-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
  IMAGE:3083036 3', mRNA sequence.
ACCESSION
  BF514910
  UI-H-BM1-app-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
  IMAGE:3083036 3', mRNA sequence.

```



```

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
  source
    High quality sequence start: 12
    High quality sequence stop: 29
    Location/Qualifiers
      source
        1..431
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="NN0045"
        /dev_stage="Adult"
        /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
        Site_2: SmaI; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        No. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."
BASE COUNT      75 a   138 c   108 g   110 t
ORIGIN
  Query Match      100.0%; Score 15; DB 14; Length 431;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||
Db 399 CCTTCTCCCCCTGTT 413

Search completed: December 11, 2002, 19:01:29
Job time : 1715.5 secs

EST.
Populus balsamifera subsp. trichocarpa.
Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 430)
Hertzberg,M., Aspeborg,H., Erlandsson,R., Bjorkbacka,H., Hiltunen
,T., Karlsson,J., Teeri,T., Gustafsson,P., Bahlerao,R., Jansson,S.,
Nilsson,O., Sundberg,B., Nilsson,P., Uhlen,M., Sandberg,G. and
Lundeberg,J.
Gene expression in Populus
Unpublished (2001)
Contact: Erlandsson R
Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
Email: rikeri@biochem.kth.se.
FEATURES
  source
    1..430
    /organism="Populus balsamifera subsp. trichocarpa"
    /db_xref="taxon:3694"
    /clone_lib="Populus flower cDNA library"
    /note="Organ: flower"
BASE COUNT      126 a   113 c   78 g   113 t
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||
Db 220 CCTTCTCCCCCTGTT 234

RESULT 15
BQ339760
LOCUS      BQ339760      431 bp      mRNA      linear      EST 20-MAY-2002
DEFINITION QV2-NN0045-211100-494-c07 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ339760
VERSION    BQ339760.1 GI:20999826
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 431)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-
211100-494-c07&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:26:07 ; Search time 1657 Seconds
(without alignments)
263.453 Million cell updates/sec

Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 cctctccccctgtt 15

Scoring table: IDENTITY_NUC
Gapox 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl : *
1: gb_ba : *
2: gb_htg : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_pro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vi : *
15: em_ba : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
26: em_ro : *
27: em_sts : *
28: em_un : *
29: em_vi : *
30: em_htg_hum : *
31: em_htg_inv : *
32: em_htg_other : *
33: em_htg_mus : *
34: em_htg_pin : *
35: em_htg_rod : *
36: em_htg_mam : *
37: em_htg_vrt : *
38: em_sy : *
39: em_htgo_hum : *
40: em_htgo_mus : *
41: em_htgo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	15	100.0	190	9	HS288489	AJ288489 Homo sapi
C 2	15	100.0	600	5	AF506010	AF506010 Gallus ga
C 3	15	100.0	1689	9	AK021867	AK021867 Homo sapi
C 4	15	100.0	1721	4	AF232676	AF232676 Sus scrofa
C 5	15	100.0	3190	9	BC000776	BC000776 Homo sapi
C 6	15	100.0	3347	5	CHKTGFEA	L01121 Gallus gall
C 7	15	100.0	3752	9	AF312211	AF312211 Homo sapi
C 8	15	100.0	4359	9	AB018279	AB018279 Homo sapi
C 9	15	100.0	11001	5	FR092H06	AL035357 Fugu rubr
C 10	15	100.0	11896	1	AE009810	AE009810 Pyrobacul
C 11	15	100.0	12602	14	AF144617	AF144617 Pestivirus
C 12	15	100.0	32802	1	BSSRFAP	X70356 B. subtilis
C 13	15	100.0	34578	9	AC107069	AC107069 Homo sapi
C 14	15	100.0	43347	9	AL138734	AL138734 Human DNA
C 15	15	100.0	56701	9	AL583852	AL583852 Human DNA
C 16	15	100.0	61720	2	AC131033	AC131033 Mus muscu
C 17	15	100.0	62755	2	AC097798	AC097798 Rattus no
C 18	15	100.0	64209	2	AC120156	AC120156 Mus muscu
C 19	15	100.0	65377	9	AL391356	AL391356 Human DNA
C 20	15	100.0	65421	2	AC129736	AC129736 Rattus no
C 21	15	100.0	66283	2	AC108314	AC108314 Rattus no
C 22	15	100.0	68171	9	AL158205	AL158205 Human DNA
C 23	15	100.0	71117	9	HSJ132F21	AL079335 Human DNA
C 24	15	100.0	88502	2	AC021967	AC021967 Homo sapi
C 25	15	100.0	99752	2	AC111526	AC111526 Rattus no
C 26	15	100.0	102853	2	AC116184	AC116184 Rattus no
C 27	15	100.0	106186	2	AC105876	AC105876 Rattus no
C 28	15	100.0	110000	2	AC103237_2	Continuation (3 of
C 29	15	100.0	110000	2	AC125066_2	Continuation (2 of
C 30	15	100.0	110000	2	AC125102_1	Continuation (2 of
C 31	15	100.0	113370	9	AL591493	AL591493 Human DNA
C 32	15	100.0	126392	2	AC018785	AC018785 Homo sapi
C 33	15	100.0	132526	2	AC120946	AC120946 Rattus no
C 34	15	100.0	141105	2	AC117134	AC117134 Rattus no
C 35	15	100.0	141289	9	AL449363	AL449363 Human DNA
C 36	15	100.0	142059	2	AC121163	AC121163 Rattus no
C 37	15	100.0	142662	2	AC118810	AC118810 Rattus no
C 38	15	100.0	142882	2	AC128133	AC128133 Rattus no
C 39	15	100.0	144201	9	HS230119	Z93942 Human DNA s
C 40	15	100.0	146191	1	D50453	D50453 Bacillus su
C 41	15	100.0	146427	2	AC124033	AC124033 Rattus no
C 42	15	100.0	148500	2	AC094249	AC094249 Rattus no
C 43	15	100.0	151514	2	AC113827	AC113827 Rattus no
C 44	15	100.0	154023	2	AC112466	AC112466 Rattus no
C 45	15	100.0	154888	2	AC114830	AC114830 Rattus no

ALIGNMENTS

RESULT 1
HSA288489/c
LOCUS HSA288489 190 bp DNA linear PRI 04-APR-2001
DEFINITION Homo sapiens partial COL4A3 gene for alpha3 type IV collagen, exon 3.
ACCESSION AJ288489
VERSION AJ288489.1 GI:13559182
KEYWORDS alpha3 type IV collagen; col4a3 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 190)
AUTHORS Heidet,L., Arrondel,C., Forestier,L., Cohen-Solal,L., Mollet,G., Gutierrez,B., Stavrou,C., Gubler,M.C. and Antignac,C.

TITLE Structure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome

J. Am. Soc. Nephrol. 12 (1), 97-106 (2001)

21064696

PUBMED 11134255

REFERENCE 2 (bases 1 to 190)

AUTORS Antignac,C.

TITLE Direct Submission

JOURNAL Submitted (28-MAR-2000) Antignac C., U423, INSERM, Hopital Necker-Enfants malades 149 rue de Sevres, 75015 Paris, FRANCE

FEATURES

source Location/Qualifiers

1..190

/organism="Homo sapiens"

/db_xref="taxon:9606"

51..140

/gene="COL4A3"

51..140

/gene="COL4A3"

/number=3

/usedin=AJ288487:cal_mRNA

/usedin=AJ288487:cal_CDS

37 a 55 c 49 g 49 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 190;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCGTT 15

|||||

Db 60 CCTTCTCCCTCGTT 46

RESULT 2

AF506010/c

LOCUS

DEFINITION Gallus gallus TNF family B cell activation factor (BAFF) mRNA, partial cds.

ACCESSION AF506010

VERSION AF506010.1 GI:22087370

KEYWORDS

SOURCE chicken.

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 600)

AUTORS Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and Staeheli,P.

TITLE A chicken homolog of the B cell activating factor of the TNF family (BAFF)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 600)

AUTORS Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and Staeheli,P.

TITLE Direct Submission

JOURNAL Submitted (24-APR-2002) Virology, University of Freiburg, Hermann-Herder-Str.11, Freiburg 79104, Germany

FEATURES

source Location/Qualifiers

1..600

/organism="Gallus gallus"

/db_xref="taxon:9031"

<1..600

/gene="BAFF"

<1..534

/gene="BAFF"

/codon_start=1

/product="TNF family B cell activation factor"

/protein_id="AA090951.1"

/db_xref="GI:22087371"

/translation="RLPGSPAESFQFEIDNRNRGRSRIVNAETVLAQCLQIAD SKDIQKDDSSIVPLWSFKRGTALEEQGNKIVIKETGYFFIYGQVLYDTDTFAMGH LIQKKARHVFDDLSLVTLPFCIQNMPQSPNNSCYTAGIAKLEGEDELQITIPRRRA

BASE COUNT 186 a 117 c 133 g 164 t

ORIGIN

Query Match 100.0%; Score 15; DB 5; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCGTT 15

|||||

Db 75 CCTTCTCCCTCGTT 61

RESULT 3

AK021867/c

LOCUS

DEFINITION Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately similar to POLY(A) POLYMERASE (EC 2.7.7.19).

ACCESSION AK021867

VERSION AK021867.1 GI:10433146

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone_lib:HEMBAL clone:HEMBAL1006278.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuno,Y. and Oshima,A.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1689)

AUTORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES

source Location/Qualifiers

1..1689

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="HEMBAL1006278"

/tissue_type="whole embryo, mainly head"

/clone_lib="HEMBAL"

/note="stage="embryo, 10 weeks"

/note="cloning vector: pME18SFL3"

186..>1689

/note="unnamed protein product"

/codon_start=1

/protein_id="BAB13919.1"

/db_xref="GI:10433147"

/translation="MKPFGVEDEELNHRVLVGLNKLNVKSWSDVSEKNLPSPVATVGGKLTFTGSY RLGVHTKGADIDALCVAPRHVRSDFQSFEEKLKHODGIRNLRAVEDAFVPIKFEF DGIEDLVFARLAIOTISDNLDRDSDRLSRSLDIRCIRSLNGCRVTDTELHLVPNKET FRLTLRAVKLWAKRGIVSNMLGLGGVSNMVLVARTCOLYPNAASTLVHKKFVLFVS KWENPNVLKQPESNLNPVWDRVNPSPFGRYHLMPIITPAYPOQNSTYNYSTRT VMVEFGQGLAVTDEILQKSDWSKLEPPPNFFQKRYHIVLTASASTENHLEWVGL VSKIRVLVGNLERNFTLAHNPQSPGPKGHHKNNYVSMWFLGIIFRVEVAES VNIDLTVDIQSFDTIVYQANNINMLKGMKIEATHVHKKKQLHHLVPAEIL"

555 a 309 c 366 g 459 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 1689;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||

Db 123 CCTTCTCCCTGTT 109

RESULT 4
AF232676/c

LOCUS AF232676 1721 bp mRNA linear MAM 22-NOV-2000
DEFINITION Sus scrofa prophet of pit-1 (Prop-1) mRNA, complete cds.
ACCESSION AF232676
VERSION AF232676.1 GI:11275672
KEYWORDS Sus scrofa.
SOURCE Sus scrofa
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 1721)
AUTHORS Sloop,K.W., McCutchan Schiller,A., Smith,T.P., Blanton,J.R. Jr., Rohrer,G.A., Meier,B.C. and Rhodes,S.J.
TITLE Biochemical and genetic characterization of the porcine Prophet of pit-1 pituitary transcription factor
JOURNAL Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)
MEDLINE 20519384
PUBMED 11064154

REFERENCE 2 (bases 1 to 1721)
AUTHORS McCutchan Schiller,A.L., Sloop,K.W., Blanton,J.R. Jr., Meier,B.C. and Rhodes,S.J.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Biology, Indiana University Purdue University Indianapolis, 723 West Michigan Street, Indianapolis, IN 46202-5132, USA

FEATURES
source
1..1721
/organism="Sus scrofa"
/db_xref="taxon:9823"
1..1721
/genes="Prop-1"
333..1013
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/note="transcription factor"
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/product="prophet of pit-1"
/protein_id="AAG33702.1"
/db_xref="GI:11275673"
/translation="MEAGRRREQKPKRGVCSLLWPEGYPAAGTLTARVDISTPRPYR NLGSGVAGRPRLSPQGGQRPHSRHRRHTFSPAOLESAFGRNOYPDIAWREGL ARDTGLSEARIQVWFONRRKORRSLLOPLAHLSPATFSGFLPPACPSYPTP PPMWCFPPHYNHLPSPSTGSGFARHQSEWDWYPTLHTPTGHLPCPPAPPVLPUS LEPPKSWN"

BASE COUNT 457 a 460 c 469 g 333 t 2 others
ORIGIN
Query Match 100.0%; Score 15; DB 4; Length 1721;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||

Db 236 CCTTCTCCCTGTT 222

RESULT 5
BC000776

LOCUS BC000776 3190 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, Similar to KIAA0736 gene product, clone IMAGE:3509807, mRNA, partial cds.
ACCESSION BC000776
VERSION BC000776.1 GI:12653962
KEYWORDS

SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
Strausberg,R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 7 Row: 1 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES
Location/Qualifiers
1..3190
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/db_xref="taxon:9606"
/clone="IMAGE:3509807"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
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/codon_start=1
/product="Similar to KIAA0736 gene product"
/protein_id="AAH00776.1"
/db_xref="GI:12653963"
/translation="CTAORRRERELEAQVEAILRECGHGFQWTFYVLGIALMAD GVEPVGVFLPSAEKDCLSNKGMLGLIYVLGMVCAFLNGGLADLRGRQCILLI LCMFMWIGGVYAAAMAWAIIPIHYSFQMSQAYQFHSRWFVFLVCAFPSPFAIGALT QPESRFFLENGKDEAMVLKQVHDTNNRKGHPERFVSHTIKTHQEDELIEIQS DMIRHLQADVARSRTKVPGRVHVFTLENOIHRGGOYFNDKFIGLRKLSVSE DSLEECYEDVTSNTFERNCTFTVYNTDLEPKFVNSRLNSTFLHNKGGCPL DVTGEGAYMVFYVSLGTLAVLPGNIVSALLMDKIGRLMAGSVMSVSCFFLS FGNSESAMIALCLFGVSIASNADLVTLVELYPSDKRTTAFGFLNALCKLAALVGI SIFTSFGITTKAAPILFASALALGSSSLAKLPETRGVQLQ"

BASE COUNT 662 a 850 c 868 g 810 t
ORIGIN
Query Match 100.0%; Score 15; DB 9; Length 3190;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
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Db 2096 CCTTCTCCCTGTT 2110

RESULT 6
CHKTGFB/c

LOCUS CHKTGFB 3347 bp mRNA linear VRT 21-JUL-1994
DEFINITION Gallus gallus transforming growth factor-beta type III receptor mRNA, complete cds.
ACCESSION L01121
VERSION L01121.1 GI:511842

KEYWORDS TGF-beta; betaglycan; plasma membrane; transforming growth factor-beta receptor; transforming growth factor-beta type III

SOURCE Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.

ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS 1 (bases 1 to 3347)

1 Barnett, J.V., Moustakas, A., Lin, W., Wang, X.F., Lin, H.Y., Galper, J.B. and Maas, R.L.

TITLE Cloning and developmental expression of the chick type II and type III TGF beta receptors

JOURNAL Dev. Dyn. 199 (1), 12-27 (1994)

MEDLINE 94220749

PUBMED 8167376

FEATURES source Location/Qualifiers 1..3347 /organism="Gallus gallus" /db_xref="taxon:9031" /tissue_type="brain" /dev_stage="embryonic" /germline /tissue_lib="lambda zap" 152..2677 /codon_start=1 /product="transforming growth factor-beta type III receptor" /protein_id="AAA49090.1" /db_xref="GI:511843" /translation="MSSSCVTPVFMILCFADGVPVRSECVLPVNSHPVHALLE SFTVLGGASRTTGLPQVHVNLNRPDEGLDHHREVTLLTPISSVHIHQKPLVF LNSPLPLKLTLPALGIRRVFVSGSIWFEKGFNSAETKFNPFERNEHL LQWAKGAYGAFSTELKISRNIYIKVGEDQVPTCNTEKFNLSIYAGVLPKRA ECLMSNIVOEREVHIELITPSNPYSFAQVDIIVDIKPSQPGAKLERNVLLKCK KSNVWIKSHDQGVLEVTNSIGFKETERSMTWSKVIPIFSSHSLIKWAYEH KYPSVTSYKAPVANRFLQLEHTEEMDEHSLPPELLEHGAKNPALSGLTFP PHNGHETGEGIFPQRSVSDTLINDEHSLSKHKEPEVOGSAVALSKGDDK VINTAVEKDSQASQYTRTELSDHSCARMNGTHFIEISLPNKGCTRTSYLDKIV YFNSIVQLSSPAEGSFDDDDMSGDNGFPGDADGVDVTFNSWPEIAFNCPLHOPEK DFFNPAMFEPPEPHTVNTYFNMLYKDLFLAPSGOLFSEANGPIYVEVSVTKADIS LGFAIQTCFVSPFSPNDRMSDYTIENICPKDES VKFYSTEKLNFPPIAHQAQDKRFS FVEKPIFNISLLFLHCLTLCNTIDKDLRPLKCPVPDEACTSLNVDMLAMHNRKT FTKPLVITHECKPEPSSLPKSNVRQPSVFGDLTVGVIAFAAEVIGALLTGALWFI YSHGGEAGRKQVPTSPSPASENSSAAHSIGSTQSTPPCSSSAT"

BASE COUNT 996 a 712 c 708 g 931 t

ORIGIN

Query Match 100.0%; Score 15; DB 5; Length 3347; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCGTT 15

Db 1368 CCTTCTCCCTCGTT 1354

RESULT 7

AF312211/c

LOCUS AF312211 3752 bp mRNA linear PRI 04-AUG-2001

DEFINITION Homo sapiens neo-poly(A) polymerase mRNA, complete cds.

ACCESSION AF312211

VERSION AF312211.1 GI:15080910

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 3752)

Topalian, S.L., Kaneko, S., Gonzales, M.I., Bond, G.L., Ward, Y. and Manley, J.L.

TITLE Identification and functional characterization of neo-poly(A) polymerase, an RNA processing enzyme overexpressed in human tumors

•

JOURNAL Mol. Cell. Biol. 21 (16), 5614-5623 (2001)

MEDLINE 21356984

PUBMED 11463842

REFERENCE 2 (bases 1 to 3752)

AUTHORS Topalian, S.L., Gonzales, M.I., Wang, X. and Wang, R.-F.

TITLE Direct Submission

JOURNAL Submitted (09-OCT-2000) Surgery Branch, NCI, National Institutes of Health, Building 10, Room 2B47, Bethesda, MD 20892, USA

FEATURES source Location/Qualifiers 1..3752 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_type="malignant melanoma" 232..2442 /note="similar to Homo sapiens poly(A) polymerase protein (PAP) encoded by GenBank Accession Number X76770" /codon_start=1 /product="neo-poly(A) polymerase" /protein_id="AAK83701.1" /db_xref="GI:15080911" /translation="MKEMSANTVLDQROQKHGYITSPISLAKPEIDHIYTKLIDA MKPFGVFDEEELNHLRLVGLKLNILKWIWSDVSEKSNLPPSVAVGKIFTFGSY RLGHTKGADIDALCVAPRHVERSDFFQFEKLKHODGIRNLRAVEDAFVPIKFEF DGIEIDLTVFARLAIQITSDNLDLDDSLRSLDIRCIRSLNGCVTDDEILHLVPNKET FRLLRAVKLWAKERGIIYNMGLFGVSWAMLVARTCQLYPNAASATLVHKKFLVFS KWENPNPVLKQEEENLNPVMDPRVNSDRYHLMPIITPAYQQNSTYVSTSTRT VVVEEFKGLAVTDEILQGGSKLLEPPNFQKYRHYIVLTASASTEENHLEWGL VESKIRVLGNLERNFEITLHVNPQSPFGNKEHKHKNYVSMWFLGIIFRRVENAES VINIDLYIQSFTDVTYRQANNIMLKEGKIEATHVKKOLHLYLPAEILOKKKKOS LSDVNRSSGSLQSLRSLDSSCLDSRDTNGTTPNSPASKSDSPSGVETERNASERA AVIVEKPLVPPAAGLSIPVIGAKVDSTYKTPVPTCTTPTTVGVGRNVIPRTYHPNP AGOGLHNGSNITKVTYKRSKSPSIDGTPKRLKQVEKFIRESLTFKDPRTAEKRK KSDAIGGESMPITDITSKRLPKSLPDDSSPPANNIRVINKSIRLTNR"

BASE COUNT 1175 a 709 c 738 g 1130 t

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 3752; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCGTT 15

Db 169 CCTTCTCCCTCGTT 155

RESULT 8

AB018279

LOCUS AB018279 4353 bp mRNA linear PRI 16-JUN-1999

DEFINITION Homo sapiens mRNA for KIAA0736 protein, complete cds.

ACCESSION AB018279

VERSION AB018279.1 GI:3882192

KEYWORDS

SOURCE Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:hk03846.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (sites)

Nagase, T., Ishikawa, K., Suyama, M., Kikuno, R., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.

TITLE Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

JOURNAL DNA Res. 5 (5), 277-286 (1998)

MEDLINE 99087487

REFERENCE 2 (bases 1 to 4353)

Ohara, O., Suyama, M., Nagase, T., Ishikawa, K. and Kikuno, R.

AUTHORS Direct Submission

TITLE Submitted (08-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)

JOURNAL Location/Qualifiers

FEATURES

intron 4655..4729
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/number=8
exon 4730..4845
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/number=9
intron 4846..4929
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exon 4930..5051
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intron 5052..5124
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intron 8123..8911

exon /gene="topialpha"
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8912..>9014
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/number=21
BASE COUNT 3155 a 2199 c 2486 g 3161 t
ORIGIN
Query Match 100.0%; Score 15; DB 5; Length 11001;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCTGTT 15
|||||
Db 6409 CCTTCTCCCTGTT 6395
RESULT 10
AE009810/c
LOCUS
DEFINITION Pyrobaculum aerophilum strain IM2 section 65 of 201 of the complete genome.
ACCESSION AE009810 AE009441
VERSION AE009810.1 GI:18159943
KEYWORDS
SOURCE
ORGANISM Pyrobaculum aerophilum.
Pyrobaculum aerophilum
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
REFERENCE 1 (bases 1 to 11896)
AUTHORS Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and Miller,J.H.
TITLE Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002)
PUBMED 11792869
REFERENCE 2 (bases 1 to 11896)
AUTHORS Fitz-Gibbon,S.T., Ladner,H., Kim,U.-J., Stetter,K.O., Simon,M.I. and Miller,J.H.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA
FEATURES
source
1..11896
/organism="Pyrobaculum aerophilum"
/strain="IM2"
/db_xref="taxon:13773"
complement(129..608)
/gene="PAE1218"
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/codon_start=1
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translation="MFKRRGLFKGVLLKSKPLSGVEILKSLRSLTSKGFVSPG
TLPLSLYLAEGLEIARSVVGRKKIYALTAAGEHLAKLMDDEFRSIQMLEG
GGREGDLLAAVRDELVIDEYDEIEGNDAEVLKEMALLKLEEKVEARLKKALGG"
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/protein_id="AAL6333.1"
/db_xref="GI:18159945"
translation="MFVYDVVNALDYKARSITITAFISQYVQAGSRGVVVVGISGGVD

STVAALAVBALGRQVRLGLLMPSLYTPPEDLKDALDVINALGVWEKRVDTITPIYDAF
VKTLPDFSQNRVPAAGNLPRIKMTVLYYYANKSNLLVWGTDGRSELLGYFTYKGDG
GVDFPLTQSLFKIQVRELAARLGFADIAKPKSPRLWQHTAEGLGASYEVIDQVLY
AVFDLKKPPEVRGFFCEVDIVITRVKKNHKLTPPAYPDITPARRNV"
complement(1424. .2608)
/gene="PAE1220"
complement(1424. .2608)
/gene="PAE1220"
/note="Fatty acid and phospholipid metabolism;
Degradation"
/codon_start=1
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/product="acetyl-CoA C-acetyltransferase"
/protein_id="AAL63334.1"
/db_xref="GI:18159946"
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KEYEEVIFGSLTLOGGMQONLSRYAALLAGLPVEYSATVNRVSSGMAIEARREIA
MGASVVVAGVDSMTQPICLPDGVWVGURHFGRREELRDLWVLDGLVDTNGLLM
GEAEAVAREKMTREELDWAVYESHMRARWATENKWFDDLEPIEGLGGVYVKLERD
EGIRPDTTMEKLAKLPAFRPDGVLTAGNSQLSDGAAVLLMSEERKAREMGVPIAR
ILGYSWHMVPWRFTAPVVAIOKLLKLGTEIDSEFDYFEANEAFVNVVLVHRLGV
PYEKLNVFGAIALGHPLGASGARIVTLLSVLRNKGRRGIAALCHGTGGGTALALE
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/note="transport and binding proteins; Unknown substrate"
/codon_start=1
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/product="ABC transporter ATP-binding protein, putative"
/protein_id="AAL63335.1"
/db_xref="GI:18159947"
/translation="MVSVTQNLKXVPPNVYALRDVNVTKDGEFLVVLGPPSSGKT
TFRLCAGLETPKGRFLGDAPVIDVERGINPPARRNVGMVFQNNALYPHMKVFDN
IAPLKIKLPKPEIERREKVEAEALISNLLDRYPLQSGQQOQVAIARALYKEPQ
VLMDPEPFLDLARLSAREFVKSQRRKLTITVTHQHDAYALADRLMNVNNGV
VOQISTDYADQPLNPANIFVAQFGDPPINILEGEGRGHDVLDGLKIPIPAQCKLOV
GIRPTIITYADQPLSPEDLEKPGRVLLVLELGTTPVAVVVKWERIEVRVWYKKEG
SIARVFLKRGVKLFQNGVRK"
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3779. .4897
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/note="Hypothetical"
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/transl_table=11
/product="hypothetical protein"
/protein_id="AAL63336.1"
/db_xref="GI:18159948"
/translation="MKWLDVLRKASQVKKKPKAVTHGGGAHADDTLAALLWRSGA
EAYRLNTEAEIKIGDVVLFIDIGDQFRLPDRYVLDHGHGVSOPAEPSVIOVSLA
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DLADAYLSKLSLDLAAFSFAFKLAELKLSFSDLAEKYPTFTQTLRMLQAASKVDITAS
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EIAAAVEENVPPAPLWNLALIDKALNGPVLIVVKDRNPGAYTVWRPDRYNIIDFR
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4887. .5378
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/protein_id="AAL63337.1"
/db_xref="GI:18159949"
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DGCAYAYIKSLFEVYKSGLLKVLAPAEISLPFADGCDSDVISAVAHHFRDIEVALR
EMVRVAKRLVAILDWTPEAGGVNPNPQPELEAKMRAADAANVKLGFIDKITRYWRL
VKP"
5401. .6453
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5401. .6453
/gene="PAE1236"
/note="DNA metabolism; DNA replication, recombination, and
repair"
/codon_start=1
/transl_table=11
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/protein_id="AAL63338.1"
/db_xref="GI:18159950"
/translation="MRFVMAALLAVILAVTPIRLQVDVAVLSPINTTKIIDYLSBA
KRAIIVETVYTKPLADALVDRKRGVDVYVLSRVYGGVPRQARDLAQYMEKNGV
RVKWNDDFPNVHTKLYVIDNQTVIIGININPTVSGFRNKGVMILVINSTLARQLATIV
LNDKFGKPYRNYPGVYSPVNSQEGLEWILTLPGDLITYAMEQIYLDGSMVPLIQHQ
RYAVVARTNADINAVDDDDIVAKIIVGQDVYVGSINLCYYSIQNRREYGLLIHNPE
LAARLARLILQWTEAGGVAPTETTETAQPTTARTPAAQATAPSLIHALAWLVVVAI
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6469. .6858
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/note="Hypothetical; Conserved"
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/protein_id="AAL63339.1"
/db_xref="GI:18159951"
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VKRSPGLFCGERYKLTQEGEKALEEWRAKIRSELAKEAEELFKGREIAEQEIVKRWDP
LPILLGLGVISIALMKLTSRLPVAEE"
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ACCESSION AF144617
VERSION AF144617.2 GI:15282441
KEYWORDS
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ORGANISM
Pestivirus giraffe-1 H138.
Pestivirus giraffe-1 H138
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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1 (bases 1 to 12602)
Becher,P., Orlich,M., Kosmidou,A., Konig,M., Baroth,M. and
Thiel,H.J.
Genetic diversity of pestiviruses: identification of novel groups
and implications for classification
Virology 262 (1), 64-71 (1999)
99420379
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2 (bases 1 to 12602)
Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
Evidence for the presence of two novel pestivirus species
Virology 286 (2), 456-465 (2001)
21378881
11485413
3 (bases 1 to 12602)
Avalos-Ramirez,R., Orlich,M., Thiel,H.-J. and Becher,P.
Complete genomic sequences of pestiviruses from giraffe and
reindeer: evidence for the presence of two novel species within the
genus pestivirus
Unpublished
4 (bases 1 to 12602)
Becher,P. and Orlich,M.
Direct Submission
Submitted (21-APR-1999) Justus-Liebig-Universitaet Giessen,
Institut fuer Virologie (Fachbereich Veterinaermedizin),
Frankfurter Str. 107, Giessen D-35392, Germany
5 (bases 1 to 12602)
Avalos-Ramirez,R., Orlich,M. and Becher,P.
Direct Submission
Submitted (26-MAR-2001) Justus-Liebig-Universitaet Giessen,
Institut fuer Virologie (Fachbereich Veterinaermedizin),
Frankfurter Str. 107, Giessen D-35392, Germany
Sequence update by submitter
On Aug 23, 2001 this sequence version replaced gi:6049239.
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RESULT 13
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DEFINITION Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.
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VERSION AC107069.5 GI:20146820
KEYWORDS HTG.
SOURCE Homo sapiens.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 34578)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 34578)
Scott,K., Kozlowicz,A., Spalding,L. and Trani,L.
The sequence of Homo sapiens BAC clone RP11-249A8
Unpublished (2001)
REFERENCE 3 (bases 1 to 34578)
Waterston,R.H.
Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 34578)
Waterston,R.H.
Direct Submission
Submitted (04-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 34578)
Waterston,R.H.
Direct Submission
Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 34578)
Waterston,R.H.
Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 13, 2002 this sequence version replaced gi:19924179.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics

Center project name: H_NH0249A08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPC11-11 human BAC library was made from the blood of one male

donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-495023, 2000 bp overlap;
the clone sequenced to the right is RP11-56366, 2000 bp overlap.
Actual start of this clone is at base position 126621 of
RP11-495023.

FEATURES

source

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Query Match 100.0%; Score 15; DB 9; Length 34578;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCTGTT 15
|||||
Db 1831 CCTTCTCCCTGTT 1817

RESULT 14

AL138734/c

LOCUS AL138734

DEFINITION Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains

ACCSSION AL138734

VERSION AL138734.6 GI:8388469

KEYWORDS HTG.

SOURCE human.

43347 bp DNA linear PRI 16-AUG-2000

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 43347)
 Tromans,A.
 Direct Submission
 Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Jun 8, 2000 this sequence version replaced gi:8247412.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C.elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
 RPI-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:pcYPAC2>
 IMPORTANT: This sequence is not the entire insert of clone RPI-310P17 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
 The true left end of clone RPI-310P17 is at 1 in this sequence. The true left end of clone RPI-413H6 is at 43244 in this sequence.

FEATURES
 source
 1..43347
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RPI-310P17"
 /clone_lib="RPCI-1"
 132..426
 /note="AluSx repeat: matches 1..295 of consensus"
 complement(428..891)
 /note="match: GSS: Em:B53078"
 complement(580..878)
 /note="match: GSS: Em:AQ269829"
 1740..1867
 /note="MIR repeat: matches 20..146 of consensus"
 1924..2090
 /note="L1MB8 repeat: matches 6005..6171 of consensus"
 2151..2266
 /note="L1MB8 repeat: matches 5874..5991 of consensus"
 2281..2431
 /note="AluY repeat: matches 158..308 of consensus"
 2432..2878
 /note="L1MB8 repeat: matches 5429..5879 of consensus"
 2879..3641
 /note="LTR17 repeat: matches 1..780 of consensus"
 3516..4013
 /note="match: GSS: Em:AQ112069"
 3642..3924
 /note="L1MB8 repeat: matches 5147..5429 of consensus"
 4063..4518
 /note="match: GSS: Em:AQ508138"
 complement(4129..4662)
 /note="match: GSS: Em:AQ316392"

misc_feature
 4657..5169
 /note="match: GSS: Em:AQ484379"
 4665..5178
 /note="match: GSS: Em:AQ432756"
 5449..5596
 /note="L2 repeat: matches 2580..2750 of consensus"
 6304..6577
 /note="AluSx repeat: matches 9..282 of consensus"
 6589..6721
 /note="AluSg/x repeat: matches 1..133 of consensus"
 6732..7036
 /note="AluSp repeat: matches 1..305 of consensus"
 7164..7253
 /note="MIR repeat: matches 47..147 of consensus"
 7584..7643
 /note="30 copies 2 mer gt 96% conserved"
 7969..8079
 /note="MIR repeat: matches 28..143 of consensus"
 8265..8544
 /note="AluJo repeat: matches 2..289 of consensus"
 8711..8799
 /note="MIR repeat: matches 59..145 of consensus"
 9753..9893
 /note="AluY repeat: matches 168..311 of consensus"
 10697..11158
 /note="L2 repeat: matches 2290..2750 of consensus"
 11255..11286
 /note="16 copies 2 mer ac 100% conserved"
 11352..11558
 /note="HERVL repeat: matches 1757..1969 of consensus"
 12998..13299
 /note="AluSx repeat: matches 1..311 of consensus"
 14005..14200
 /note="MIR repeat: matches 1..208 of consensus"
 14674..14748
 /note="L1ME3 repeat: matches 5872..5956 of consensus"
 15052..15480
 /note="L1M4 repeat: matches 3375..3822 of consensus"
 15481..15498
 /note="AluS repeat: matches 152..170 of consensus"
 15499..15731
 /note="AluSg/x repeat: matches 71..308 of consensus"
 15732..15790
 /note="AluS repeat: matches 1..152 of consensus"
 15822..16105
 /note="L1PA16 repeat: matches 5830..6110 of consensus"
 16106..16416
 /note="AluSp repeat: matches 1..313 of consensus"
 16417..17711
 /note="L1PA16 repeat: matches 4517..5830 of consensus"
 17737..18032
 /note="MER61A repeat: matches 7..314 of consensus"
 18038..18426
 /note="L1PA16 repeat: matches 4125..4510 of consensus"
 18427..18706
 /note="L1M4 repeat: matches 3826..4124 of consensus"
 18703..19271
 /note="L1MD2 repeat: matches 5774..6331 of consensus"
 19272..19892
 /note="L2 repeat: matches 1452..2147 of consensus"
 19893..19948
 /note="MADE1 repeat: matches 5..80 of consensus"
 19949..20211
 /note="L2 repeat: matches 1194..1452 of consensus"
 20944..21113
 /note="AluSg/x repeat: matches 129..299 of consensus"
 21140..21264
 /note="AluSc repeat: matches 1..125 of consensus"
 21581..21650
 /note="35 copies 2 mer tt 68% conserved"
 21747..21896
 /note="L1MD3 repeat: matches 7476..7579 of consensus"
 complement(21823..22281)
 misc_feature


```
misc_feature /note="match: GSS: Em:AQ714858"
22304..22755
/note="match: GSS: Em:AQ357726"
22608..22697
/note="L2 repeat: matches 2620..2710 of consensus"
22829..22868
/note="20 copies 2 mer aa 80% conserved"
22998..23085
/note="L2R22 repeat: matches 413..509 of consensus"
23148..23417
/note="L2R22 repeat: matches 38..312 of consensus"
23454..23569
/note="L2 repeat: matches 2005..2146 of consensus"
23645..23819
/note="MIR repeat: matches 61..243 of consensus"
24043..25714
/note="L1MEC repeat: matches 281..1953 of consensus"
25721..26938
/note="L1MEC repeat: matches 2151..3045 of consensus"
complement(26913..27340)
/note="match: GSS: Em:AQ225006"
28135..28460
/note="MER7A repeat: matches 4..346 of consensus"
28538..29022
/note="L1MC3 repeat: matches 7250..7739 of consensus"
29898..30315
/note="MLT1B repeat: matches 6..390 of consensus"
30318..31382
/note="Charlie2 repeat: matches 2658..3755 of consensus"
31290..31766
/note="match: GSS: Em:AQ735362"
31390..31669
/note="L2R16C repeat: matches 102..387 of consensus"
32151..32455
/note="AluJb repeat: matches 1..304 of consensus"
33318..33468
/note="Charlie2 repeat: matches 327..504 of consensus"
34076..34305
/note="MIR repeat: matches 6..260 of consensus"
34434..34535
/note="L2 repeat: matches 2574..2687 of consensus"
34633..35136
/note="MER9 repeat: matches 1..511 of consensus"
36692..37186
/note="Cheshire repeat: matches 27..548 of consensus"
37183..38826
/note="Cheshire repeat: matches 723..2420 of consensus"

Query Match 100.0%; Score 15; DB 9; Length 43347;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCCTCCCTGTT 15
|||||
Db 27556 CCTTCCTCCCTGTT 27542

RESULT 15
AL583852
LOCUS AL583852 56701 bp DNA linear PRI 03-DEC-2001
DEFINITION Human DNA sequence from clone RP11-17G2 on chromosome 10, complete
sequence.
ACCESSION AL583852 AC011691
VERSION AL583852.6 GI:14702147
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 56701)
AUTHORS Chapman,J.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
```

COMMENT

Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On or before Jul 12, 2001 this sequence version replaced gi:7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep>

This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>

RP11-17G2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-17G2. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-17G2 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this sequence.

Location/Qualifiers

1..56701
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-17G2"
/clone_lib="RPCI-11.1"
1..284
/note="MER1B repeat: matches 1..285 of consensus"
285..400
/note="MER20 repeat: matches 103..218 of consensus"
1266..1301
/note="L2 repeat: matches 2580..2615 of consensus"
1305..1352
/note="24 copies 2 mer ga 75% conserved"
complement(2038..2434)
/note="match: GSS: Em:AQ358591"
2479..2823
/note="match: GSS: Em:AQ812738"
2586..2791
/note="MIR repeat: matches 45..258 of consensus"
2979..3119
/note="MIR repeat: matches 61..212 of consensus"
complement(3478..3937)
/note="match: GSS: Em:AQ475942"
4218..4317
/note="L2 repeat: matches 2645..2749 of consensus"
5477..5644
/note="MLT1I repeat: matches 68..240 of consensus"
complement(5738..6110)
/note="match: STS: Em:G53244"
/note="match: GSS: Em:AQ083388"
6206..6292
/note="MER91A repeat: matches 5..95 of consensus"
6293..6521
/note="MIR repeat: matches 9..234 of consensus"
8688..8929

```
repeat_region /note="L2 repeat: matches 2284. .2534 of consensus"
8947. .9112
repeat_region /note="MIR repeat: matches 70. .248 of consensus"
9173. .9416
misc_feature /note="MLT1A1 repeat: matches 337. .568 of consensus"
9753. .10220
repeat_region /note="match: GSS: Em:AQ497216"
10458. .10642
repeat_region /note="L2 repeat: matches 2129. .2318 of consensus"
13448. .13763
repeat_region /note="MLT1A1 repeat: matches 1. .341 of consensus"
13847. .13898
repeat_region /note="2 copies 26 mer 94% conserved"
15428. .15572
repeat_region /note="MER5A repeat: matches 18. .178 of consensus"
16288. .16546
repeat_region /note="L2 repeat: matches 2242. .2521 of consensus"
16664. .16777
repeat_region /note="L2 repeat: matches 2596. .2708 of consensus"
16779. .16842
repeat_region /note="16 copies 4 mer gga 81% conserved"
16817. .16998
repeat_region /note="7 copies 26 mer 62% conserved"
16861. .16944
repeat_region /note="21 copies 4 mer gga 75% conserved"
16951. .16994
repeat_region /note="11 copies 4 mer gga 81% conserved"
17973. .18165
repeat_region /note="MIR repeat: matches 22. .214 of consensus"
18174. .18509
repeat_region /note="MER46C repeat: matches 7. .338 of consensus"
18670. .18785
repeat_region /note="MER5A repeat: matches 45. .163 of consensus"
18833. .19044
repeat_region /note="MIR repeat: matches 28. .260 of consensus"
21936. .22145
repeat_region /note="LIME repeat: matches 5599. .5820 of consensus"
22148. .22199
repeat_region /note="13 copies 4 mer caca 82% conserved"
22199. .22596
repeat_region /note="MSTA repeat: matches 1. .426 of consensus"
22480. .22743
misc_feature /note="match: STS: Em:HS094YH3"
22597. .22638
repeat_region /note="21 copies 2 mer ca 92% conserved"
22599. .22638
repeat_region /note="10 copies 4 mer caca 92% conserved"
22770. .22846
repeat_region /note="MIR repeat: matches 87. .165 of consensus"
22959. .23149
repeat_region /note="MER3 repeat: matches 1. .200 of consensus"
23508. .23698
repeat_region /note="L2 repeat: matches 2539. .2748 of consensus"
24378. .24458
repeat_region /note="L1 repeat: matches 2136. .2213 of consensus"
24486. .24581
repeat_region /note="48 copies 2 mer tt 63% conserved"
25073. .25451
misc_feature /note="MLTIF repeat: matches 1. .371 of consensus"
complement(25325. .25729)
repeat_region /note="match: GSS: Em:AQ507252"
26471. .26619
repeat_region /note="MLTIF repeat: matches 105. .257 of consensus"
26933. .27097
repeat_region /note="MER5A repeat: matches 1. .188 of consensus"
27101. .27219
repeat_region /note="MIR repeat: matches 13. .134 of consensus"
27767. .27813
repeat_region /note="MIR repeat: matches 49. .103 of consensus"
28697. .28879
repeat_region /note="MIR repeat: matches 31. .225 of consensus"
29356. .29488
repeat_region /note="MER5A repeat: matches 50. .184 of consensus"
```

```
repeat_region 29578. .29664
/note="MIR repeat: matches 82. .175 of consensus"
31386. .31508
repeat_region /note="MIR repeat: matches 42. .164 of consensus"
31974. .32354
misc_feature /note="MLT1I repeat: matches 1. .410 of consensus"
32596. .33015
repeat_region /note="match: GSS: Em:AQ604754"
33407. .33823
repeat_region /note="MLT1H repeat: matches 128. .547 of consensus"
33833. .34015
repeat_region /note="MIR repeat: matches 50. .251 of consensus"
34122. .34214
misc_feature /note="match: GSS: Em:AQ551831"
35380. .35474
repeat_region /note="MIR repeat: matches 46. .140 of consensus"
37028. .37195
repeat_region /note="MER63A repeat: matches 45. .210 of consensus"
37274. .37413
repeat_region /note="L2 repeat: matches 2137. .2276 of consensus"
37801. .38057
repeat_region /note="L2 repeat: matches 2469. .2750 of consensus"
38541. .39465
repeat_region /note="L2 repeat: matches 1655. .2599 of consensus"
39625. .39782
repeat_region /note="MIR repeat: matches 59. .220 of consensus"
41102. .41277
repeat_region /note="L2 repeat: matches 2517. .2691 of consensus"
41278. .41718
repeat_region /note="MLT1C repeat: matches 5. .462 of consensus"
41719. .41924
repeat_region /note="L2 repeat: matches 2308. .2517 of consensus"
42387. .42468
repeat_region /note="MIR repeat: matches 162. .246 of consensus"
42496. .42577
repeat_region /note="L2 repeat: matches 2605. .2692 of consensus"
43328. .43400
repeat_region /note="L2 repeat: matches 2646. .2731 of consensus"
43505. .43769
repeat_region /note="L2 repeat: matches 2161. .2419 of consensus"

Query Match 100.0%; Score 15; DB 9; Length 56701;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCTGT 15
|||||
Db 2530 CCTTCTCCCTCTGT 2544
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Search completed: December 11, 2002, 14:35:48
Job time : 1686 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:23:57 ; Search time 212.5 Seconds
(without alignments)
158.965 Million cell updates/sec

Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 cttctcccccgtgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
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- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	15	100.0	15	22	AAH28085	Probe for human no
2	15	100.0	352	21	AAC09241	Human secreted pro
3	15	100.0	445	23	ABV50337	Human prostate exp
4	15	100.0	549	23	AAS66052	DNA encoding novel
5	15	100.0	827	22	AAH04051	Human cDNA clone (
6	15	100.0	1689	22	AAH15437	Human cDNA sequenc
7	15	100.0	1854	22	AAH28083	DNA encoding human
8	15	100.0	1854	22	AAH28087	DNA encoding human
9	15	100.0	2159	23	ABK43728	DNA encoding novel

c 10	15	100.0	2451	23	AAS83288	DNA encoding novel
c 11	15	100.0	2520	24	ABL90474	Human polynucleoti
c 12	15	100.0	2522	23	ABK4004	DNA encoding novel
c 13	15	100.0	3580	21	AAH16697	Human secreted pro
c 14	15	100.0	3580	24	ABK35630	CDNA sequence #21
c 15	15	100.0	4215	23	ABV22746	Human prostate exp
c 16	15	100.0	4215	23	ABV28574	Human prostate exp
c 17	15	100.0	4366	22	AAH57556	Human brain cell s
c 18	15	100.0	15857	22	AAS26730	Human genomic DNA
c 19	15	100.0	31122	14	AAQ40706	Bacillus subtilis
c 20	14	93.3	389	24	ABN96737	Gene #3235 used to
c 21	14	93.3	389	24	ABL66267	Lung cancer relate
c 22	14	93.3	482	24	ABT04065	Human ovary specif
c 23	14	93.3	594	22	ABA62115	Human foetal liver
c 24	14	93.3	594	22	AAK10435	Human brain expres
c 25	14	93.3	594	22	AAK36337	Human bone marrow
c 26	14	93.3	594	22	AAI42060	Probe #10746 used
c 27	14	93.3	599	23	AAS85439	DNA encoding novel
c 28	14	93.3	2349	21	AAAT6376	Human secreted pro
c 29	14	93.3	2415	18	AAT62067	Fission yeast prot
c 30	14	93.3	2775	22	AAH13954	Human cDNA sequenc
c 31	14	93.3	6959	23	AAS85443	DNA encoding novel
c 32	14	93.3	8894	22	AAL36698	Human musculoskele
c 33	14	93.3	8894	22	AAS26718	Human genomic DNA
c 34	14	93.3	16877	22	ABA20494	Human nervous syst
c 35	14	93.3	16877	22	AAL36984	Human musculoskele
c 36	14	93.3	61710	22	AAK83782	Human immune/haema
c 37	13.4	89.3	15	22	AAH28084	Probe for human no
c 38	13.4	89.3	108	19	AAH28085	Human biallelic po
c 39	13.4	89.3	134	21	AAC04726	Human secreted pro
c 40	13.4	89.3	198	24	ABK76772	Bacillus lichenifo
c 41	13.4	89.3	303	20	ABK76772	EST clone BG388.
c 42	13.4	89.3	315	22	AAH52042	Mycobacterium tube
c 43	13.4	89.3	332	22	AAD08846	Human G-protein co
c 44	13.4	89.3	337	21	AAC11522	Human secreted pro
c 45	13.4	89.3	342	22	AAS38882	Novel human diagno

ALIGNMENTS

RESULT 1

AAH28085
ID AAH28085 standard; DNA; 15 BP.

XX AAH28085;

XX 05-SEP-2001 (first entry)

DT Probe for human norepinephrine transporter gene A457P variant allele.

DE Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; probe; ss.

XX Homo sapiens.

XX WO200148246-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35491.

PR 29-DEC-1999; 99US-0173682.

PR 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

PI Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

PT Screening for susceptibility to sub-optimal norepinephrine transport.

PT particularly orthostatic intolerance in a subject by detecting a
 PT polymorphism of norepinephrine transporter gene -
 PS Claim 15; Page 69; 133pp; English.
 XX
 CC The present sequence represents a probe for the A457P variant allele of
 CC a human norepinephrine transporter gene. The specification a method
 CC for screening for susceptibility to sub-optimal norepinephrine transport
 CC in a subject. The method comprises obtaining a biological sample from
 CC the subject and detecting a polymorphism of a norepinephrine transporter
 CC gene in the sample from the subject, the presence of the polymorphism
 CC indicating the susceptibility of the subject to sub-optimal
 CC norepinephrine transport. The method is useful for screening for
 CC susceptibility of a subject to orthostatic intolerance. Norepinephrine
 CC transporter genes are useful for gene therapy for modulating
 CC norepinephrine transport in a target cell and treating susceptibility
 CC to impaired norepinephrine transporter function, orthostatic intolerance
 CC or other relevant diseases in humans and animals such as mental illness,
 CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
 CC amphetamine abuse.
 XX
 SQ Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
 |||||
 Db 1 CCTTCTCCCTGTT 15

RESULT 2
 AAC09241/c
 ID AAC09241 standard; cDNA; 352 BP.
 AC AAC09241;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 13316.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 OS Homo sapiens.
 OS
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 13316; 71pp + CD-ROM; English.
 XX

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. NO ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;

Query Match 100.0%; Score 15; DB 21; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
 |||||
 Db 149 CCTTCTCCCTGTT 135

RESULT 3
 ABV50337
 ID ABV50337 standard; cDNA; 445 BP.
 XX
 AC ABV50337;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 50328.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 9798; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;

Query Match 100.0%; Score 15; DB 23; Length 445;
Best Local Similarity 100.0%; Pred. NO. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
Db 370 CCTTCTCCCCCTGTT 384

RESULT 4
AAS66052
ID AAS66052 standard; cDNA; 549 BP.
XX
AC AAS66052;
XX
DT 13-FEB-2002 (first entry)
DE DNA encoding novel human diagnostic protein #1856.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR P-PSDB; ABG01865.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 1856; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 549;
Best Local Similarity 100.0%; Pred. NO. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
Db 423 CCTTCTCCCCCTGTT 437

RESULT 5
AAH04051/c
ID AAH04051 standard; cDNA; 827 BP.
XX
AC AAH04051;
XX
DT 26-JUN-2001 (first entry)
DE Human cDNA clone (5'-primer) SEQ ID NO:886.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 1; SEQ ID 886; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification

```
CC of the present invention.
XX Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;
SQ

Query Match      100.0%; Score 15; DB 22; Length 827;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCGCTGT 15
    |||||
Db 123 CCTTCTCCCGCTGT 109

RESULT 6
AAH15437/c
ID AAH15437 standard; cDNA; 1689 BP.
XX
AC AAH15437;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:13660.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
XX
PR 27-AUG-1999; 99JP-0300253.
XX
PR 11-JAN-2000; 2000JP-0118776.
XX
PR 02-MAY-2000; 2000JP-0183767.
XX
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 13660; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC

CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;
Query Match      100.0%; Score 15; DB 22; Length 1689;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCGCTGT 15
    |||||
Db 123 CCTTCTCCCGCTGT 109

RESULT 7
AAH28083
ID AAH28083 standard; cDNA; 1854 BP.
XX
AC AAH28083;
XX
DT 05-SEP-2001 (first entry)
XX
DE DNA encoding human norepinephrine transporter variant A457P.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1854
FT /tag= a
FT /product= "norepinephrine transporter"
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
XX
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45.
XX
DR P-PSDB; AAB84533.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
PS Claim 43; Page 104-108; 133pp; English.
XX
CC The present sequence encodes a variant norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;
```

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
Db 1362 CCTTCTCCCCCTGTT 1376

RESULT 8
AAH28087
ID AAH28087 standard; cDNA; 1854 BP.

XX AC AAH28087;
XX DT 05-SEP-2001 (first entry)
XX DE DNA encoding human norepinephrine transporter variant.
XX KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1..1854
FT /*tag= a
FT /product= "norepinephrine transporter"

XX WO200148246-A1.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35491.

XX PR 29-DEC-1999; 99US-0173682.

XX PR 11-JAN-2000; 2000US-0175456.

XX PA (UYVA-) UNIV VANDERBILT.

XX PI Robertson D, Blakely RD;

XX DR WPI: 2001-425681/45.

XX DR P-PSDB; AAB84535.

XX PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene

XX PS Claim 43; Page 119-121; 133pp; English.

XX CC The present sequence encodes a variant norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.

SQ Sequence 1854 BP; 357 A; 554 C; 493 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
Db 1362 CCTTCTCCCCCTGTT 1376

RESULT 9
ABK43728

ID ABK43728 standard; cDNA; 2159 BP.

XX AC ABK43728;

XX DT 05-JUN-2002 (first entry)

XX DE DNA encoding novel central nervous system protein #308.

XX KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.

XX OS Homo sapiens.

XX PN WO200155318-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01332.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 11-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 11-JUL-2000; 2000US-0217496.

XX PR 14-JUL-2000; 2000US-0218290.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 26-JUL-2000; 2000US-0220964.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

XX PR 14-AUG-2000; 2000US-0225757.

XX PR 14-AUG-2000; 2000US-0225758.

XX PR 14-AUG-2000; 2000US-0225759.

XX PR 18-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0228668.

XX PR 22-AUG-2000; 2000US-0227182.

XX PR 23-AUG-2000; 2000US-0227009.

XX PR 30-AUG-2000; 2000US-0228924.

XX PR 01-SEP-2000; 2000US-0229287.

XX PR 01-SEP-2000; 2000US-0229343.

PR	01-SEP-2000;	2000US-0229344;
PR	01-SEP-2000;	2000US-0229345;
PR	01-SEP-2000;	2000US-0229509;
PR	05-SEP-2000;	2000US-0229513;
PR	05-SEP-2000;	2000US-0230437;
PR	06-SEP-2000;	2000US-0230438;
PR	08-SEP-2000;	2000US-0231242;
PR	08-SEP-2000;	2000US-0231243;
PR	08-SEP-2000;	2000US-0231244;
PR	08-SEP-2000;	2000US-0231413;
PR	08-SEP-2000;	2000US-0231414;
PR	08-SEP-2000;	2000US-0232080;
PR	08-SEP-2000;	2000US-0232081;
PR	12-SEP-2000;	2000US-0231968;
PR	14-SEP-2000;	2000US-0232297;
PR	14-SEP-2000;	2000US-0232398;
PR	14-SEP-2000;	2000US-0232399;
PR	14-SEP-2000;	2000US-0232400;
PR	14-SEP-2000;	2000US-0232401;
PR	14-SEP-2000;	2000US-0233063;
PR	14-SEP-2000;	2000US-0233064;
PR	14-SEP-2000;	2000US-0233065;
PR	21-SEP-2000;	2000US-0234274;
PR	25-SEP-2000;	2000US-0234957;
PR	25-SEP-2000;	2000US-0234958;
PR	26-SEP-2000;	2000US-0235484;
PR	27-SEP-2000;	2000US-0235834;
PR	27-SEP-2000;	2000US-0235836;
PR	29-SEP-2000;	2000US-0236327;
PR	29-SEP-2000;	2000US-0236367;
PR	29-SEP-2000;	2000US-0236368;
PR	29-SEP-2000;	2000US-0236369;
PR	29-SEP-2000;	2000US-0236370;
PR	02-OCT-2000;	2000US-0236802;
PR	02-OCT-2000;	2000US-0237037;
PR	02-OCT-2000;	2000US-0237038;
PR	02-OCT-2000;	2000US-0237039;
PR	02-OCT-2000;	2000US-0237040;
PR	13-OCT-2000;	2000US-0239035;
PR	13-OCT-2000;	2000US-0239937;
PR	20-OCT-2000;	2000US-0240960;
PR	20-OCT-2000;	2000US-0241221;
PR	20-OCT-2000;	2000US-0241785;
PR	20-OCT-2000;	2000US-0241786;
PR	20-OCT-2000;	2000US-0241787;
PR	20-OCT-2000;	2000US-0241808;
PR	20-OCT-2000;	2000US-0241809;
PR	01-NOV-2000;	2000US-0244617;
PR	08-NOV-2000;	2000US-0246474;
PR	08-NOV-2000;	2000US-0246475;
PR	08-NOV-2000;	2000US-0246476;
PR	08-NOV-2000;	2000US-0246477;
PR	08-NOV-2000;	2000US-0246478;
PR	08-NOV-2000;	2000US-0246523;
PR	08-NOV-2000;	2000US-0246524;
PR	08-NOV-2000;	2000US-0246525;
PR	08-NOV-2000;	2000US-0246526;
PR	08-NOV-2000;	2000US-0246527;
PR	08-NOV-2000;	2000US-0246528;
PR	08-NOV-2000;	2000US-0246532;
PR	08-NOV-2000;	2000US-0246609;
PR	08-NOV-2000;	2000US-0246610;
PR	08-NOV-2000;	2000US-0246613;
PR	17-NOV-2000;	2000US-0249207;
PR	17-NOV-2000;	2000US-0249208;
PR	17-NOV-2000;	2000US-0249209;
PR	17-NOV-2000;	2000US-0249211;
PR	17-NOV-2000;	2000US-0249212;
PR	17-NOV-2000;	2000US-0249213;

PR	17-NOV-2000;	2000US-0249214.	
PR	17-NOV-2000;	2000US-0249215.	
PR	17-NOV-2000;	2000US-0249216.	
PR	17-NOV-2000;	2000US-0249217.	
PR	17-NOV-2000;	2000US-0249218.	
PR	17-NOV-2000;	2000US-0249244.	
PR	17-NOV-2000;	2000US-0249245.	
PR	17-NOV-2000;	2000US-0249264.	
PR	17-NOV-2000;	2000US-0249265.	
PR	17-NOV-2000;	2000US-0249297.	
PR	17-NOV-2000;	2000US-0249299.	
PR	17-NOV-2000;	2000US-0249300.	
PR	01-DEC-2000;	2000US-0250160.	
PR	01-DEC-2000;	2000US-0250391.	
PR	05-DEC-2000;	2000US-0251030.	
PR	05-DEC-2000;	2000US-0251988.	
PR	05-DEC-2000;	2000US-0256719.	
PR	06-DEC-2000;	2000US-0251479.	
PR	08-DEC-2000;	2000US-0251856.	
PR	08-DEC-2000;	2000US-0251868.	
PR	08-DEC-2000;	2000US-0251869.	
PR	08-DEC-2000;	2000US-0251989.	
PR	08-DEC-2000;	2000US-0251990.	
PR	11-DEC-2000;	2000US-0254097.	
PR	05-JAN-2001;	2001US-0259678.	
XX	(HUMA-)	HUMAN GENOME SCI INC	

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1: SEO ID No 318: 837pp: English:

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

```

Query Match      100.0%: Score 15: DB 23; Length 2159;
Best Local Similarity 100.0%: Pred. NO. 4.4e+02;
Matches 15: Conservative 0: Mismatches 0; Indels 0; Gaps 0;

```

09 1 CCTTCTCCCCCTGTT 15

Db 1070 CCTTCTCCCCCTGTT 1084

RESULT 10


```

AAS83288/c
ID AAS83288 standard; cDNA: 2451 BP.
XX
AC AAS83288;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19092.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG19101.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 19092; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (I) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2451 BP; 670 A; 631 C; 671 G; 479 T; 0 other;
XX
Query Match 100.0%; Score 15; DB 23; Length 2451;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCTTCTCCCCCTGTT 15
Db 164 CCTTCTCCCCCTGTT 150
XX
RESULT 11
ABL90474
ID ABL90474 standard; cDNA: 2520 BP.
XX
AAS83288/c
ID AAS83288 standard; cDNA: 2451 BP.
XX
AC AAS83288;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19092.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG19101.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 19092; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (I) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2451 BP; 670 A; 631 C; 671 G; 479 T; 0 other;
XX
Query Match 100.0%; Score 15; DB 23; Length 2451;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCTTCTCCCCCTGTT 15
Db 164 CCTTCTCCCCCTGTT 150
XX
RESULT 11
ABL90474
ID ABL90474 standard; cDNA: 2520 BP.
XX
ABL90474;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1036.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI: 2002-122018/16.
DR P-PSDB; ABB90065.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders
XX
PS Claim 4; SEQ ID NO 1036; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2520 BP; 583 A; 687 C; 623 G; 626 T; 1 other;
XX
Query Match 100.0%; Score 15; DB 24; Length 2520;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCTTCTCCCCCTGTT 15
Db 1062 CCTTCTCCCCCTGTT 1076
XX
RESULT 12
ABK44004/c
ID ABK44004 standard; cDNA: 2522 BP.
XX
AC ABK44004;
XX
```

DT 05-JUN-2002 (first entry)
XX DNA encoding novel central nervous system protein #584.
DE Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
XX food additive; food preservative; gene therapy; gene; ss.
OS Homo sapiens.
XX WO200155318-A2.
PN 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01332.
PD 31-JAN-2000; 2000US-0179065.
PF 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 11-JUL-2000; 2000US-0217487.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.
XX 14-SEP-2000; 2000US-0232400.
XX 14-SEP-2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0233063.
XX 14-SEP-2000; 2000US-0233064.
XX 14-SEP-2000; 2000US-0233065.
XX 21-SEP-2000; 2000US-0234223.
XX 21-SEP-2000; 2000US-0234274.
XX 25-SEP-2000; 2000US-0234997.
XX 25-SEP-2000; 2000US-0234998.
XX 26-SEP-2000; 2000US-0235484.
XX 27-SEP-2000; 2000US-0235834.
XX 27-SEP-2000; 2000US-0235836.
XX 29-SEP-2000; 2000US-0236327.
XX 29-SEP-2000; 2000US-0236367.
XX 29-SEP-2000; 2000US-0236368.
XX 29-SEP-2000; 2000US-0236369.
XX 29-SEP-2000; 2000US-0236370.
XX 02-OCT-2000; 2000US-0236802.
XX 02-OCT-2000; 2000US-0237037.
XX 02-OCT-2000; 2000US-0237038.
XX 02-OCT-2000; 2000US-0237039.
XX 02-OCT-2000; 2000US-0237040.
XX 13-OCT-2000; 2000US-0239935.
XX 13-OCT-2000; 2000US-0239937.
XX 20-OCT-2000; 2000US-0240960.
XX 20-OCT-2000; 2000US-0241221.
XX 20-OCT-2000; 2000US-0241785.
XX 20-OCT-2000; 2000US-0241786.
XX 20-OCT-2000; 2000US-0241787.
XX 20-OCT-2000; 2000US-0241808.
XX 20-OCT-2000; 2000US-0241809.
XX 20-OCT-2000; 2000US-0241826.
XX 01-NOV-2000; 2000US-0244617.
XX 08-NOV-2000; 2000US-0246474.
XX 08-NOV-2000; 2000US-0246475.
XX 08-NOV-2000; 2000US-0246476.
XX 08-NOV-2000; 2000US-0246477.
XX 08-NOV-2000; 2000US-0246478.
XX 08-NOV-2000; 2000US-0246523.
XX 08-NOV-2000; 2000US-0246524.
XX 08-NOV-2000; 2000US-0246525.
XX 08-NOV-2000; 2000US-0246526.
XX 08-NOV-2000; 2000US-0246527.
XX 08-NOV-2000; 2000US-0246528.
XX 08-NOV-2000; 2000US-0246532.
XX 08-NOV-2000; 2000US-0246609.
XX 08-NOV-2000; 2000US-0246610.
XX 08-NOV-2000; 2000US-0246611.
XX 08-NOV-2000; 2000US-0246613.
XX 17-NOV-2000; 2000US-0249207.
XX 17-NOV-2000; 2000US-0249208.
XX 17-NOV-2000; 2000US-0249209.
XX 17-NOV-2000; 2000US-0249210.
XX 17-NOV-2000; 2000US-0249211.
XX 17-NOV-2000; 2000US-0249212.
XX 17-NOV-2000; 2000US-0249213.
XX 17-NOV-2000; 2000US-0249214.
XX 17-NOV-2000; 2000US-0249215.
XX 17-NOV-2000; 2000US-0249216.
XX 17-NOV-2000; 2000US-0249217.
XX 17-NOV-2000; 2000US-0249218.
XX 17-NOV-2000; 2000US-0249244.
XX 17-NOV-2000; 2000US-0249245.
XX 17-NOV-2000; 2000US-0249265.
XX 17-NOV-2000; 2000US-0249266.
XX 17-NOV-2000; 2000US-0249297.
XX 17-NOV-2000; 2000US-0249299.
XX 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-581633/65.
 DR P-PSDB; AAU87674.

PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -

XX Claim 1; SEQ ID No 594; 837pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (III) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC anglogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 100.0%; Score 15; DB 23; Length 2522;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTCTCCCCCTGTT 15
 |||||
 Db 1460 CCTTCTCCCTGTT 1446

RESULT 13
 AAA16697

ID AAA16697 standard; cDNA; 3580 BP.

XX

AC AAA16697;

DT 16-JUN-2000 (first entry)

DE Human secreted protein clone as180_1 nucleotide sequence SEQ ID NO:159.
 XX Human; secreted protein; immunestimulant; immunesuppressant; virucide;
 KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
 KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;

KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
 KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
 KW connective tissue disease; multiple sclerosis; erythematosis;
 KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
 KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 KW insulin dependent diabetes mellitus; graft-versus-host-disease;
 KW autoimmune inflammatory eye disease; allergy; ss.

XX Homo sapiens.

XX WO200009552-A1.

XX 24-FEB-2000.

XX 13-AUG-1999; 99WO-US18298.

XX 14-AUG-1998; 98US-0096622.

PR 17-AUG-1998; 98US-0096815.

PR 04-SEP-1998; 98US-0099229.

PR 23-OCT-1998; 98US-0105368.

PR 08-JAN-1999; 99US-0115234.

PR 12-FEB-1999; 99US-0119931.

PR 18-FEB-1999; 99US-0120575.

PR 30-APR-1999; 99US-0132020.

PR 11-AUG-1999; 99US-0096622.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;
 PI Wong GG, Clark HF, Fechtel K;

XX WPI; 2000-205979/18.

DR P-PSDB; AA94977.

XX New polynucleotides encoding secreted proteins, which may have e.g.
 PT nutritional, chemokine, immune stimulating or suppressing,
 PT hematopoiesis regulating, tissue growth, activin/inhibin
 PT antiinflammatory or tumor inhibition activity -

XX Claim 168; Page 613-614; 641pp; English.

XX AAA16618 to AAA16697 encode the human secreted proteins given in
 CC AA94898 to AA94980, isolated from human adult brain, adult thyroid,
 CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,
 CC adult placenta, adult testis, whole embryo, adult cartilage, kidney,
 CC foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,
 CC and adult bladder, cDNA libraries. The polynucleotides and proteins are
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans
 CC and animals. The polynucleotides can be used as markers for tissues in
 CC which the protein is preferentially expressed, as molecular weight
 CC markers on Southern gels, and as chromosome markers or tags to identify
 CC chromosomes or to map gene positions. The proteins can be used in the
 CC treatment of immune deficiencies and disorders, such as severe combined
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
 CC infections. These infections include human immunodeficiency virus (HIV),
 CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
 CC candidiasis. The proteins can be used to treat autoimmune disorders such
 CC as connective tissue disease, multiple sclerosis, systemic lupus
 CC erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation,
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
 CC autoimmune inflammatory eye disease. The proteins can also be used to
 CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent
 CC probes for the human secreted proteins from the present invention.

SQ Sequence 3580 BP; 734 A; 942 C; 1024 G; 880 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 15; DB 21; Length 3580;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
DB 2528 CCTTCTCCCCCTGTT 2542

RESULT 14
ABK35630/C
ID ABK35630 standard: cDNA; 3580 BP.

XX AC ABK35630;
XX DT 08-MAY-2002 (first entry)
XX DE cDNA sequence #21 encoding novel human secreted protein.

XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX KW immune deficiency disorder; blood disorder; inflammatory disorder;
XX KW infectious disorder; allergic condition; neurodegenerative disorder;
XX KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
XX KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.

XX OS Homo sapiens.
XX PN WO200177289-A2.
XX PD 18-OCT-2001.

XX PF 29-MAR-2001; 2001WO-US10232.
XX PR 06-APR-2000; 2000US-195605P.

XX PA (GEMV) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
XX PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX DR WPI; 2002-179322/23.

XX PT Six hundred and twenty three polynucleotides derived from a variety of
XX PT human tissue sources which encode secreted proteins, useful for
XX PT treating immune deficiencies and disorders such as autoimmune disorders

XX PS Claim 1; Page 85-86; 393pp; English.

XX CC The present invention relates to the isolation of novel cDNA sequences
XX CC which encode human secreted proteins. The cDNA sequences have been
XX CC derived from a variety of human tissues. The invention also provides
XX CC a method for producing proteins from these polynucleotide sequences.
XX CC The proteins are useful for identifying compounds that modulate their
XX CC activity and production. The sequences of the invention are
XX CC useful for treating diseases such as hyperproliferative disorders
XX CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
XX CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
XX CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
XX CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
XX CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
XX CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
XX CC haemophilia), and tumours. The polynucleotide sequences of the
XX CC invention are also useful in gene therapy. ABK35610-ABK36232 represent
XX CC the cDNA sequences of the invention that encode for novel human
XX CC secreted proteins.

XX SQ Sequence 3580 BP; 880 A; 1024 C; 942 G; 734 T; 0 other;
Query Match 100.0%; Score 15; DB 24; Length 3580;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
DB 1053 CCTTCTCCCCCTGTT 1039

RESULT 15
ABV22746/C

ID ABV22746 standard: cDNA; 4215 BP.

XX AC ABV22746;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 22737.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.

XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer

XX PS Claim 1; Page 4005-4006; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring the progression of prostate cancer in a patient;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound;
XX CC (g) determining whether prostate cancer has metastasized in a patient;
XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 4215 BP; 1325 A; 808 C; 818 G; 1251 T; 13 other;
Query Match 100.0%; Score 15; DB 23; Length 4215;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
DB 166 CCTTCTCCCCCTGTT 152

Search completed: December 11, 2002, 13:38:16
Job time : 213.5 secs

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 747
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(738)
OTHER INFORMATION: n-A,T,C or G
US-09-605-785-747

Query Match 89.3%; Score 13.4; DB 4; Length 738;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
||||| |||||
Db 469 CCTTCTCCCCCTGTT 455

RESULT 3
US-08-975-316-54/c
Sequence 54, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:

NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-54

Query Match 89.3%; Score 13.4; DB 2; Length 1074;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
||||| |||||
Db 581 CCTTCTCCCCCTGTT 567

RESULT 4
US-09-615-192A-54/c
Sequence 54, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 1074
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-54

Query Match 89.3%; Score 13.4; DB 4; Length 1074;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
||||| |||||
Db 581 CCTTCTCCCCCTGTT 567

RESULT 5
US-08-975-316-55/c
Sequence 55, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-55

Query Match 89.3%; Score 13.4; DB 2; Length 1075;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
DB 582 CCTTCTCCCCCTTT 568

RESULT 6
US-09-615-192A-55/c
Sequence 55, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55
LENGTH: 1075
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-55

Query Match 89.3%; Score 13.4; DB 4; Length 1075;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
DB 582 CCTTCTCCCCCTTT 568

RESULT 7
US-08-482-746-9
Sequence 9, Application US/08482746B
Patent No. 6399315
GENERAL INFORMATION:
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Vale Jr., Wylie W.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: CRF Receptor(s)
FILE REFERENCE: P41-90002
CURRENT APPLICATION NUMBER: US/08/482,746B
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1995-01-17
EARLIER APPLICATION NUMBER: US 08/353,537
EARLIER FILING DATE: 1994-12-09
EARLIER APPLICATION NUMBER: PCT/US94/05908
EARLIER FILING DATE: 1994-05-25
EARLIER APPLICATION NUMBER: US 08/110,286
EARLIER FILING DATE: 1993-08-23
EARLIER APPLICATION NUMBER: US 08/079,320
EARLIER FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1374
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (79)...(1371)
US-08-482-746-9

Query Match 89.3%; Score 13.4; DB 4; Length 1374;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
DB 1080 CCTTCTCCCCCTGTT 1094

RESULT 8
US-08-381-433A-1
Sequence 1, Application US/08381433A
Patent No. 5786203
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy W.
APPLICANT: Oltersdorf, Tilman
APPLICANT: Liaw, Chen
APPLICANT: Grigoriadis, Dimitri E.
APPLICANT: Desouza, Errol B.
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/381,433A
;; FILING DATE: 31-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 690068.401C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; TELEX: 3723836 SEEDANDBERRY
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1514 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 44..1336
US-08-381-433A-1

Query Match 89.3%; Score 13.4; DB 1; Length 1514;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCGTGT 15
||| |||||
DB 1045 CCTCTCCCCCGTGT 1059

RESULT 9

US-08-381-433A-3
;; Sequence 3, Application US/08381433A
;; Patent No. 5786203

GENERAL INFORMATION:

;; APPLICANT: Lovenberg, Timothy W.
;; APPLICANT: Oltersdorf, Tilman
;; APPLICANT: Liaw, Chen
;; APPLICANT: Grigoriadis, Dimitri E.
;; APPLICANT: DeSouza, Errol B.
;; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SEED and BERRY
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98104-7092

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/381,433A
;; FILING DATE: 31-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 690068.401C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; TELEX: 3723836 SEEDANDBERRY
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1626 base pairs

;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 216..1449
US-08-381-433A-3

Query Match 89.3%; Score 13.4; DB 1; Length 1626;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCGTGT 15
||| |||||
DB 1157 CCTCTCCCCCGTGT 1171

RESULT 10

US-09-258-373-21
;; Sequence 21, Application US/09258373
;; Patent No. 6150110

GENERAL INFORMATION:

;; APPLICANT: Fletcher, Jonathan A.
;; APPLICANT: Xiao, Sheng
;; TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
;; FILE REFERENCE: B0801/7135/ERP
;; CURRENT APPLICATION NUMBER: US/09/258,373
;; CURRENT FILING DATE: 1999-02-26
;; EARLIER APPLICATION NUMBER: 60/076,401
;; EARLIER FILING DATE: 1998-02-28
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 21
;; LENGTH: 1875

TYPE: DNA

ORGANISM: Homo Sapiens

US-09-258-373-21

Query Match 89.3%; Score 13.4; DB 3; Length 1875;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCGTGT 15
||| |||||
DB 1755 CCTCTCCCCCGTGT 1769

RESULT 11

US-08-379-496-1/c
;; Sequence 1, Application US/08379496
;; Patent No. 5593833

GENERAL INFORMATION:

;; APPLICANT: MORRISON, Nigel A
;; APPLICANT: EISMAN, John A
;; APPLICANT: KELLY, Paul J
;; TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
;; STREET: Suite 701-E, 555 13th Street.N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/379,496

; FILING DATE: 02-MAR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ERNST, Barbara G
 ; REGISTRATION NUMBER: 30,377
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202 783-6040
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2169 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-379-496-1

Query Match 89.3%; Score 13.4; DB 1; Length 2169;
 Best Local Similarity 93.3%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
 Db 164 CCTTCTCCCCCTGTT 150

RESULT 12
 US-08-484-044-11
 ; Sequence 11, Application US/08484044
 ; Patent No. 552282
 ; GENERAL INFORMATION:
 ; APPLICANT: Caskey, C. T.
 ; APPLICANT: Fu, Ying-Hui
 ; APPLICANT: Friedman, David L.
 ; APPLICANT: Pizzuti, Antonio
 ; APPLICANT: Fenwick, Raymond G.
 ; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,044
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/019,940
 ; FILING DATE: 19-FEB-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5443
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; TELEX: 762829
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3182 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-484-044-11

Query Match 89.3%; Score 13.4; DB 1; Length 3182;
 Best Local Similarity 93.3%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
 Db 414 CCTTCTCCCCCTGTT 428

RESULT 13
 US-08-965-729A-2
 ; Sequence 2, Application US/08965729A
 ; Patent No. 6200751
 ; GENERAL INFORMATION:
 ; APPLICANT: Jian-Ming Gu and Charles T. Esmon
 ; TITLE OF INVENTION: ENDOTHELIAL SPECIFIC EXPRESSION
 ; TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
 ; CITY: Atlanta
 ; STATE: GA
 ; COUNTRY: USA
 ; ZIP: 30309-4530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/965,729A
 ; FILING DATE: 07-NOV-1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/030,718
 ; FILING DATE: 08-NOV-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: OMRF 164 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-873-8794
 ; TELEFAX: 404-873-8795
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3224 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: /note= "Nucleotides 2272 through 2729 are a
 ; OTHER INFORMATION: thrombin responsive element"; Human
 US-08-965-729A-2

Query Match 89.3%; Score 13.4; DB 4; Length 3224;
 Best Local Similarity 93.3%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
 Db 2759 CCTTCTCCCCCTTT 2773

RESULT 14
 PCT-US93-03077-2
 ; Sequence 2, Application PC/TUS9303077
 ; GENERAL INFORMATION:

APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Gaynor, Richard B.
APPLICANT: Wu, Foon Kin
TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
TITLE OF INVENTION: REGULATING GENE EXPRESSION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03077
FILING DATE: 19930331
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/862,025
FILING DATE: April 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: UTFD270PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1540
TELEFAX: 713-749-2679
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3279 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
PCT-US93-03077-2

Query Match 89.3%; Score 13.4; DB 5; Length 3279;
Best Local Similarity 93.3%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||

Db 724 CCTTCTCTCTCTGTT 738

RESULT 15
US-08-965-729A-1
Sequence 1, Application US/08965729A
Patent No. 6200751
GENERAL INFORMATION:
APPLICANT: Jian-Ming Gu and Charles T. Esmon
TITLE OF INVENTION: ENDOTHELIAL SPECIFIC EXPRESSION
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,729A
FILING DATE: 07-NOV-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,718
FILING DATE: 08-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 164 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: /note= "Nucleotides 2270 through 2840 are a
OTHER INFORMATION: large endothelial specific element"; murine
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: /note= "Nucleotides 2990 through 3061 are a
OTHER INFORMATION: serum response element"; murine
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: /note= "Nucleotides 3007 through 3014 are a
OTHER INFORMATION: thrombin responsive element"; murine
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: /note= "Nucleotides 3130 through 3350 are an
OTHER INFORMATION: endothelial specific element"; murine
US-08-965-729A-1

Query Match 89.3%; Score 13.4; DB 4; Length 3481;
Best Local Similarity 93.3%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||

Db 3053 CCTTCTCCCCCTTTT 3067

Search completed: December 11, 2002, 15:30:47
Job time : 51 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:35:52 ; Search time 52.5 Seconds
(without alignments)
111.409 Million cell updates/sec

Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 ccttctccccctgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	14	93.3	389	10	US-09-954-456-1577
3	14	93.3	389	10	US-09-880-107-3234
4	14	93.3	482	9	US-10-001-835-84
5	14	93.3	493	10	US-09-833-381-1570
6	14	93.3	594	10	US-09-864-761-13104
7	14	93.3	8894	10	US-09-764-864-1692
8	14	93.3	8894	10	US-09-764-877-3063
9	14	93.3	16877	10	US-09-764-877-3349
10	13.4	89.3	198	10	US-09-974-300-4063
11	13.4	89.3	264	10	US-09-783-590-10753
12	13.4	89.3	315	9	US-09-712-363-96
13	13.4	89.3	363	10	US-09-783-590-10470
14	13.4	89.3	401	9	US-09-946-807-1267
15	13.4	89.3	401	9	US-09-946-807-1268
16	13.4	89.3	401	9	US-09-946-807-1269
17	13.4	89.3	401	10	US-09-795-668-1267
18	13.4	89.3	401	10	US-09-795-668-1268
19	13.4	89.3	401	10	US-09-795-668-1269

20	13.4	89.3	401	10	US-09-795-686-1267	Sequence 1267, Ap
21	13.4	89.3	401	10	US-09-795-686-1268	Sequence 1268, Ap
22	13.4	89.3	401	10	US-09-795-686-1269	Sequence 1269, Ap
c 23	13.4	89.3	419	9	US-09-954-531-332	Sequence 332, App
c 24	13.4	89.3	419	9	US-09-954-531-355	Sequence 555, App
c 25	13.4	89.3	419	10	US-09-962-832-210	Sequence 210, App
c 26	13.4	89.3	419	10	US-09-954-456-1100	Sequence 1100, Ap
c 27	13.4	89.3	419	10	US-09-954-456-1784	Sequence 1784, Ap
c 28	13.4	89.3	419	10	US-09-880-107-2007	Sequence 2007, Ap
c 29	13.4	89.3	419	10	US-09-967-768A-134	Sequence 134, App
c 30	13.4	89.3	469	10	US-09-864-761-551	Sequence 551, App
c 31	13.4	89.3	477	10	US-09-917-800A-701	Sequence 701, App
c 32	13.4	89.3	738	10	US-09-759-143-747	Sequence 747, App
c 33	13.4	89.3	738	10	US-09-780-669-747	Sequence 747, App
c 34	13.4	89.3	738	10	US-09-822-827-747	Sequence 747, App
c 35	13.4	89.3	928	10	US-09-770-445-393	Sequence 393, App
c 36	13.4	89.3	1016	10	US-09-925-301-438	Sequence 438, App
c 37	13.4	89.3	1374	10	US-09-191-724-9	Sequence 9, Appli
c 38	13.4	89.3	1514	10	US-09-881-401-1	Sequence 1, Appli
c 39	13.4	89.3	1557	10	US-09-900-700-1	Sequence 1, Appli
c 40	13.4	89.3	1626	10	US-09-881-401-3	Sequence 3, Appli
c 41	13.4	89.3	1802	10	US-09-822-830A-401	Sequence 401, App
c 42	13.4	89.3	1945	9	US-09-974-298-189	Sequence 189, App
c 43	13.4	89.3	2617	10	US-09-853-386-123	Sequence 123, App
c 44	13.4	89.3	2766	9	US-09-938-842A-703	Sequence 703, App
c 45	13.4	89.3	3282	10	US-09-864-864-298	Sequence 298, App

ALIGNMENTS

RESULT 1
US-09-764-864-1704
; Sequence 1704, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 15857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1704

Query Match 100.0%; Score 15; DB 10; Length 15857;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCCCTGTT 15
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Db 13094 CCTTCTCCCCCTGTT 13108

RESULT 2
US-09-954-456-1577/c
; Sequence 1577, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; FILE REFERENCE: 68290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052

;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: US/60/234,923
;; PRIOR FILING DATE: 2000-09-25
;; PRIOR APPLICATION NUMBER: US/60/235,134
;; PRIOR FILING DATE: 2000-09-25
;; PRIOR APPLICATION NUMBER: US/60/235,637
;; PRIOR FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US/60/235,638
;; PRIOR FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US/60/235,711
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,720
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,840
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,863
;; PRIOR FILING DATE: 2000-09-27
;; NUMBER OF SEQ ID NOS: 2276
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 1577
;; LENGTH: 389
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1577

Query Match 93.3%; Score 14; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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DB 296 CCTTCTCCCCCTGT 283

RESULT 3
US-09-880-107-3234/c
; Sequence 3234, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3234
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 T84491
; NAME/KEY: unsure
; LOCATION: (1)..(389)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3234

Query Match 93.3%; Score 14; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 296 CCTTCTCCCCCTGT 283
RESULT 4
US-10-001-835-84/c
; Sequence 84, Application US/10001835
; Patent No. US20020160387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Caferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,997
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-835-84

Query Match 93.3%; Score 14; DB 9; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCCCTGTT 15
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DB 188 CTTCTCCCCCTGTT 175

RESULT 5
US-09-833-381-1570/c
; Sequence 1570, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1570
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1570

Query Match 93.3%; Score 14; DB 10; Length 493;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
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DB 120 CCTTCTNCCCCTGTT 106

RESULT 6
US-09-864-761-13104
; Sequence 13104, Application US/09864761

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13104
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136968.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
US-09-864-761-13104
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Query Match          93.3%; Score 14; DB 10; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCTCTCTCCCTGT 14
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DB 192 CCTCTCTCCCTGT 205
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RESULT 7
US-09-764-864-1692/c
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; Sequence 1692, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1692
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-864-1692
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Query Match          93.3%; Score 14; DB 10; Length 8894;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCTTCTCCCTGT 14
      |||||||
DB 4843 CCTTCTCCCTGT 4830
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RESULT 8

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US-09-764-877-3063
; Sequence 3063, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3063
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-3063
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Query Match          93.3%; Score 14; DB 10; Length 8894;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCTTCTCCCTGT 14
      |||||||
DB 4052 CCTTCTCCCTGT 4065
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RESULT 9

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US-09-764-877-3349/c
; Sequence 3349, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-3349
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Query Match 93.3%; Score 14; DB 10; Length 16877;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCTGT 14
|||||
Db 1269 CCTTCTCCCTGT 1256

RESULT 10
US-09-974-300-4063
; Sequence 4063, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4063
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-4063

Query Match 89.3%; Score 13.4; DB 10; Length 198;
Best Local Similarity 93.3%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 15
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Db 69 CCCTCTCCCTGT 83

RESULT 11
US-09-783-590-10753
; Sequence 10753, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10753
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-783-590-10753
Query Match 89.3%; Score 13.4; DB 10; Length 264;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 15
|||||
Db 124 CCTTCTCCCTGT 138

RESULT 12
US-09-712-363-96/c
; Sequence 96, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-96

Query Match 89.3%; Score 13.4; DB 9; Length 315;
Best Local Similarity 93.3%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 15
|||||
Db 106 CCTTCTCCCTGT 92

RESULT 13
US-09-783-590-10470/c
; Sequence 10470, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15

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; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10470
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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US-09-783-590-10470
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Best Local Similarity 93.3%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 41 CCTTCTCCACCTGTT 27
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RESULT 14
US-09-946-807-1267
; Sequence 1267, Application US/09946807
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; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1267
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1267
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Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; Sequence 1268, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
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; SEQ ID NO 1268
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1268
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Query Match      89.3%; Score 13.4; DB 9; Length 401;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Search completed: December 11, 2002, 17:01:30
Job time : 58.5 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:27:12 : Search time 1661 Seconds
(without alignments)
146.257 Million cell updates/sec

Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 ccttctccccctgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	181	17	AZ284882
2	15	100.0	226	10	AV335397
c 3	15	100.0	246	9	AL708655
c 4	15	100.0	297	9	AV067076
5	15	100.0	378	14	F07213
6	15	100.0	393	14	T08889

c 7	15	100.0	399	9	AJ449549
8	15	100.0	401	17	TA8E07P
c 9	15	100.0	403	13	BI706542
c 10	15	100.0	410	10	AW139708
c 11	15	100.0	420	10	AW504644
c 12	15	100.0	421	12	BF514910
c 13	15	100.0	430	13	BG961625
14	15	100.0	430	13	BI136273
15	15	100.0	431	14	BQ339760
16	15	100.0	433	17	AQ640984
c 17	15	100.0	434	10	AW699666
c 18	15	100.0	445	14	BQ778842
c 19	15	100.0	452	12	BF926997
c 20	15	100.0	458	9	AI629376
c 21	15	100.0	469	17	BH635764
c 22	15	100.0	471	17	TA299E02P
23	15	100.0	473	14	R24819
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25	15	100.0	476	14	R87939
26	15	100.0	478	17	BH622683
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c 29	15	100.0	534	9	AJ446382
30	15	100.0	555	17	TA311G03P
c 31	15	100.0	557	9	AL700490
c 32	15	100.0	575	9	AJ397416
33	15	100.0	580	10	BE265171
c 34	15	100.0	590	12	BF674237
c 35	15	100.0	593	9	AJ447956
c 36	15	100.0	599	9	AJ398497
c 37	15	100.0	602	17	AQ656394
c 38	15	100.0	608	12	BF962681
c 39	15	100.0	611	17	AQ661274
40	15	100.0	643	10	BE875768
41	15	100.0	649	10	AW956920
c 42	15	100.0	650	9	AJ450711
c 43	15	100.0	659	9	AJ454058
c 44	15	100.0	667	13	BI859096
c 45	15	100.0	676	9	AJ450146

ALIGNMENTS

RESULT 1
AZ284882
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ284882
RPCI-23-442E20.TV
RPCI-23
Mus musculus genomic clone
DNA
linear
GSS 27-JUL-2000
RPCI-23-442E20
DNA sequence.
AZ284882
GI:9526668
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 181)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-442E20.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 442 row: E column: 20
 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-442E20"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1: EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 54 a 54 c 26 g 47 t

Query Match 100.0%; Score 15; DB 17; Length 181;

Best Local Similarity 100.0%; Pred. No. 5.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

Db 165 CCTTCTCCCCCTGTT 179

RESULT 2

AV335397 226 bp mRNA linear EST 11-NOV-1999
 LOCUS AV335397 RIKEN full-length enriched, adult male medulla oblongata
 DEFINITION Mus musculus cDNA clone 6330571M18 3' similar to AF06196 Mus musculus metalloprotease-disintegrin MDC15 mRNA, mRNA sequence.
 AV335397
 AV335397.1 GI:6375449

ACCSSION AV335397.1

VERSION AV335397.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 226)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,

Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,

Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai

,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,

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,Y., Shigemoto,X., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,

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Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
 Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers
 1. .226
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="6330571M18"
 /clone_lib="RIKEN full-length enriched, adult male medulla oblongata"
 /sex="male"
 /tissue_type="medulla oblongata"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site:1: SalI; Site:2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

BASE COUNT 55 a 51 c 63 g 56 t 1 others

Query Match 100.0%; Score 15; DB 10; Length 226;

Best Local Similarity 100.0%; Pred. No. 5.7e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

Db 77 CCTTCTCCCCCTGTT 91

RESULT 3

LOCUS AL708655/c

DEFINITION

DKFZp686J0853.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

AL708655

ACCESSION

VERSION

KEYWORDS

SOURCE

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

EST.

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
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 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-442E20"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1: EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 54 a 54 c 26 g 47 t

Query Match 100.0%; Score 15; DB 17; Length 181;

Best Local Similarity 100.0%; Pred. No. 5.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

Db 165 CCTTCTCCCCCTGTT 179

RESULT 2

AV335397 226 bp mRNA linear EST 11-NOV-1999
 LOCUS AV335397 RIKEN full-length enriched, adult male medulla oblongata
 DEFINITION Mus musculus cDNA clone 6330571M18 3' similar to AF06196 Mus musculus metalloprotease-disintegrin MDC15 mRNA, mRNA sequence.
 AV335397
 AV335397.1 GI:6375449

ACCSSION AV335397.1

VERSION AV335397.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 226)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,

Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,

Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai

,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,

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Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

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Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

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Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T.,

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
 Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers
 1. .226
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="6330571M18"
 /clone_lib="RIKEN full-length enriched, adult male medulla oblongata"
 /sex="male"
 /tissue_type="medulla oblongata"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site:1: SalI; Site:2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

BASE COUNT 55 a 51 c 63 g 56 t 1 others

Query Match 100.0%; Score 15; DB 10; Length 226;

Best Local Similarity 100.0%; Pred. No. 5.7e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

Db 77 CCTTCTCCCCCTGTT 91

RESULT 3

LOCUS AL708655/c

DEFINITION

DKFZp686J0853.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

AL708655

ACCESSION

VERSION

KEYWORDS

SOURCE

EST.

EST.

EST.

EST.

EST.

EST.

EST.

Transcriptional sequencing: A method for DNA sequencing using RNA

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

No sl sequence available.
This clone (DKF2p86J0853) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Source

1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p86J0853"
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/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
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BASE COUNT 71 a 47 c 88 g 40 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

Db 176 CCTTCTCCCCCTGTT 162

RESULT 4

AV067076/c

LOCUS

DEFINITION AV067076 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA clone 2010200P09, mRNA sequence.

ACCESSION

AV067076

VERSION

AV067076.1 GI:5186904

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 297)

AUTHORS

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE

RIKEN Mouse ESTs

JOURNAL

Unpublished (1999)

COMMENT

Contact: Chie Owa

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Source

1..297
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="2010200P09"
/clone_lib="Mus musculus small intestine C57BL/6J adult"
/sex="male"
/tissue_type="small intestine"
/dev_stage="adult"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTCGGAGCGCGGATGGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 95 a 62 c 79 g 61 t

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 297;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCCCCCTGTT 15

Db 45 CTTCTCCCCCTGTT 31

RESULT 5

F07213

LOCUS

DEFINITION F07213 HSC12B021 normalized infant brain cDNA Homo sapiens cDNA clone c-1zb02, mRNA sequence.

ACCESSION

F07213

VERSION

F07213.1 GI:672862

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 378)
Aufrey, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabakchis, C. and Tessier, A.

TITLE

IMAGE: molecular integration of the analysis of the human genome and its expression

JOURNAL

MEDLINE

COMMENT

95277534

Contact: Genethon

Genexpress-Genethon

Genethon Centre de recherche sur le Genome Humain

1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE

Tel: 33169472800

Fax: 33160778698

Email: genexpress@genethon.fr

Single read.

Genexpress_library_id: C; Genexpress_sequence_id: yic-1zb02

Seq primer: (-21)M13_universal.

Location/Qualifiers

1..378

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="c-1zb02"

/clone_lib="normalized infant brain cDNA"

/sex="Female"

/tissue_type="total brain"

/dev_stage="3 months old"

/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex:Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the

```

lafmid BA vector. Clone library from B.Soaress, Psychiatry
Dept. Columbia University, USA.
Normalization_method:
Bento Soares, P.N.A.S in press"
BASE COUNT      68 a 111 c 99 g 98 t 2 others
ORIGIN

Query Match      100.0%; Score 15; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
    |||||
Db 193 CCTTCTCCCCCTGTT 207

RESULT 6
T08889
LOCUS      T08889          393 bp      mRNA      linear      EST 03-AUG-1993
DEFINITION EST06781 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBL71
5' end similar to p87 transporter-like protein, mRNA sequence.
ACCESSION  T08889
VERSION     T08889.1 GI:389917
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 393)
AUTHORS   Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
TITLE     Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
JOURNAL   Nat. Genet. 4, 373-380 (1993)
MEDLINE   94004965
COMMENT   Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: W13 Reverse

FEATURES             source
    source
    1..393
    /organism="Homo sapiens"
    /db_xref="ATCC (inhost):85383"
    /db_xref="taxon:9606"
    /clone="HIBL71"
    /clone_lib="Infant Brain, Bento Soares"
    /note="Vector: Lafmid; The IB library was constructed by
directional cloning and oligo(dT)-priming in the Lafmid
vector, utilizing a three month old infant human brain
(total brain)."
```

```

BASE COUNT      78 a 114 c 101 g 99 t 1 others
ORIGIN

Query Match      100.0%; Score 15; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
    |||||
Db 130 CCTTCTCCCCCTGTT 144
```

```

RESULT 7
AJ449549/c
LOCUS      AJ449549      399 bp      mRNA      linear      EST 19-APR-2002
DEFINITION AJ449549 riken1 Gallus gallus cDNA clone 22g1lrl, mRNA sequence.
ACCESSION  AJ449549
VERSION     AJ449549.1 GI:20216770
KEYWORDS   EST.
SOURCE     chicken.
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 399)
Buerstedde,J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
    source
    1..399
    /organism="Gallus gallus"
    /db_xref="taxon:9031"
    /clone="22g1lrl"
    /clone_lib="riken1"
    /cell_type="bursal lymphocyte"
    /dev_stage="2-3 weeks old"
    /note="CB inbred strain"
BASE COUNT      120 a 78 c 103 g 97 t 1 others
ORIGIN

Query Match      100.0%; Score 15; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
    |||||
Db 107 CCTTCTCCCCCTGTT 93

RESULT 8
TA8E07P
LOCUS      TA8E07P          401 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 8e07, forward sequence, genomic
survey sequence.
ACCESSION  AL452614
VERSION     AL452614.1 GI:11861158
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 401)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE     Direct Submission
JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrel@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT   Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
    source
    1..401
    /organism="Trypanosoma brucei"
    /strain="TREU927"
    /db_xref="taxon:5691"
    /clone="8e07"
BASE COUNT      81 a 91 c 118 g 111 t
ORIGIN
```

Query Match 100.0%; Score 15; DB 17; Length 401;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
 |||||
 Db 67 CCTTCTCCCCCTGTT 81

RESULT 9
 BI706542/c
 LOCUS
 DEFINITION 403 bp mRNA linear EST 13-FEB-2002
 fg07c03.y1 zebrafish adult retina cDNA Danio rerio cDNA clone
 4790765.5, similar to TR:Q9UH03 Q9UH03 BK250D10.3 ;, mRNA sequence.
 BI706542
 ACCESSION BI706542.1 GI:15682237
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM zebrafish.
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Danio.

REFERENCE
 AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
 , S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
 , K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Gibbons, M., Fape, D., Harvey, N., Schurk, R., Ritter, E.,
 Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
 and Wilson, R.

TITLE WashU Zebrafish EST Project 1998
 JOURNAL Unpublished (1998)
 COMMENT Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: zbrfish@wustl.wustl.edu
 Library constructed by: Chandra Tucker and Gregory Niemi DNA
 Sequencing by: Washington University Genome Sequencing Center Clone
 distribution: RessourcenzentrumPrimaDatenbank, Berlin, Germany
 (web address: www.rzpd.de)
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 396.

FEATURES
 Source
 1..403
 /organism="Danio rerio"
 /strain="wild-type"
 /db_xref="taxon:7955"
 /clone="4790765"
 /clone_lib="zebrafish adult retina cDNA"
 /sex="mixed"
 /dev_stage="1-2 years"
 /lab_host="E.Coli XL1-Blue MRF"
 /note="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
 EcoRI; Site_2: SalI; This Zebrafish library was
 constructed by Dr. Susan E. Brockerhoff (email:
 sbrocker@u.washington.edu) RZPD library number: 760"
 BASE COUNT 105 a 89 c 116 g 93 t
 ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 403;
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
 |||||
 Db 114 CCTTCTCCCCCTGTT 100

RESULT 10
 AW139708/c
 LOCUS

DEFINITION UI-H-BII-aeb-a-03-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
 IMAGE:2718605 3', mRNA sequence.
 ACCESSION AW139708
 VERSION AW139708.1 GI:6144426
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 410)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Oligo-dt track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NCI_CGAP clone distribution
 information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html The following repetitive
 elements were found in this cDNA sequence: 151-216, >(GGGA
)n#Simple_repeat
 Seq primer: M13 Forward
 POLYA=No.

FEATURES
 source
 1..410
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2718605"
 /clone_lib="NCI_CGAP_Sub3"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NCI_CGAP Sub3 library is a subtracted library derived from
 the NCI_CGAP Sub1 library, which is a subtracted library
 derived from B1. B1 constitutes a mixture of 21
 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
 , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
 NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
 NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
 NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_GLL1, NCI_CGAP_Le12,
 NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
 NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
 NCI_CGAP_Brn25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below:
 NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
 3798-3803 (IMAGE Clones 1322376-1323911, 1456008-1456775
 , 1500552-1502855); NCI_CGAP_Kid5 pool 1, LLAM 3338-3342
 , 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831,
 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991,
 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,
 1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones
 985608-986759, 1101192-1101959, 1217928-1220615);
 NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
 Clones 1057416-1061255, 1144584-1145351). Subtraction
 was performed as previously described [Bonaldi, Lennon &
 Soares (1996)]: Normalization and Subtraction: Two
 Approaches To Facilitate Gene Discovery. Genome Research
 6, 791-806.

TAG_LIB=NCI_CGAP_Kid3
 TAG_TISSUE=Kidney
 TAG_SEQ=AATGC"
 BASE COUNT 110 a 124 c 91 g 85 t
 ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 410;
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
Db 396 CCTTCTCCCCCTGTT 382

RESULT 11
AW504644/c
LOCUS
DEFINITION
  AW504644 420 bp mRNA linear EST 02-MAR-2000
  UI-HF-BN0-alk-h-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
  IMAGE:3079943 5', mRNA sequence.
ACCESSION
  AW504644
VERSION
  AW504644.1 GI:7142311
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 420)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-re@mail.nih.gov
  Eco RI site shown at the beginning of the sequence.
  Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
  cDNA Library Preparation: M.B. Soares Lab
  cDNA Library Arrayed by: M.B. Soares Lab
  DNA Sequencing by: M.B. Soares Lab
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Seq primer: M13 Forward.

FEATURES
  source
    1..420
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:3079943"
      /clone_lib="NIH_MGC_50"
      /tissue_type="lymph"
      /cell_type="germinal center B cells"
      /cell_line="MGC85"
      /lab_host="DH10B (LTI)"
      /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
      Constructed from size fractionated cytoplasmic mRNA
      (3.5-4.4kb). Directionally cloned. Cells provided by
      Louis M. Staudt, Ph.D. Library preparation by Maria de
      Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

BASE COUNT 124 a 72 c 126 g 98 t
ORIGIN
  Query Match 100.0%; Score 15; DB 10; Length 420;
  Best Local Similarity 100.0%; Pred. No. 6.5e+03;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
Db 159 CCTTCTCCCCCTGTT 145

RESULT 12
BF514910/c
LOCUS
DEFINITION
  BF514910 421 bp mRNA linear EST 07-DEC-2000
  UI-H-BW1-anp-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
  IMAGE:3083036 3', mRNA sequence.
ACCESSION
  BF514910
VERSION
  BF514910.1 GI:11600078
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 421)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first A
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes

FEATURES
source

Location/Qualifiers
1..421
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3083036"
/clone_lib="NCI_CGAP_Sub7"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73B-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub7
is a subtracted library derived from NCI_CGAP_Sub6. The
NCI_CGAP_Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones
1322376-1323911, 1456008-1456775,1500552-1502855);
NCI_CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-3778
(IMAGE Clones 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439
); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720
3733-3735 (IMAGE Clones 1257096-1258631,1469064-1470983
, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clones 985608-986759,
1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255
,114584-1145351). (6% of the driver population), plus a
pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE
Clones 2710536-2710535) and NCI_CGAP_Sub2 (IMAGE
Clones 2710536-2712455) (4% of the driver population
, plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
Clones 2712456-2723591) (10% of the driver population),
plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
Clones 2723592-2729326) (40% of the driver population),
plus a pool of 4032 clones from NCI_CGAP_Sub6 (IMAGE
Clones 2728969-2733190) (40% of the driver population).
Subtraction was performed as previously described (Bonaldo
, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG_LIB=NCI_CGAP_Brn50
TAG_TISSUE=brain
TAG_SEQ=TTTCG"

BASE COUNT 114 a 95 c 111 g 101 t
ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 421;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
Db 130 CCTTCTCCCCCTGTT 116

RESULT 13
BG961625/c

```

LOCUS      BG961625          430 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION PM0-CT0642-240401-007-C09 CT0642 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG961625
VERSION     BG961625.1  GI:14379796
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 430)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Gene expression in Populus
            Lundberg,J.
            Contact: Erlandsson R
            Department of Biotechnology
            Royal Institute of Technology
            Teknikringen 30, Stockholm S-10044, Sweden
            Tel: 46 8 790 8287
            Fax: 46 8 245452
            Email: rikerl@biochem.kth.se.
FEATURES    Location/Qualifiers
            source          1..430
                        /organism="Populus balsamifera subsp. trichocarpa"
                        /db_xref="taxon:3694"
                        /clone_lib="Populus flower cDNA library"
                        /note="Organ: flower"
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Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
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Db 220 CCTTCTCCCCCTGTT 234

RESULT 15
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DEFINITION QV2-NN0045-211100-494-c07 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ339760
VERSION     BQ339760.1  GI:209999826
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 431)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&t2=QV2-NN0045-
            211100-494-c07&t3=2000-11-21&t4=1)
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            High quality sequence start: 12
            High quality sequence stop: 29.
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DEFINITION F065P87Y Populus flower cDNA library Populus balsamifera subsp.
            trichocarpa cDNA, mRNA sequence.
ACCESSION  B1136273
VERSION     B1136273.1  GI:18017201
KEYWORDS    EST.
SOURCE      Populus balsamifera subsp. trichocarpa.
            Populus balsamifera subsp. trichocarpa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
FEATURES    Location/Qualifiers
            source          1..430
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                        /db_xref="taxon:9606"
                        /clone_lib="CT0642"
                        /dev_stage="Adult"
                        /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                        SmaI; A mini-library was made by cloning products derived
                        from ORESTES PCR (U.S. Letters Patent application No. 196
                        ,716 - Ludwig Institute for Cancer Research) profiles
                        into the puc 18 vector. Reverse transcription of tissue
                        mRNA and cDNA amplification were performed under low
                        stringency conditions."
BASE COUNT  141 a 83 c 118 g 88 t
ORIGIN
Query Match      100.0%; Score 15; DB 13; Length 430;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
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Db 132 CCTTCTCCCCCTGTT 118

RESULT 14
B1136273
LOCUS      B1136273          430 bp      mRNA      linear      EST 31-DEC-2001
DEFINITION F065P87Y Populus flower cDNA library Populus balsamifera subsp.
            trichocarpa cDNA, mRNA sequence.
ACCESSION  B1136273
VERSION     B1136273.1  GI:18017201
KEYWORDS    EST.
SOURCE      Populus balsamifera subsp. trichocarpa.
            Populus balsamifera subsp. trichocarpa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

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/clone_lib="NN0045"  
/dev_stage="Adult"  
/notes="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;  
Site_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT      75 a 138 c 108 g 110 t  
ORIGIN
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Query Match      100.0%; Score 15; DB 14; Length 431;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCTTCTCCCCCTGTT 15  
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Db 399 CCTTCTCCCCCTGTT 413
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Search completed: December 11, 2002, 15:28:57  
Job time : 1665 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:30:52 : Search time 1652 Seconds
(without alignments)
264.251 Million cell updates/sec

Title: US-09-750-609-9

Perfect score: 15
Sequence: 1 cctctcgcgcctgtt 15

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:

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- 4: gb.ov.*
- 5: gb.pat.*
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- 32: em.htg_other.*
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- 34: em.htg_pln.*
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- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	100.0	920	6	AX194629	Sequence
2	15	100.0	920	6	AX194634	Sequence
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4	15	100.0	1411	9	BC000563	Homo sapi
5	15	100.0	1983	9	HUMNORTR	M65105 Human nad
6	15	100.0	2127	9	HUMCOLA1XV	L01697 Homo sapien
7	15	100.0	5161	9	HUMCOLXVAL	L25286 Homo sapien
8	15	100.0	14621	2	AC020425	AC020425 Drosophill
9	15	100.0	61956	2	AC101376	Mus muscu
10	15	100.0	65851	2	AC124280	Homo sapi
11	15	100.0	80669	2	AC130797	Chlamydom
12	15	100.0	90280	2	AC009031	Homo sapi
13	15	100.0	110000	2	LMFICHR12_1	Continuation (2 of
14	15	100.0	150765	2	AC094766	Rattus no
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16	15	100.0	167094	9	AC007602	Homo sapi
17	15	100.0	169763	2	AC120748	Rattus no
18	15	100.0	178965	2	AC096167	Rattus no
19	15	100.0	181066	2	AC099635	Mus muscu
20	15	100.0	181650	2	AC097825	Rattus no
21	15	100.0	183105	3	AC104606	Drosophill
22	15	100.0	187359	8	OSJN00259	AL731609 Oryza sat
23	15	100.0	188913	9	AC026802	Homo sapi
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25	15	100.0	285272	3	AE003441	AE003441 Drosophill
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27	14	93.3	1773	9	AB057774	Homo sapi
28	14	93.3	1987	10	AF158025	Rattus no
29	14	93.3	1989	10	MUSCAT2A	L03290 Mus musculu
30	14	93.3	1989	10	MUSCAT2X	L11600 Mouse catio
31	14	93.3	2072	3	AF145606	AF145606 Drosophill
32	14	93.3	2306	9	AK054811	AK054811 Homo sapi
33	14	93.3	2324	8	SCYGR002C	272787 S.cerevisia
34	14	93.3	2393	8	AF435646	Oryza sat
35	14	93.3	2397	6	AR054116	AR054116 Sequence
36	14	93.3	2397	6	IL13751	IL13751 Sequence 5
37	14	93.3	2723	10	MUSTEAB	M62838 Mouse T cel
38	14	93.3	3507	10	AF301152	AF301152 Mus muscu
39	14	93.3	3698	10	MUSMEMPROT	L29006 Mouse membr
40	14	93.3	4420	1	CGL300822	AF300822 Corynebacc
41	14	93.3	5245	1	AF130462	AF130462 Corynebacc
42	14	93.3	12563	1	AE000769	AE000769 Aquifex a
43	14	93.3	13782	1	AE009777	AE009777 Pyrobacul
44	14	93.3	16387	5	AP002935	AP002935 Poromitra
45	14	93.3	18518	1	AE001068	AE001068 Archaeogl
46	14	93.3	20539	9	HS349E10	AL022341 Human DNA
47	14	93.3	20603	9	AL359534	AL359534 Human DNA
48	14	93.3	28235	2	AC014089	AC014089 Drosophill
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50	14	93.3	66789	2	AC103807	AC103807 Homo sapi
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52	14	93.3	71605	2	AC119332	AC119332 Rattus no
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57	14	93.3	104268	9	AC068120	AC068120 Homo sapi
58	14	93.3	104492	2	AC124910	AC124910 Takifugu
59	14	93.3	110977	2	AC103120	AC103120 Rattus no
60	14	93.3	113375	9	AC073878	AC073878 Homo sapi
61	14	93.3	114715	2	AC103165	AC103165 Rattus no
62	14	93.3	120937	10	AL591911	AL591911 Mouse DNA
63	14	93.3	123520	9	HSJ447E21	AL050336 Human DNA
64	14	93.3	130926	9	HS453A3	283745 Human DNA s
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c 66	14	93.3	138335	8	AC119148	Genomic s	139	13	86.7	1090	8	AY042856	Arabidops
c 67	14	93.3	139884	10	AC110379	Mus muscu	c 140	13	86.7	1117	1	AB016861	Burkholde
c 68	14	93.3	140403	2	AC109444	Homo sapi	c 141	13	86.7	1122	1	STMDRG	M51029 S.typhimuri
c 69	14	93.3	144949	2	AC040935	Homo sapi	c 142	13	86.7	1122	1	STYLF2MDH	M95049 Salmonella
c 70	14	93.3	145679	2	AC027249	Homo sapi	c 143	13	86.7	1359	3	AY061092	AY061092 Drosophil
c 71	14	93.3	147910	2	AC105988	Mus muscu	c 144	13	86.7	1369	1	RRU317975	AJ317975 Rhodospir
c 72	14	93.3	153533	2	AC095199	Rattus no	c 145	13	86.7	1385	10	BC025516	BC025516 Mus muscu
c 73	14	93.3	155001	2	AL356474	Homo sapi	c 146	13	86.7	1465	9	HSTSHR	AF035361 Homo sapi
c 74	14	93.3	155001	2	AL356474	Homo sapi	c 147	13	86.7	1681	1	SC6GL0A	AF035361 Homo sapi
c 75	14	93.3	155670	3	AC012097	Drosophil	c 148	13	86.7	1721	8	AY086007	AL45343 Streptomy
c 76	14	93.3	156413	9	HSAL19E20	Human DNA	c 149	13	86.7	1811	9	ABU18602	U18602 Alouatta be
c 77	14	93.3	160376	2	AC036118	Homo sapi	c 150	13	86.7	1886	5	AB067770	AB067770 Oncorhync
c 78	14	93.3	160379	2	AC118296	Rattus no	c 151	13	86.7	2001	6	AR163597	AR163597 Sequence
c 79	14	93.3	161519	9	AC097459	Homo sapi	c 152	13	86.7	2003	1	ECNDAG	V00274 E. coli dna
c 80	14	93.3	163395	2	AC103726	Homo sapi	c 153	13	86.7	2161	9	AK094594	AK094594 Homo sapi
c 81	14	93.3	166447	2	AC121202	Rattus no	c 154	13	86.7	2232	6	AX280771	AX280771 Sequence
c 82	14	93.3	168706	2	AC092199	Typanoso	c 155	13	86.7	2292	6	AX280775	AX280775 Sequence
c 83	14	93.3	169457	2	AC009216	Drosophil	c 156	13	86.7	2292	6	AX280779	AX280779 Sequence
c 84	14	93.3	169633	2	AC111280	Rattus no	c 157	13	86.7	2292	6	AX280783	AX280783 Sequence
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c 87	14	93.3	177126	2	AC123188	Rattus no	c 160	13	86.7	2292	6	AX280795	AX280795 Sequence
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c 89	14	93.3	181596	2	AC069467	Mus muscu	c 162	13	86.7	2413	9	HUMTSHR	M73747 Homo sapien
c 90	14	93.3	182301	9	AC012498	Homo sapi	c 163	13	86.7	2415	6	A34990	A34990 H.sapiens T
c 91	14	93.3	182749	2	AC094882	Rattus no	c 164	13	86.7	2415	6	A34990	A34990 H.sapiens T
c 92	14	93.3	182755	2	AC127835	Rattus no	c 165	13	86.7	2415	6	A34990	A34990 H.sapiens T
c 93	14	93.3	183269	9	AP001024	Homo sapi	c 166	13	86.7	2470	9	HUMTSRX	M32175 Human thyro
c 94	14	93.3	184338	2	AC124901	Rattus no	c 167	13	86.7	2470	9	HUMTSRX	M32175 Human thyro
c 95	14	93.3	185174	2	AC118184	Rattus no	c 168	13	86.7	2475	10	MMU02601	U02601 Mus musculu
c 96	14	93.3	186748	3	AC101263	Drosophil	c 169	13	86.7	2512	10	MMU02602	U02602 Mus musculu
c 97	14	93.3	187035	2	AC109750	Rattus no	c 170	13	86.7	2545	3	AY118724	AY118724 Drosophil
c 98	14	93.3	193024	2	AC108538	Rattus no	c 171	13	86.7	2934	3	AY118724	AY118724 Drosophil
c 99	14	93.3	193159	9	AC006946	Homo sapi	c 172	13	86.7	2934	3	AY118724	AY118724 Drosophil
c 100	14	93.3	194355	2	AC116511	Mus muscu	c 173	13	86.7	2936	1	AF007804	AF007804 Brucella
c 101	14	93.3	197183	2	AC102636	Mus muscu	c 174	13	86.7	3239	3	DROSERCA	BC032200 Mus muscu
c 102	14	93.3	197743	10	AL591711	Mouse DNA	c 175	13	86.7	3239	3	DROSERCA	BC032200 Mus muscu
c 103	14	93.3	199386	8	NCB14D6	Neurospor	c 176	13	86.7	3240	8	AF056976	AF056976 Acremoniu
c 104	14	93.3	202605	9	AP002353	Homo sapi	c 177	13	86.7	3249	3	AY095510	AY095510 Drosophil
c 105	14	93.3	213386	2	AC115746	Mus muscu	c 178	13	86.7	3349	6	AX280963	AX280963 Sequence
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c 107	14	93.3	219414	2	AC101931	Mus muscu	c 180	13	86.7	3366	3	AY119446	AY119446 Drosophil
c 108	14	93.3	219564	2	AC103021	Mus muscu	c 181	13	86.7	3366	3	AY119446	AY119446 Drosophil
c 109	14	93.3	220898	2	AC098941	Rattus no	c 182	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 110	14	93.3	221951	10	AC122857	Mus muscu	c 183	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 111	14	93.3	225016	2	AC063967	Mus muscu	c 184	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 112	14	93.3	226402	2	AC105706	Rattus no	c 185	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 113	14	93.3	229422	2	AC097544	Rattus no	c 186	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 114	14	93.3	235302	2	AC073784	Rattus no	c 187	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 115	14	93.3	242048	2	AC110537	Mus muscu	c 188	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 116	14	93.3	256073	9	AE006464	Homo sapi	c 189	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 117	14	93.3	297308	3	AE003507	Drosophil	c 190	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 118	14	93.3	349980	6	AX127144	Sequence	c 191	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 119	13	86.7	107	19	DOGSF1RB	L7224 Canis famil	c 192	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 120	13	86.7	107	19	DOGSF1RB	L7224 Canis famil	c 193	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 121	13	86.7	392	11	RSPPUFA03	M00899 R.rubrum pu	c 194	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 122	13	86.7	392	11	AU047565	AU047565 Rattus no	c 195	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 123	13	86.7	416	5	AF012928	AF012928 Gallus ga	c 196	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 124	13	86.7	485	6	AR163602	AR163602 Sequence	c 197	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 125	13	86.7	491	6	AR163603	AR163603 Sequence	c 198	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 126	13	86.7	497	6	AR163604	AR163604 Sequence	c 199	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 127	13	86.7	625	1	AB051733	AB051733 Unculture	c 200	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 128	13	86.7	809	8	AY072470	AY072470 Arabidops	c 201	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 129	13	86.7	827	2	AF230658	AF230658 Escherich	c 202	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 130	13	86.7	849	1	SEU04765	U04765 Salmonella	c 203	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 131	13	86.7	849	1	SEU04765	U04765 Salmonella	c 204	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 132	13	86.7	927	9	HSCOLXV16	HSCOLXV16	c 205	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 133	13	86.7	927	9	HSCOLXV16	HSCOLXV16	c 206	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 134	13	86.7	964	5	L231072	L231072 Lampetra	c 207	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 135	13	86.7	979	14	AF118618	AF118618 Hepatitis	c 208	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 136	13	86.7	979	14	AF118619	AF118619 Hepatitis	c 209	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 137	13	86.7	1027	3	AY118621	AY118621 Hepatitis	c 210	13	86.7	3486	6	E03374	E03374 DNA sequenc
c 138	13	86.7	1049	8	AY084467	AY084467 Arabidops	c 211	13	86.7	3486	6	E03374	E03374 DNA sequenc

c 212	13	86.7	9000	1	AB032368	AB032368 Thermus t	285	13	86.7	65446	2	AC105034	AC105034 Homo sapi
c 213	13	86.7	9241	2	AC017570	AC017570 Drosophill	286	13	86.7	65875	2	AC101523	AC101523 Mus muscu
c 214	13	86.7	9785	6	I24403	I24403 Sequence 1	287	13	86.7	65902	2	AC100235	AC100235 Mus muscu
c 215	13	86.7	10029	1	AE009572	AE009572 Brucella	288	13	86.7	67129	2	AC095673	AC095673 Rattus no
c 216	13	86.7	10029	1	AE011656	AE011656 Xanthomon	c 289	13	86.7	67129	2	AC127128	AC127128 Rattus no
c 217	13	86.7	10124	1	TP036839	TP036839 Treponema p	c 290	13	86.7	67349	8	AF003752	AF003752 Rattus no
c 218	13	86.7	10140	1	AE009086	AE009086 Agrobacte	c 291	13	86.7	68631	2	AC020051	AC020051 Drosophill
c 219	13	86.7	10334	1	AE000388	AE000388 Escherich	c 292	13	86.7	69169	2	AC102380	AC102380 Mus muscu
c 220	13	86.7	10365	1	AE005536	AE005536 Escherich	c 293	13	86.7	69201	9	AC004109	AC004109 Homo sapi
c 221	13	86.7	10576	1	AE000957	AE000957 Archaeogl	c 294	13	86.7	69314	2	AC090447	AC090447 Homo sapi
c 222	13	86.7	10576	1	AE011689	AE011689 Xanthomon	c 295	13	86.7	71538	2	AC118243	AC118243 Mus muscu
c 223	13	86.7	10683	1	AE008052	AE008052 Agrobacte	c 296	13	86.7	72893	2	AC113515	AC113515 Mus muscu
c 224	13	86.7	10750	1	AE012010	AE012010 Xanthomon	c 297	13	86.7	76334	2	AC128007	AC128007 Rattus no
c 225	13	86.7	10986	1	AE005188	AE005188 Escherich	c 298	13	86.7	77630	7	AF222060	AF222060 Halovirus
c 226	13	86.7	11069	1	AE004124	AE004124 Vibrio ch	c 299	13	86.7	77670	8	AC007260	AC007260 Arabidops
c 227	13	86.7	11411	1	AE007649	AE007649 Clostridi	c 300	13	86.7	78500	8	SCD9461	SCD9461 Saccharomyc
c 228	13	86.7	11584	1	AE006049	AE006049 Pasteurel	c 301	13	86.7	80460	10	AL513014	AL513014 Mouse DNA
c 229	13	86.7	11622	1	AE004519	AE004519 Pseudomon	c 302	13	86.7	80609	1	AF116907	AF116907 Rhodococc
c 230	13	86.7	12248	1	AE001929	AE001929 Delnococe	c 303	13	86.7	80610	1	AF001204	AF001204 Rhodococc
c 231	13	86.7	12541	9	AL162736	AL162736 Human DNA	c 304	13	86.7	81344	9	AC079770	AC079770 Homo sapi
c 232	13	86.7	12600	1	AE006102	AE006102 Pasteurel	c 305	13	86.7	85219	9	AC073520	AC073520 Homo sapi
c 233	13	86.7	13041	1	AE005983	AE005983 Caenorhab	c 306	13	86.7	85829	9	AC011382	AC011382 Homo sapi
c 234	13	86.7	13205	1	AE001225	AE001225 Treponema	c 307	13	86.7	87166	2	AC014242	AC014242 Drosophill
c 235	13	86.7	13605	1	AE009309	AE009309 Agrobacte	c 308	13	86.7	87217	2	AC012260	AC012260 Homo sapi
c 236	13	86.7	13899	1	AE013637	AE013637 Yersinia	c 309	13	86.7	87526	2	AC018485	AC018485 Drosophill
c 237	13	86.7	14309	1	AE004759	AE004759 Pseudomon	c 310	13	86.7	88028	9	AC004938	AC004938 Homo sapi
c 238	13	86.7	14939	1	AE008304	AE008304 Agrobacte	c 311	13	86.7	88080	2	AC097591	AC097591 Rattus no
c 239	13	86.7	15304	1	AE000692	AE000692 Aquifex a	c 312	13	86.7	89286	2	AC095922	AC095922 Rattus no
c 240	13	86.7	15861	3	AF036685	AF036685 Caenorhab	c 313	13	86.7	91268	8	AF004895	AF004895 Lotus jap
c 241	13	86.7	16876	1	AE000002	AE000002 Mycoplasma	c 314	13	86.7	91331	9	AL450386	AL450386 Human DNA
c 242	13	86.7	20285	3	AC024852	AC024852 Caenorhab	c 315	13	86.7	92491	8	ATF17114	ATF17114 Arabidops
c 243	13	86.7	20674	1	AE008854	AE008854 Salmonell	c 316	13	86.7	94984	9	AC114804	AC114804 Homo sapi
c 244	13	86.7	23838	2	AC019968	AC019968 Drosophill	c 317	13	86.7	95922	9	AL358934	AL358934 Human DNA
c 245	13	86.7	24089	2	AC013138	AC013138 Drosophill	c 318	13	86.7	96208	1	AL596174	AL596174 Listeria
c 246	13	86.7	25464	2	AC104234	AC104234 Homo sapi	c 319	13	86.7	96975	9	AC004975	AC004975 Homo sapi
c 247	13	86.7	25638	1	EC028379	EC028379 Escherichia	c 320	13	86.7	97846	9	AC015980	AC015980 Homo sapi
c 248	13	86.7	26536	1	AE001244	AE001244 Treponema	c 321	13	86.7	98597	9	AC008416	AC008416 Homo sapi
c 249	13	86.7	27653	2	AC094247	AC094247 Rattus no	c 322	13	86.7	98645	3	AC005267	AC005267 Drosophill
c 250	13	86.7	29774	1	AF193754	AF193754 Zymomonas	c 323	13	86.7	98770	9	HS36411	HS36411 Human DNA
c 251	13	86.7	31427	3	AF013843	AF013843 Drosophill	c 324	13	86.7	99329	2	AC099247	AC099247 Rattus no
c 252	13	86.7	32727	3	AF047660	AF047660 Caenorhab	c 325	13	86.7	100002	2	AC020372	AC020372 Drosophill
c 253	13	86.7	33001	1	SCC123	SCC123 Streptomy	c 326	13	86.7	101607	8	AF004334	AF004334 Oryza sat
c 254	13	86.7	33148	2	AC094247	AC094247 Streptomy	c 327	13	86.7	103242	9	AC097649	AC097649 Homo sapi
c 255	13	86.7	33810	1	SCB6	SCB6 Streptomy	c 328	13	86.7	103531	2	AC106260	AC106260 Rattus no
c 256	13	86.7	34074	1	SCF81	SCF81 Streptomy	c 329	13	86.7	106553	2	AC094270	AC094270 Rattus no
c 257	13	86.7	35100	6	I96182	I96182 Sequence 19	c 330	13	86.7	107262	2	AC105668	AC105668 Rattus no
c 258	13	86.7	36413	2	AC097272	AC097272 Hylobates	c 331	13	86.7	107372	2	AC098415	AC098415 Rattus no
c 259	13	86.7	36615	2	AC014144	AC014144 Drosophill	c 332	13	86.7	110000	2	AC091528_1	AC091528_1 Continuation (2 of
c 260	13	86.7	39250	1	SV1011500	SV1011500 Streptomy	c 333	13	86.7	110000	2	AC125124_0	AC125124_0 Mus muscu
c 261	13	86.7	40835	2	AC101263	AC101263 Mus muscu	c 334	13	86.7	110000	2	AC125124_3	AC125124_3 Continuation (4 of
c 262	13	86.7	42006	2	AC018022	AC018022 Drosophill	c 335	13	86.7	111701	2	AC130906	AC130906 Rattus no
c 263	13	86.7	42706	2	AC115087	AC115087 Homo sapi	c 336	13	86.7	113794	2	AC129353	AC129353 Rattus no
c 264	13	86.7	42947	8	SPAC343	SPAC343 Human CSF-1	c 337	13	86.7	113916	9	HUAC003007	HUAC003007 Human Chr
c 265	13	86.7	44151	9	AL831769	AL831769 S.pombe c	c 338	13	86.7	114259	2	AC117057	AC117057 Rattus no
c 266	13	86.7	44334	3	AF077534	AF077534 Caenorhab	c 339	13	86.7	114963	2	AC100180	AC100180 Mus muscu
c 267	13	86.7	44334	3	AF077534	AF077534 Caenorhab	c 340	13	86.7	116481	9	AC092287	AC092287 Homo sapi
c 268	13	86.7	44496	10	AL645975	AL645975 Mouse DNA	c 341	13	86.7	116679	9	AC123416	AC123416 Rattus no
c 269	13	86.7	44588	2	AC020529	AC020529 Drosophill	c 342	13	86.7	118068	9	AC1356798	AC1356798 Human DNA
c 270	13	86.7	45848	2	AC013885	AC013885 Drosophill	c 343	13	86.7	118294	2	AC121447	AC121447 Rattus no
c 271	13	86.7	51288	9	AL627210	AL627210 Human DNA	c 344	13	86.7	119087	2	CNS08C86	AL731876 Oryza sat
c 272	13	86.7	51411	2	AC101008	AC101008 Mus muscu	c 345	13	86.7	119141	2	AC096826	AC096826 Rattus no
c 273	13	86.7	52286	2	AC115957	AC115957 Mus muscu	c 346	13	86.7	119593	2	AC015799	AC015799 Homo sapi
c 274	13	86.7	54233	2	AC100456	AC100456 Mus muscu	c 347	13	86.7	119806	9	AL137795	AL137795 Human DNA
c 275	13	86.7	56376	2	AC084338	AC084338 Homo sapi	c 348	13	86.7	120510	9	AL356457	AL356457 Human DNA
c 276	13	86.7	59096	2	AC101634	AC101634 Mus muscu	c 349	13	86.7	120841	9	AC008162	AC008162 Homo sapi
c 277	13	86.7	59389	2	AC095557	AC095557 Rattus no	c 350	13	86.7	120849	2	AC0087148	AC0087148 Mus muscu
c 278	13	86.7	59805	2	AC101151	AC101151 Mus muscu	c 351	13	86.7	121492	8	OSJN00104	AL606653 Oryza sat
c 279	13	86.7	60009	39	AC015507	AC015507 Homo sapi	c 352	13	86.7	121679	2	AC120952	AC120952 Rattus no
c 280	13	86.7	60740	8	AB016557	AB016557 Homo sapi	c 353	13	86.7	122557	9	AC069013	AC069013 Mus muscu
c 281	13	86.7	61290	8	AB017065	AB017065 Arabidops	c 354	13	86.7	123907	9	AC083851	AC083851 Homo sapi
c 282	13	86.7	62355	3	AC084472	AC084472 Caenorhab	c 355	13	86.7	125099	9	AC006251	AC006251 Homo sapi
c 283	13	86.7	63229	2	AC111184	AC111184 Homo sapi	c 356	13	86.7	126128	2	AC111941	AC111941 Rattus no
c 284	13	86.7	63493	2	AC102474	AC102474 Mus muscu	c 357	13	86.7	126220	2	AC103157	AC103157 Rattus no

C 358	13	86.7	127452	2	AC110099	AC110099 Rattus no	C 431	13	86.7	157546	9	AC108360	Homo sapi
C 359	13	86.7	127824	9	AL592205	Human DNA	C 432	13	86.7	157968	2	AC118890	Rattus no
C 360	13	86.7	128137	2	AP003798	Oryza sat	C 433	13	86.7	158043	2	AC105270	Homo sapi
C 361	13	86.7	129413	9	AC020992	Homo sapi	C 434	13	86.7	158382	2	AC016507	Homo sapi
C 362	13	86.7	129923	2	AC126617	Rattus no	C 435	13	86.7	158395	9	AC010614	Homo sapi
C 363	13	86.7	130569	9	CNS08CBB	Human chr	C 436	13	86.7	158897	2	AC116207	Rattus no
C 364	13	86.7	130628	2	AC010992	Drosophill	C 437	13	86.7	158919	2	AC108624	Rattus no
C 365	13	86.7	132419	1	D90907	D90907 synecocyst	C 438	13	86.7	159158	9	AL359915	Human DNA
C 366	13	86.7	133213	2	AC109059	Rattus no	C 439	13	86.7	159688	9	AC087311	Homo sapi
C 367	13	86.7	133276	2	AC087147	Mus muscu	C 440	13	86.7	160083	2	AC129367	Rattus no
C 368	13	86.7	134353	2	AC125305	Rattus no	C 441	13	86.7	160141	8	AP003142	Oryza sat
C 369	13	86.7	134965	9	AL354923	Human DNA	C 442	13	86.7	160147	8	OSJN00232	Oryza sat
C 370	13	86.7	136062	2	AC118514	Rattus no	C 443	13	86.7	160678	2	AC097200	Rattus no
C 371	13	86.7	136767	8	AP005443	Oryza sat	C 444	13	86.7	161150	2	AC126240	Felis cat
C 372	13	86.7	137956	2	AC010918	Drosophill	C 445	13	86.7	161970	2	AC027706	Homo sapi
C 373	13	86.7	138340	2	AP005128	Oryza sat	C 446	13	86.7	162000	2	AC126666	Rattus no
C 374	13	86.7	138953	9	AC022778	Homo sapi	C 447	13	86.7	162609	2	AC097083	Rattus no
C 375	13	86.7	139152	8	AP003525	AF325155 Spodopter	C 448	13	86.7	162923	3	AC008236	Drosophill
C 376	13	86.7	139342	14	AF325155	AF325155 Spodopter	C 449	13	86.7	162996	2	AL391359	Homo sapi
C 377	13	86.7	140619	9	AC007285	AP005558 Oryza sat	C 450	13	86.7	163849	2	AC044808	Mus muscu
C 378	13	86.7	141428	2	AP005558	AC120739 Rattus no	C 451	13	86.7	163888	2	AC024432	Homo sapi
C 379	13	86.7	142127	2	AC120739	AP002899 Oryza sat	C 452	13	86.7	163908	9	AC007050	Homo sapi
C 380	13	86.7	143710	8	AP002899	AC120290 Rattus no	C 453	13	86.7	164018	2	AC097104	Homo sapi
C 381	13	86.7	144097	2	AC120290	AC097178 Rattus no	C 454	13	86.7	164304	2	AC095537	Rattus no
C 382	13	86.7	144348	2	AC097178	AC123948 Mus muscu	C 455	13	86.7	164468	2	AC112594	Rattus no
C 383	13	86.7	144734	2	AC123948	AC096856 Oryza sat	C 456	13	86.7	165080	3	AC018490	Rattus no
C 384	13	86.7	145472	2	AC096856	AC027473 Homo sapi	C 457	13	86.7	165399	2	AL840627	Danio rer
C 385	13	86.7	146017	2	AC027473	AC123262 Rattus no	C 458	13	86.7	166299	2	AC127244	Mus muscu
C 386	13	86.7	146308	2	AC123262	AC128902 Rattus no	C 459	13	86.7	166697	2	AC115290	Mus muscu
C 387	13	86.7	146587	2	AC128902	AC127100 Rattus no	C 460	13	86.7	166922	9	AC008393	Homo sapi
C 388	13	86.7	146853	2	AC127100	AP004675 Oryza sat	C 461	13	86.7	166997	2	AC015290	Mus muscu
C 389	13	86.7	146884	2	AP004675	AC120235 Rattus no	C 462	13	86.7	166997	2	AC015290	Mus muscu
C 390	13	86.7	147327	9	AC097455	AC094684 Rattus no	C 463	13	86.7	166847	9	AC008393	Homo sapi
C 391	13	86.7	147522	2	AC120235	AC126100 Rattus no	C 464	13	86.7	167022	9	AC010238	Homo sapi
C 392	13	86.7	147554	2	AC094684	AC012615 Homo sapi	C 465	13	86.7	167164	2	AC098167	Rattus no
C 393	13	86.7	147688	2	AC126100	AC012615 Homo sapi	C 466	13	86.7	167667	2	AL449084	Homo sapi
C 394	13	86.7	148252	9	AC012615	AC123735 Rattus no	C 467	13	86.7	167735	2	AC009794	Homo sapi
C 395	13	86.7	149599	2	AC123735	AP000556 Homo sapi	C 468	13	86.7	167830	2	AC027768	Homo sapi
C 396	13	86.7	149618	9	AP000556	AL072263 Danio rer	C 469	13	86.7	167926	3	AC023685	Drosophill
C 397	13	86.7	150036	9	AP000557	AC119667 Rattus no	C 470	13	86.7	168008	9	AC008544	Homo sapi
C 398	13	86.7	150259	2	AL772263	AL592285 Human DNA	C 471	13	86.7	168263	9	AC009124	Homo sapi
C 399	13	86.7	151021	2	AC119667	AC016747 Homo sapi	C 472	13	86.7	168316	2	AC101775	Mus muscu
C 400	13	86.7	151465	2	AC117371	AC016506 Homo sapi	C 473	13	86.7	168344	9	AL513307	Human DNA
C 401	13	86.7	152113	9	AL592285	AC128193 Rattus no	C 474	13	86.7	168601	3	AC007471	Drosophill
C 402	13	86.7	152345	9	AC016747	AC016506 Homo sapi	C 475	13	86.7	168820	2	AC131149	Homo sapi
C 403	13	86.7	152533	2	AC016506	AC006020 Homo sapi	C 476	13	86.7	169335	2	AP005566	Oryza sat
C 404	13	86.7	152668	2	AC128193	AC093981 Rattus no	C 477	13	86.7	169464	2	AC098176	Rattus no
C 405	13	86.7	152811	9	AC006020	AC093981 Rattus no	C 478	13	86.7	170094	2	AC120811	Rattus no
C 406	13	86.7	153166	2	AC093981	AC008332 Drosophill	C 479	13	86.7	170163	3	AC009457	Drosophill
C 407	13	86.7	153250	3	AC008332	AC022953 Homo sapi	C 480	13	86.7	170596	2	AC099185	Rattus no
C 408	13	86.7	153315	2	AC022953	AC090484 Genomic s	C 481	13	86.7	170924	2	AC128333	Rattus no
C 409	13	86.7	153322	8	AC090484	AC018933 Homo sapi	C 482	13	86.7	171004	2	AC034202	Homo sapi
C 410	13	86.7	153348	2	AC018933	AC098544 Rattus no	C 483	13	86.7	172400	9	AC090883	Homo sapi
C 411	13	86.7	153568	2	AC098544	AC108343 Rattus no	C 484	13	86.7	172462	2	AL833789	Danio rer
C 412	13	86.7	153798	2	AC108343	AC097886 Rattus no	C 485	13	86.7	172854	3	AC023706	Drosophill
C 413	13	86.7	153904	2	AC097886	AC006197 Homo sapi	C 486	13	86.7	172902	2	AL358816	Homo sapi
C 414	13	86.7	154354	9	AC006197	AC073620 Homo sapi	C 487	13	86.7	173249	2	AC123468	Rattus no
C 415	13	86.7	154608	2	AC073620	AC079472 Mus muscu	C 488	13	86.7	173302	2	AC008137	Drosophill
C 416	13	86.7	154673	3	AC079472	AC099018 Drosophill	C 489	13	86.7	173441	2	AC080112	Homo sapi
C 417	13	86.7	154840	3	AC099018	AP004222 Oryza sat	C 490	13	86.7	173713	2	AC095840	Rattus no
C 418	13	86.7	155263	8	AP004222	AL354997 Human DNA	C 491	13	86.7	173765	9	AC090457	Homo sapi
C 419	13	86.7	156077	2	AL354997	AC109563 Rattus no	C 492	13	86.7	173836	9	AC027125	Homo sapi
C 420	13	86.7	156088	2	AC109563	AC006472 Drosophill	C 493	13	86.7	173836	9	AC118421	Rattus no
C 421	13	86.7	156346	3	AC006472	AL357774 Human DNA	C 494	13	86.7	173909	2	AC128406	Rattus no
C 422	13	86.7	156498	9	AL357774	AC013363 Homo sapi	C 495	13	86.7	174151	2	AC120483	Rattus no
C 423	13	86.7	156619	2	AC013363	AL049594 Human DNA	C 496	13	86.7	174157	3	AC023711	Drosophill
C 424	13	86.7	156791	9	HSJ2B60B4	AC127950 Rattus no	C 497	13	86.7	174265	2	AL772355	Rattus no
C 425	13	86.7	156874	2	AC127950	AC020006 Drosophill	C 498	13	86.7	174406	3	AC104516	Homo sapi
C 426	13	86.7	156908	2	OSJN00030	AL606591 Oryza sat	C 499	13	86.7	174569	9	AC022533	Homo sapi
C 427	13	86.7	156935	2	AC020006	AC011095 Homo sapi	C 500	13	86.7	174661	2	AC098609	Rattus no
C 428	13	86.7	157051	9	AC011095	AL358856 Homo sapi	C 501	13	86.7	174688	2	AC124395	Mus muscu
C 429	13	86.7	157080	2	AL358856	AC036212 Homo sapi	C 502	13	86.7	174719	2	AL840636	Danio rer
C 430	13	86.7	157393	2	AC036212		C 503	13	86.7	175507	2	AL807799	Danio rer

504	13	86.7	175511	2	AC023924	AC023924 Homo sapi	c	577	13	86.7	193690	2	AC121603	AC121603 Mus muscu
c 505	13	86.7	175669	3	AC008235	AC008235 Drosophi	c	578	13	86.7	193924	2	AC098275	AC098275 Rattus no
c 506	13	86.7	175945	2	AC022147	AC022147 Homo sapi	c	579	13	86.7	194056	9	AL590708	AL590708 Human DNA
c 507	13	86.7	176051	9	AC023490	AC023490 Homo sapi	c	580	13	86.7	194056	9	AL590708	AL590708 Human DNA
c 508	13	86.7	176099	2	AC167779	AC167779 Mus muscu	c	581	13	86.7	194718	9	AL590708	AL590708 Human DNA
c 509	13	86.7	176310	2	AC109004	AC109004 Rattus no	c	582	13	86.7	194718	9	AL590708	AL590708 Human DNA
c 510	13	86.7	176547	2	AC126433	AC126433 Mus muscu	c	583	13	86.7	195783	2	AC109104	AC109104 Rattus no
c 511	13	86.7	176933	3	AC009350	AC009350 Drosophi	c	584	13	86.7	196560	2	AC023640	AC023640 Homo sapi
c 512	13	86.7	176954	2	AC126680	AC126680 Mus muscu	c	585	13	86.7	196724	10	AL590963	AL590963 Mouse DNA
c 513	13	86.7	177028	3	AC008315	AC008315 Drosophi	c	586	13	86.7	197389	9	AL358791	AL358791 Human DNA
c 514	13	86.7	177407	9	AC073916	AC073916 Homo sapi	c	587	13	86.7	197561	2	AC093407	AC093407 Mus muscu
c 515	13	86.7	177514	2	AC126919	AC126919 Bos tauru	c	588	13	86.7	197841	2	AC105322	AC105322 Mus muscu
c 516	13	86.7	177739	2	AC127423	AC127423 Mus muscu	c	589	13	86.7	198412	2	AC098236	AC098236 Rattus no
c 517	13	86.7	178254	9	AL731541	AL731541 Human DNA	c	590	13	86.7	198413	2	AC130022	AC130022 Rattus no
c 518	13	86.7	178254	9	AL731541	AL731541 Human DNA	c	591	13	86.7	198489	2	AC067809	AC067809 Homo sapi
c 519	13	86.7	178676	2	AC087868	AC087868 Mus muscu	c	592	13	86.7	199016	3	AC008204	AC008204 Drosophi
c 520	13	86.7	178892	2	AC130794	AC130794 Fells cat	c	593	13	86.7	199050	1	AJ414159	AJ414159 Yersinia
c 521	13	86.7	180154	2	AC123464	AC123464 Rattus no	c	594	13	86.7	199268	2	AC099523	AC099523 Homo sapi
c 522	13	86.7	180179	2	AC018881	AC018881 Homo sapi	c	595	13	86.7	199420	9	CNS01DVV	AL136040 Human chr
c 523	13	86.7	180355	2	AC022167	AC022167 Homo sapi	c	596	13	86.7	199777	2	AC098064	AC098064 Rattus no
c 524	13	86.7	180425	3	AC008229	AC008229 Drosophi	c	597	13	86.7	199794	2	AC026633	AC026633 Homo sapi
c 525	13	86.7	180485	2	AC027145	AC027145 Homo sapi	c	598	13	86.7	200123	2	AC126764	AC126764 Homo sapi
c 526	13	86.7	180766	9	AC090691	AC090691 Homo sapi	c	599	13	86.7	200289	2	AC090681	AC090681 Homo sapi
c 527	13	86.7	180790	9	AC012173	AC012173 Homo sapi	c	600	13	86.7	200594	9	AC005632	AC005632 Homo sapi
c 528	13	86.7	181026	2	AC119640	AC119640 Rattus no	c	601	13	86.7	200883	2	AL590107	AL590107 Homo sapi
c 529	13	86.7	181261	2	AC010189	AC010189 Mus muscu	c	602	13	86.7	201105	2	AC118088	AC118088 Rattus no
c 530	13	86.7	181320	2	AC095303	AC095303 Rattus no	c	603	13	86.7	201105	9	AC025668	AC025668 Mus muscu
c 531	13	86.7	181827	2	AC055854	AC055854 Homo sapi	c	604	13	86.7	201155	9	AC020703	AC020703 Homo sapi
c 532	13	86.7	182280	9	AL136981	AL136981 Human DNA	c	605	13	86.7	201155	9	AC009086	AC009086 Homo sapi
c 533	13	86.7	182289	2	AC115341	AC115341 Rattus no	c	606	13	86.7	203216	2	AC097328	AC097328 Pan trogl
c 534	13	86.7	182427	2	AC061992	AC061992 Homo sapi	c	607	13	86.7	204379	2	AC131113	AC131113 Mus muscu
c 535	13	86.7	182601	3	AC009904	AC009904 Drosophi	c	608	13	86.7	204442	3	AE003747	AE003747 Drosophi
c 536	13	86.7	183089	10	AL663115	AL663115 Mouse DNA	c	609	13	86.7	206030	9	AC021439	AC021439 Homo sapi
c 537	13	86.7	183342	9	AC087490	AC087490 Homo sapi	c	610	13	86.7	207380	2	AC124566	AC124566 Mus muscu
c 538	13	86.7	183402	2	AC126231	AC126231 Bos tauru	c	611	13	86.7	207424	10	AC090489	AC090489 Genomic s
c 539	13	86.7	183591	9	AC008462	AC008462 Homo sapi	c	612	13	86.7	207739	2	AC113528	AC113528 Mus muscu
c 540	13	86.7	183656	9	AC009487	AC009487 Homo sapi	c	613	13	86.7	208064	9	AL392043	AL392043 Human DNA
c 541	13	86.7	183675	2	AL845320	AL845320 Danio rer	c	614	13	86.7	209320	2	AC096076	AC096076 Homo sapi
c 542	13	86.7	183714	2	AC103508	AC103508 Rattus no	c	615	13	86.7	209502	2	AC093930	AC093930 Rattus no
c 543	13	86.7	184026	2	AC098923	AC098923 Rattus no	c	616	13	86.7	209706	2	AC067885	AC067885 Homo sapi
c 544	13	86.7	184140	9	AC090630	AC090630 Homo sapi	c	617	13	86.7	210472	9	AC035139	AC035139 Homo sapi
c 545	13	86.7	184346	2	AC069138	AC069138 Homo sapi	c	618	13	86.7	210514	10	AC117199	AC117199 Mus muscu
c 546	13	86.7	185329	2	AC023587	AC023587 Homo sapi	c	619	13	86.7	210727	2	AC122864	AC122864 Mus muscu
c 547	13	86.7	185415	9	HS121M24	AL354046 Homo sapi	c	620	13	86.7	212208	2	AC079024	AC079024 Mus muscu
c 548	13	86.7	185509	2	AC098143	AC098143 Rattus no	c	621	13	86.7	213288	2	AL773558	AL773558 Danio rer
c 549	13	86.7	185600	8	AP003563	AP003563 Oryza sat	c	622	13	86.7	213732	1	AE001862	AE001862 Deinococc
c 550	13	86.7	185617	2	AC126920	AC126920 Bos tauru	c	623	13	86.7	214465	9	AC023027	AC023027 Mus muscu
c 551	13	86.7	186241	3	AC007086	AC007086 Drosophi	c	624	13	86.7	214702	9	AC020689	AC020689 Homo sapi
c 552	13	86.7	186341	2	AC126841	AC126841 Rattus no	c	625	13	86.7	215050	1	AL646057	AL646057 Ralstonia
c 553	13	86.7	186542	2	AL844197	AL844197 Danio rer	c	626	13	86.7	215366	10	AL603836	AL603836 Mouse DNA
c 554	13	86.7	186980	2	AC130961	AC130961 Rattus no	c	627	13	86.7	215788	9	AC007308	AC007308 Homo sapi
c 555	13	86.7	187215	2	AC093667	AC093667 Homo sapi	c	628	13	86.7	216105	10	AC091777	AC091777 Mus muscu
c 556	13	86.7	187336	9	AL158822	AL158822 Human DNA	c	629	13	86.7	217422	9	AC108721	AC108721 Homo sapi
c 557	13	86.7	187347	2	AC025880	AC025880 Homo sapi	c	630	13	86.7	217629	3	AE003743	AE003743 Drosophi
c 558	13	86.7	188563	9	AL136965	AL136965 Homo sapi	c	631	13	86.7	217859	2	AC112891	AC112891 Rattus no
c 559	13	86.7	188696	2	AL512629	AL512629 Human DNA	c	632	13	86.7	218952	2	AL606984	AL606984 Mus muscu
c 560	13	86.7	188926	9	AC012182	AC012182 Homo sapi	c	633	13	86.7	219125	2	AL772165	AL772165 Mus muscu
c 561	13	86.7	189050	1	AL646069	AL646069 Ralstonia	c	634	13	86.7	219200	10	AL589701	AL589701 Mouse DNA
c 562	13	86.7	189333	1	RME603647	AL603647 Rhizobium	c	635	13	86.7	219218	2	AC020817	AC020817 Mus muscu
c 563	13	86.7	189534	2	AL354656	AL354656 Homo sapi	c	636	13	86.7	219809	2	AC125058	AC125058 Mus muscu
c 564	13	86.7	189805	2	AC109479	AC109479 Homo sapi	c	637	13	86.7	220940	10	AL671913	AL671913 Mouse DNA
c 565	13	86.7	190301	3	AC009352	AC009352 Drosophi	c	638	13	86.7	221049	2	AL691421	AL691421 Mus muscu
c 566	13	86.7	190757	10	AC087840	AC087840 Mus muscu	c	639	13	86.7	221792	2	AC124711	AC124711 Mus muscu
c 567	13	86.7	190856	2	AC009160	AC009160 Homo sapi	c	640	13	86.7	222235	2	AC074148	AC074148 Mus muscu
c 568	13	86.7	190944	2	AC122960	AC122960 Rattus no	c	641	13	86.7	222574	2	AL772227	AL772227 Mus muscu
c 569	13	86.7	191023	2	AC128255	AC128255 Rattus no	c	642	13	86.7	224067	2	AC092259	AC092259 Mus muscu
c 570	13	86.7	191108	9	AC097265	AC097265 Pan trogl	c	643	13	86.7	225448	2	AC122296	AC122296 Mus muscu
c 571	13	86.7	191358	9	AC012533	AC012533 Homo sapi	c	644	13	86.7	225514	2	AC024142	AC024142 Mus muscu
c 572	13	86.7	191549	9	AC010582	AC010582 Homo sapi	c	645	13	86.7	226903	2	AC079272	AC079272 Mus muscu
c 573	13	86.7	191590	3	AC023722	AC023722 Drosophi	c	646	13	86.7	229655	3	AE003707	AE003707 Drosophi
c 574	13	86.7	191630	2	AC114875	AC114875 Rattus no	c	647	13	86.7	236043	2	AC115234	AC115234 Rattus no
c 575	13	86.7	191672	2	AC020794	AC020794 Mus muscu	c	648	13	86.7	239679	2	AC118545	AC118545 Mus muscu
c 576	13	86.7	192802	9	AC011753	AC011753 Homo sapi	c	649	13	86.7	241753	2	AC019149	AC019149 Homo sapi

650	13	86.7	243076	3	AE003683	AE003683 Drosophill	c 723	12	80.0	414	5	AF401585	AF401585 Ictalarus
c 651	13	86.7	250688	2	AC098059	AC098059 Rattus no	c 724	12	80.0	414	6	AX329865	AX329865 Sequence
c 652	13	86.7	253648	3	AE003638	AE003638 Drosophill	c 725	12	80.0	414	6	AX331438	AX331438 Sequence
c 653	13	86.7	254438	3	AE003814	AE003814 Drosophill	c 726	12	80.0	438	8	ZMFBFERUM	X73300 Z.mays sequ
654	13	86.7	256972	2	AC116577	AC116577 Mus muscu	727	12	80.0	447	6	ARI53967	ARI53967 Sequence
655	13	86.7	260699	2	AC006893	AC006893 Caenorhab	728	12	80.0	455	9	HSSPGSC02	AF080512 Homo sapi
c 656	13	86.7	266574	2	AC087129	AC087129 Mus muscu	c 729	12	80.0	461	6	AX331371	AX331371 Sequence
c 657	13	86.7	267759	2	AC079418	AC079418 Mus muscu	c 730	12	80.0	462	9	HSEMX1	X68879 H.sapiens E
658	13	86.7	268200	1	AP000061	AP000061 Aeropyrum	c 731	12	80.0	480	9	AB041354S2	AB041355 Homo sapi
c 659	13	86.7	271743	3	AE003835	AE003835 Drosophill	c 732	12	80.0	490	11	G72657	G72657 MARC 5847-5
c 660	13	86.7	281530	1	AP002550	AP002550 Escherich	c 733	12	80.0	495	1	AY072237	AY072237 Unculture
c 661	13	86.7	294250	1	AP001517	AP001517 Bacillus	c 734	12	80.0	495	1	AY072238	AY072238 Unculture
c 662	13	86.7	296992	3	AE003833	AE003833 Drosophill	c 735	12	80.0	495	9	AF392405	AF392405 Homo sapi
c 663	13	86.7	298705	3	AE003510	AE003510 Drosophill	c 736	12	80.0	497	9	AY052945	AY052945 Homo sapi
c 664	13	86.7	298750	1	AP005375	AP005375 Thermosyn	c 737	12	80.0	504	9	HSLCC1F01	226256 H.sapiens i
c 665	13	86.7	299350	1	SME591786	AL591786 Sinorhizo	c 738	12	80.0	519	1	AY072232	AY072232 Unculture
c 666	13	86.7	303823	3	AE003462	AE003462 Drosophill	c 739	12	80.0	536	9	AF208488	AF208488 Homo sapi
c 667	13	86.7	307120	1	CNSPAX03	AJ248285 Pyrococcu	c 740	12	80.0	540	8	CNS01DPI	AL117101 Botrytis
668	13	86.7	307962	1	AP002564	AP002564 Escherich	741	12	80.0	543	1	AF246422	AF246422 Acidithio
669	13	86.7	311208	6	AX417049	AX417049 Sequence	742	12	80.0	550	6	AX154863	AX154863 Sequence
c 670	13	86.7	319012	3	AE003596	AE003596 Drosophill	c 743	12	80.0	552	1	AV123697	AV123697 Granulica
c 671	13	86.7	323461	3	AE003491	AE003491 Drosophill	c 744	12	80.0	552	8	AB075378	AB075378 Oryza sat
c 672	13	86.7	327927	3	AE003439	AE003439 Drosophill	c 745	12	80.0	576	6	ARI74766	ARI74766 Sequence
c 673	13	86.7	337133	2	AC110384	AC110384 Rattus no	746	12	80.0	588	6	AX381056	AX381056 Sequence
c 674	13	86.7	340857	1	AP003010	AP003010 Mesorhizo	747	12	80.0	605	8	AF284970	AF284970 Carex bas
c 675	13	86.7	341880	1	AP003589	AP003589 Nostoc sp	748	12	80.0	607	8	AF284972	AF284972 Carex ros
c 676	13	86.7	347800	1	AP000060	AP000060 Aeropyrum	749	12	80.0	608	8	AF27427	AF27427 Carex sup
c 677	13	86.7	349980	6	AX041919	AX041919 Sequence	750	12	80.0	608	8	AF285057	AF285057 Cymophyll
c 678	13	86.7	349980	6	AX417036	AX417036 Sequence	751	12	80.0	608	9	DB6059	DB6059 Homo sapien
c 679	12	80.0	19	6	AX129897	AX129897 Sequence	752	12	80.0	609	8	AF027425	AF027425 Carex wil
680	12	80.0	19	6	AX129898	AX129898 Sequence	753	12	80.0	610	8	AF284977	AF284977 Carex pen
681	12	80.0	19	6	AX129899	AX129899 Sequence	754	12	80.0	634	9	HS326873	HS326873 Homo sapi
c 682	12	80.0	49	6	AX194378	AX194378 Sequence	c 755	12	80.0	636	8	CNS01DGO	AL116776 Botrytis
c 683	12	80.0	76	10	MMCA21V6	X02899 Mouse gene	c 756	12	80.0	644	9	HUMCOL22	U76585 Human 180 k
c 684	12	80.0	108	4	AB073620	AB073620 Oryctolog	c 757	12	80.0	647	4	OCU291432	AJ291432 Oryctolog
c 685	12	80.0	173	6	AX438778	AX438778 Sequence	c 758	12	80.0	651	9	HS342792	AJ342792 Unculture
c 686	12	80.0	198	8	AB019982	AB019982 Nclana sp	c 759	12	80.0	660	1	AF315434	AF315434 Unculture
687	12	80.0	198	10	MMEMX1	X68881 M.musculus	c 760	12	80.0	660	1	AF315444	AF315444 Unculture
c 688	12	80.0	221	8	AF027412	AF027412 Carex sax	c 761	12	80.0	660	1	AF315447	AF315447 Unculture
c 689	12	80.0	221	8	AF027413	AF027413 Carex sax	c 762	12	80.0	660	1	AF315448	AF315448 Unculture
c 690	12	80.0	221	8	AF027414	AF027414 Carex sax	c 763	12	80.0	660	1	AF315453	AF315453 Unculture
c 691	12	80.0	221	8	AF027417	AF027417 Carex jun	c 764	12	80.0	660	1	AF315456	AF315456 Unculture
c 692	12	80.0	221	8	AF027418	AF027418 Carex jun	c 765	12	80.0	660	1	AF315457	AF315457 Unculture
c 693	12	80.0	221	8	AF027419	AF027419 Carex jun	c 766	12	80.0	660	1	AF361791	AF361791 Azospiril
c 694	12	80.0	221	8	AF027420	AF027420 Carex jam	c 767	12	80.0	660	1	AF361795	AF361795 Alcaligen
c 695	12	80.0	221	8	AF027421	AF027421 Carex jam	c 768	12	80.0	660	1	AY074762	AY074762 Azospiril
c 696	12	80.0	221	8	AF027423	AF027423 Carex jam	c 769	12	80.0	661	6	AX381052	AX381052 Sequence
c 697	12	80.0	221	8	AF027430	AF027430 Carex bas	c 770	12	80.0	666	1	AF315441	AF315441 Unculture
c 698	12	80.0	222	8	AF027409	AF027409 Carex bac	c 771	12	80.0	667	6	AX401398	AX401398 Sequence
c 699	12	80.0	222	8	AF027411	AF027411 Carex bac	c 772	12	80.0	677	9	HSPFC2	AF048784 Actinomyc
c 700	12	80.0	222	8	AF027415	AF027415 Carex lat	c 773	12	80.0	681	1	AF048784	AF048784 Actinomyc
c 701	12	80.0	222	8	AF027416	AF027416 Carex lat	774	12	80.0	682	8	D64038	D64038 Oryza sativ
c 702	12	80.0	222	8	AF027424	AF027424 Carex wil	775	12	80.0	684	5	AF168081	AF168081 Guira gui
c 703	12	80.0	222	8	AF027426	AF027426 Carex wil	c 776	12	80.0	684	5	AY072227	AY072227 Achromoba
c 704	12	80.0	222	8	AF027431	AF027431 Carex bas	c 777	12	80.0	696	3	AF153423	AF153423 Drosophill
c 705	12	80.0	223	8	AF027410	AF027410 Carex bac	c 778	12	80.0	696	3	AF153424	AF153424 Drosophill
c 706	12	80.0	223	8	AF027428	AF027428 Carex sup	c 779	12	80.0	696	3	AF153425	AF153425 Drosophill
c 707	12	80.0	223	8	AF027429	AF027429 Carex sup	c 780	12	80.0	696	3	AF153426	AF153426 Drosophill
c 708	12	80.0	223	8	AF027432	AF027432 Carex bas	c 781	12	80.0	696	3	AF153427	AF153427 Drosophill
c 709	12	80.0	239	11	G45463	GA5463 Z33659_1 ze	c 782	12	80.0	696	3	AF153428	AF153428 Drosophill
c 710	12	80.0	281	9	HS164H12F	Z57122 H.sapiens C	c 783	12	80.0	696	3	AF153429	AF153429 Drosophill
c 711	12	80.0	318	1	AF246423	AF246423 Acidithio	c 784	12	80.0	696	8	CNS01AXV	AL113531 Botrytis
c 712	12	80.0	336	8	AY023844	AY023844 Oryza sat	c 785	12	80.0	696	9	HSTRUPFC6	AF158732 Homo sapi
c 713	12	80.0	348	11	G36234	G36234 STS h14a225	786	12	80.0	700	2	AX046342	AX046342 Sequence
c 714	12	80.0	350	6	AX629602	AX069602 Sequence	787	12	80.0	711	6	AX046342	AX046342 Sequence
c 715	12	80.0	358	6	A24556	A24556 S.gghanaensi	788	12	80.0	721	11	PM6F7G	AL684955 Penicilli
c 716	12	80.0	358	6	A24557	A24557 S.gghanaensi	789	12	80.0	728	10	MUSMK2P	M35833 Mouse retin
c 717	12	80.0	360	9	HS234973	AJ234973 Homo sapi	790	12	80.0	730	10	MUSMK2	BC012244 Mus muscu
c 718	12	80.0	366	1	AY072240	AY072240 Unculture	791	12	80.0	753	10	BC012244	BC012244 Mus muscu
c 719	12	80.0	391	8	AF439938	AF439938 Talaromyc	c 792	12	80.0	754	9	HS327691	HS327691 Homo sapi
c 720	12	80.0	402	11	HUM077564A	L30503 Human STS u	793	12	80.0	766	2	AX123427	AX123427 Sequence
c 721	12	80.0	407	5	CHKP561CK	M85043 Chicken tyr	c 794	12	80.0	774	6	AX123427	AX123427 Sequence
c 722	12	80.0					c 795	12	80.0	790	9	HS326425	HS326425 Homo sapi

c 796	12	80.0	800	8	AY078938	AY078938 Arabidops	869	12	80.0	1437	9	AK058126	AK058126 Homo sapi
c 797	12	80.0	801	3	DMU11824	U11824 Drosophila	c 870	12	80.0	1442	3	AY060686	AY060686 Drosophill
c 798	12	80.0	806	10	AB049954	AB049954 Mus muscu	c 871	12	80.0	1443	3	AY119570	AY119570 Drosophill
c 799	12	80.0	808	8	AF302807	AF302807 Sesamum i	c 872	12	80.0	1443	8	FSOKCH	L29381 Fusarium ox
c 800	12	80.0	815	8	AY074640	AY074640 Arabidops	c 873	12	80.0	1450	9	HSRARA1A1	AF088888 Homo sapi
c 801	12	80.0	819	10	AF033270	AF033270 Mus saxic	c 874	12	80.0	1471	10	MMU421520	AJ421520 Mus muscu
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c 806	12	80.0	837	6	AX123429	AX123429 Sequence	c 879	12	80.0	1473	6	A23955	A23955 Endoglucana
c 807	12	80.0	843	8	AY098941	AY098941 Solanum t	c 880	12	80.0	1473	6	A41660	A41660 Sequence 3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE 1 (bases 1 to 920)						
AUTHORS Chu,T., Blumenfeld,M. and Cohen,D.						
TITLE Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders						
JOURNAL Patent: WO 0151659-A 99 19-JUL-2001;						
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE 1 (bases 1 to 920)						
AUTHORS Chu,T., Blumenfeld,M. and Cohen,D.						
TITLE Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders						
JOURNAL Patent: WO 0151659-A 104 19-JUL-2001;						
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KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES

HSNETEX9
Homo sapiens partial SLC6A2 gene for norepinephrine transporter, exons 9-10.
X91127
X91127.1 GI:1143488
norepinephrine transporter; SLC6A2 gene.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
Porzgen, P., Bonisch, H. and Bruss, M.
Molecular cloning and organization of the coding region of the human norepinephrine transporter gene
Biochem. Biophys. Res. Commun. 215 (3), 1145-1150 (1995)
96078050
7488042
2 (bases 1 to 980)
Porzgen, P., Bonisch, H., Hammermann, R. and Bruss, M.
The human noradrenaline transporter gene contains multiple polyadenylation sites and two alternatively spliced C-terminal exons
Biochim. Biophys. Acta 1398 (3), 365-370 (1998)
98322125
9655936
3 (bases 1 to 980)
Bonisch, H.
Direct Submission
Submitted (30-AUG-1995) H. Bonisch, Institut fuer Pharmacologie und Toxikologie, Universitaet Bonn, Reuterstr 2b, 53113 Bonn, FRG
Related sequences: M65105 and X57700.
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
BC000563
LOCUS
DEFINITION
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REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

BC000563
Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.
BC000563
BC000563.1 GI:12653576
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1411)
Strausberg, R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland.
Web site: http://www.nisc.nih.gov/nisc_mgc/nigr1.nih.gov
Contact: nisc_mgc@nigr1.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Zhang, L., E.H., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 5 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES
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BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 496 CCTTCTCGCCCTGTT 510

RESULT 5
LOCUS HUMNORTR 1983 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human noradrenaline transporter mRNA, complete cds.
ACCESSION M65105
VERSION M65105.1 GI:189257
KEYWORDS noradrenaline transporter.
SOURCE Human, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1983)
AUTHORS Pacholczyk,T., Blakely,R.D. and Amara,S.G.
TITLE Expression cloning of a cocaine- and antidepressant-sensitive human
noradrenaline transporter
JOURNAL Nature 350 (6316), 350-354 (1991)
MEDLINE 91179515
PUBMED 2008212
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    EATSLSGSTFWAVFFVMLLALGLDSMGMEAVITGLADDFQVLRKRLKLTFTGVT
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BASE COUNT 383 a 602 c 530 g 468 t
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 46;
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QY 1 CCTTCTCGCCCTGTT 15
Db 1422 CCTTCTCGCCCTGTT 1436

RESULT 6
LOCUS HUMCOLALXV/c 2127 bp mRNA linear PRI 27-APR-1993
DEFINITION Homo sapiens alpha-1 type XV collagen mRNA sequence.
ACCESSION L01697
VERSION L01697.1 GI:180858
KEYWORDS alpha-1 type XV collagen.
SOURCE Homo sapiens (library: gtl1 from Cloneteck Laboratories) placenta
cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2127)
AUTHORS Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
Pihlajaniemi,T.
TITLE Identification of a previously unknown human collagen chain, alpha
1(XV), characterized by extensive interruptions in the
triple-helical region
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)
MEDLINE 93066196
PUBMED 1279671
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FGRGDPGPPGPPGPPGPAIIGAVALPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP
KAHLVTEGFIYLRDSTEFFIRVRDGMKQLQGLGELIPADSPPPVLTSSNPQLLPP
PNPISANYEKPALHIAALNMPFSGDIRADQCFKQARAAGLLSTYRAFLSSHLQDLS
TVIKRAERYSLPTNLKGOVLNFDNWDISIFSGHGQFMNHIPIYSEFGRDITMDPSWQ
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mat_peptide

3'UTR

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polyA_signal

polyA_signal

polyA_signal

polyA_site

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Query Match      100.0%; Score 15; DB 9; Length 5161;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 2673 CCTTCTCGCCCTGTT 2659
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RESULT 8
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LOCUS      Drosophila melanogaster, 14621 bp DNA linear HTG 03-JAN-2000
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
ACCESSION AC020425
VERSION AC020425.1 GI:6664472
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 14621)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10213135 by the submitter.
For more information on this record e-mail to flycelera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 4882 CCTTCTCGCCCTGTT 4896
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RESULT 9
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LOCUS      Mus musculus clone RP23-117121, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC101376
ACCESSION AC101376
VERSION AC101376.1 GI:17060151
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 61956)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-117121
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 61956)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Hearford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneu, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L16579

Center clone name: 117_I_21

* NOTE: This record contains 79 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1 630: contig of 630 bp in length

* 631 730: gap of 100 bp

* 731 1391: contig of 661 bp in length

* 1392 1491: gap of 100 bp

* 1492 2138: contig of 647 bp in length

* 2139 2238: gap of 100 bp

* 2239 3005: contig of 767 bp in length

* 3006 3105: gap of 100 bp

* 3106 3860: contig of 755 bp in length

* 3861 3960: gap of 100 bp

* 3961 4639: contig of 679 bp in length

* 4640 4739: gap of 100 bp

* 4740 5414: contig of 675 bp in length

* 5415 5514: gap of 100 bp

* 5515 6290: contig of 776 bp in length

* 6291 6390: gap of 100 bp

* 6391 7071: contig of 681 bp in length

* 7072 7171: gap of 100 bp

* 7172 7853: contig of 682 bp in length

* 7854 7953: gap of 100 bp

* 7954 8627: contig of 674 bp in length

* 8628 8727: gap of 100 bp

* 8728 9409: contig of 682 bp in length

* 9410 9509: gap of 100 bp

* 9510 10180: contig of 671 bp in length

* 10181 10280: gap of 100 bp

* 10281 10969: contig of 689 bp in length

* 10970 11069: gap of 100 bp

* 11070 11740: contig of 671 bp in length

* 11741 11840: gap of 100 bp

* 11841 12509: contig of 669 bp in length

* 12510 12609: gap of 100 bp

* 12610 13254: contig of 645 bp in length

* 13255 13354: gap of 100 bp

* 13355 14028: contig of 674 bp in length

* 14029 14128: gap of 100 bp

* 14129 14795: contig of 667 bp in length

* 14796 14895: gap of 100 bp

* 14896 15570: contig of 675 bp in length

* 15571 15670: gap of 100 bp

* 15671 16330: contig of 660 bp in length

* 16331 16430: gap of 100 bp

* 16431 17099: contig of 669 bp in length

* 17100 17199: gap of 100 bp

* 17200 17903: contig of 704 bp in length

* 17904 18003: gap of 100 bp

* 18004 18693: contig of 689 bp in length

* 18693 18792: gap of 100 bp

* 18793 19467: contig of 675 bp in length

* 19468 19567: gap of 100 bp

* 19568 20238: contig of 671 bp in length

* 20239 20338: gap of 100 bp

* 20339 21007: contig of 669 bp in length

* 21008 21107: gap of 100 bp

* 21109 21852: contig of 745 bp in length

* 21853 21952: gap of 100 bp

* 21953 22635: contig of 683 bp in length

* 22636 22735: gap of 100 bp

* 22736 23384: contig of 649 bp in length

* 23385 23484: gap of 100 bp

* 23485 24154: contig of 670 bp in length

* 24155 24254: gap of 100 bp

* 24255 24914: contig of 660 bp in length

* 24915 25014: gap of 100 bp

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* 27329 27428: gap of 100 bp

* 27429 28117: contig of 689 bp in length

* 28118 28217: gap of 100 bp

* 28218 28864: contig of 647 bp in length

* 28865 28964: gap of 100 bp

* 28965 29633: contig of 669 bp in length

* 29634 29734: gap of 100 bp

* 29734 30482: contig of 749 bp in length

* 30483 30582: gap of 100 bp

* 30583 31343: contig of 761 bp in length

* 31344 31443: gap of 100 bp

* 31444 32204: contig of 761 bp in length

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* 40344 41003: contig of 660 bp in length

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* 44197 44852: contig of 656 bp in length
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* 45628 45727: gap of 100 bp
* 45728 46410: contig of 683 bp in length
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* 46511 47187: contig of 677 bp in length
* 47188 47287: gap of 100 bp
* 47288 48012: contig of 725 bp in length
* 48013 48112: gap of 100 bp
* 48113 48784: contig of 672 bp in length
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* 48885 49549: contig of 665 bp in length
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* 49650 50338: contig of 689 bp in length
* 50339 50438: gap of 100 bp
* 50439 51107: contig of 669 bp in length
* 51108 51207: gap of 100 bp
* 51208 51871: contig of 664 bp in length
* 51872 51971: gap of 100 bp
* 51972 52651: contig of 680 bp in length
* 52652 52751: gap of 100 bp
* 52752 53427: contig of 676 bp in length
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* 53528 54200: contig of 673 bp in length
* 54201 54300: gap of 100 bp

Query Match 100.0%; Score 15; DB 2; Length 61956;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 57817 CCTTCGCCCTGTT 57831

RESULT 10
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LOCUS
DEFINITION Homo sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS
AC124280 65851 bp DNA linear HTG 30-JUL-2002
SEQUENCE SAMPLING.
AC124280
VERSION AC124280.3 GI:22004380
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 65851)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP13-519019
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 65851)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campolano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,

Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
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Theodore,J., Topham,K., Travers,M., Travis,N., Trioglio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 65851)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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Gardyna,S., Gordon,S., Graham,L., Grand-Pierre,N., Hagos,B.,
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Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 30, 2002 this sequence version replaced gi:21699374.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27356
Center clone name: 519_O_19

* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 707: contig of 707 bp in length
* 708 807: gap of 100 bp
* 808 1542: contig of 735 bp in length
* 1543 1642: gap of 100 bp
* 1643 2336: contig of 694 bp in length
* 2337 2436: gap of 100 bp
* 2437 3166: contig of 730 bp in length
* 3167 3266: gap of 100 bp
* 3267 3987: contig of 721 bp in length
* 3988 4087: gap of 100 bp
* 4088 4813: contig of 726 bp in length
* 4814 4913: gap of 100 bp
* 4914 5651: contig of 738 bp in length
* *

TITLE
JOURNAL

COMMENT

TITLE
JOURNAL
REFERENCE
AUTHORS

* 5652 5751: gap of 100 bp
* 5752 6473: contig of 722 bp in length
* 6474 6573: gap of 100 bp
* 6574 7300: contig of 727 bp in length
* 7301 7400: gap of 100 bp
* 7401 8134: contig of 734 bp in length
* 8135 8234: gap of 100 bp
* 8235 8966: contig of 732 bp in length
* 8967 9066: gap of 100 bp
* 9067 9714: contig of 648 bp in length
* 9715 9814: gap of 100 bp
* 9815 10534: contig of 720 bp in length
* 10535 10634: gap of 100 bp
* 10635 11348: contig of 714 bp in length
* 11349 11448: gap of 100 bp
* 11449 12160: contig of 712 bp in length
* 12161 12260: gap of 100 bp
* 12261 12986: contig of 726 bp in length
* 12987 13086: gap of 100 bp
* 13087 13816: contig of 730 bp in length
* 13817 13916: gap of 100 bp
* 13917 14633: contig of 717 bp in length
* 14634 14733: gap of 100 bp
* 14734 15446: contig of 713 bp in length
* 15447 15546: gap of 100 bp
* 15547 16272: contig of 726 bp in length
* 16273 16372: gap of 100 bp
* 16373 17115: contig of 743 bp in length
* 17116 17215: gap of 100 bp
* 17216 17930: contig of 715 bp in length
* 17931 18030: gap of 100 bp
* 18031 18748: contig of 718 bp in length
* 18749 18848: gap of 100 bp
* 18849 19574: contig of 726 bp in length
* 19575 19674: gap of 100 bp
* 19675 20393: contig of 719 bp in length
* 20394 20493: gap of 100 bp
* 20494 21206: contig of 713 bp in length
* 21207 21306: gap of 100 bp
* 21307 22020: contig of 714 bp in length
* 22021 22120: gap of 100 bp
* 22121 22852: contig of 732 bp in length
* 22853 22952: gap of 100 bp
* 22953 23692: contig of 740 bp in length
* 23693 23792: gap of 100 bp
* 23793 24520: contig of 728 bp in length
* 24521 24620: gap of 100 bp
* 24621 25368: contig of 748 bp in length
* 25369 25468: gap of 100 bp
* 25469 26186: contig of 718 bp in length
* 26187 26286: gap of 100 bp
* 26287 27015: contig of 729 bp in length
* 27016 27115: gap of 100 bp
* 27116 27837: contig of 722 bp in length
* 27838 27937: gap of 100 bp
* 27938 28649: contig of 712 bp in length
* 28650 28749: gap of 100 bp
* 28750 29479: contig of 730 bp in length
* 29480 29579: gap of 100 bp
* 29580 30264: contig of 685 bp in length
* 30265 30364: gap of 100 bp
* 30365 31103: contig of 739 bp in length
* 31104 31203: gap of 100 bp
* 31204 31943: contig of 740 bp in length
* 31944 32043: gap of 100 bp
* 32044 32786: contig of 743 bp in length
* 32787 32886: gap of 100 bp
* 32887 33595: contig of 709 bp in length
* 33596 33695: gap of 100 bp
* 33696 34433: contig of 738 bp in length
* 34434 34533: gap of 100 bp
* 34534 35276: contig of 743 bp in length
* 35277 35376: gap of 100 bp

* 35377 36124: contig of 748 bp in length
* 36125 36224: gap of 100 bp
* 36225 36946: contig of 722 bp in length
* 36947 37046: gap of 100 bp
* 37047 37776: contig of 730 bp in length
* 37777 37876: gap of 100 bp
* 37877 38577: contig of 701 bp in length
* 38578 38677: gap of 100 bp
* 38678 39398: contig of 721 bp in length
* 39399 39498: gap of 100 bp
* 39499 40210: contig of 712 bp in length
* 40211 40310: gap of 100 bp
* 40311 41043: contig of 733 bp in length
* 41044 41143: gap of 100 bp
* 41144 41859: contig of 716 bp in length
* 41860 41959: gap of 100 bp
* 41960 42683: contig of 724 bp in length
* 42684 42783: gap of 100 bp
* 42784 43521: contig of 738 bp in length
* 43522 43621: gap of 100 bp
* 43623 44359: contig of 738 bp in length
* 44360 44459: gap of 100 bp
* 44460 45198: contig of 739 bp in length
* 45199 45298: gap of 100 bp
* 45299 46011: contig of 713 bp in length
* 46012 46111: gap of 100 bp
* 46112 46840: contig of 729 bp in length
* 46841 46940: gap of 100 bp

Query Match 100.0%; Score 15; DB 2; Length 65851;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 63511 CCTTCTCGCCCTGTT 63525

RESULT 11

AC130797 80669 bp DNA linear HTG 14-AUG-2002
LOCUS Chlamydomonas reinhardtii clone cr-1j6, WORKING DRAFT SEQUENCE, 1
DEFINITION ordered piece.
AC130797
AC130797.1 GI:22218470
VERSION HTG; HTGS_PHASE2; HTGS_DRAFT.
KEYWORDS Chlamydomonas reinhardtii.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 80669)
Wu, H., Lin, S., Jia, H., Dutcher, S. and Roe, B. A.
Chlamydomonas reinhardtii BAC Clone cr-1j6
Unpublished
2 (bases 1 to 80669)
Wu, H., Lin, S., Jia, H., Dutcher, S. and Roe, B. A.
Direct Submission
TITLE Submitted (14-AUG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code: UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

FEATURES	source	* the accession number will be preserved. 1 80669: contig of 80669 bp in length. Location/Qualifiers 1. 80669 /organism="Chlamydomonas reinhardtii" /db_xref="taxon:3055" /clone="cr-lj6" /clone_lib="cr-lj6" /note="This is one of two clone in the same well cr-lj6"	
BASE COUNT	14154 a 25825 c 24793 g 15894 t	3 others	
ORIGIN			
Query Match	100.0%; Score 15; DB 2; Length 80669;		
Best Local Similarity	100.0%; Pred. No. 38;		
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CCTTCTGCGCCCTGTT 15		
Db	70450 CCTTCTGCGCCCTGTT 70464		
RESULT 12			
AC009031/c			
LOCUS	AC009031	90280 bp DNA linear HTG 26-JAN-2000	
DEFINITION	Homo sapiens chromosome 16 clone RP11-13M21, LOW-PASS SEQUENCE		
ACCESSION	AC009031		
VERSION	AC009031.2 GI:67589938		
KEYWORDS	HTG; HTGS_PHASE0.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Sequencing of Human Chromosome 16		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 90280)		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
COMMENT	On Jan 26, 2000 this sequence version replaced gi:5686044. -----Genome Center Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov ***** * NOTE: This record contains 87 individual * sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely * arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows * overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that * the record is updated, the accession number will * be preserved. * 1 649: contig of 649 bp in length * gap of unknown length * 650 1313: contig of 664 bp in length * gap of unknown length * 1314 1981: contig of 668 bp in length * gap of unknown length * 1982 2621: contig of 640 bp in length * gap of unknown length * 2622 3298: contig of 677 bp in length * gap of unknown length * 3299 3768: contig of 470 bp in length * gap of unknown length * 3769 4417: contig of 649 bp in length * gap of unknown length *****		

* * * * *
* 30771 gap of unknown length
* 31472: contig of 702 bp in length
* gap of unknown length
* 32518: contig of 1046 bp in length
* gap of unknown length
* 32519: contig of 1211 bp in length
* gap of unknown length
* 33730: contig of 75 bp in length
* gap of unknown length
* 33805: contig of 971 bp in length
* gap of unknown length
* 34776: contig of 793 bp in length
* gap of unknown length
* 35569: contig of 958 bp in length
* gap of unknown length
* 36527: contig of 652 bp in length
* gap of unknown length
* 37179: contig of 1419 bp in length
* gap of unknown length
* 38598: contig of 802 bp in length
* gap of unknown length
* 39400: contig of 1133 bp in length
* gap of unknown length
* 40533: contig of 1079 bp in length
* gap of unknown length
* 41612: contig of 1046 bp in length
* gap of unknown length
* 42658: contig of 987 bp in length
* gap of unknown length
* 43645: contig of 1164 bp in length
* gap of unknown length
* 44809: contig of 1339 bp in length
* gap of unknown length
* 46148: contig of 1070 bp in length
* gap of unknown length
* 47218: contig of 1304 bp in length
* gap of unknown length
* 48522: contig of 788 bp in length
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* 49310: contig of 1534 bp in length
* gap of unknown length
* 50844: contig of 1350 bp in length
* gap of unknown length
* 52194: contig of 1124 bp in length
* gap of unknown length
* 53318: contig of 1146 bp in length
* gap of unknown length
* 54464: contig of 1248 bp in length
* gap of unknown length
* 55712: contig of 972 bp in length
* gap of unknown length
* 56684: contig of 1526 bp in length
* gap of unknown length
* 58210: contig of 1554 bp in length
* gap of unknown length
* 59764: contig of 1446 bp in length
* gap of unknown length
* 61210: contig of 1706 bp in length
* gap of unknown length
* 62916: contig of 1219 bp in length
* gap of unknown length
* 64135: contig of 1864 bp in length
* gap of unknown length
* 65999: contig of 1327 bp in length
* gap of unknown length
* 67326: contig of 1285 bp in length
* gap of unknown length
* 68611: contig of 1476 bp in length
* gap of unknown length
* 70087: contig of 1202 bp in length
* gap of unknown length
* 71289: contig of 2022 bp in length
* gap of unknown length

* 73311 74258: contig of 948 bp in length
* gap of unknown length
* 74259 75836: contig of 1578 bp in length
* gap of unknown length

Query Match 100.0%; Score 15; DB 2; Length 90280;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 63309 CCTTCTCGCCCTGTT 63295

RESULT 13
LMFLCHR12_1
WPCOMMENT
Sequence split into 8 fragments LOCUS LMFLCHR12 Accession AL390114
Fragment Name Begin End
LMFLCHR12_0 1 110000
LMFLCHR12_1 100001 210000
LMFLCHR12_2 200001 310000
LMFLCHR12_3 300001 410000
LMFLCHR12_4 400001 510000
LMFLCHR12_5 500001 610000
LMFLCHR12_6 600001 710000
LMFLCHR12_7 700001 757191

Continuation (2 of 8) of LMFLCHR12 from base 100001 (AL390114 Leishmania major chromosome)

Query Match 100.0%; Score 15; DB 2; Length 110000;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 46567 CCTTCTCGCCCTGTT 46581

RESULT 14
AC094766
LOCUS
DEFINITION Rattus norvegicus clone CH230-5L5, *** SEQUENCING IN PROGRESS ***,
65 unordered pieces.
AC094766
AC094766.2 GI:17941546
VERSION HTG: HTGS_PHASE1.
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
REFERENCE 1 (bases 1 to 150765)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alb Brooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsif,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,


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Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
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Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogulu,H., Okwouonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaie,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczkyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 150765)
Worley,K.C.
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624602.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GBID
Center clone name: CH230-5L5
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 115371 bases at least Q40
Consensus quality: 123148 bases at least Q30
Consensus quality: 129020 bases at least Q20
Estimated insert size: 114258; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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* 13033
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* 19365
* 24766: contig of 5402 bp in length
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* 24866: gap of unknown length
* 24867
* 29281: contig of 4415 bp in length
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* 29381: gap of unknown length
* 29382
* 35253: contig of 5872 bp in length
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* 35353: gap of unknown length
* 35354
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* 38907
* 39006: gap of unknown length
* 39007
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* 43063
* 43162: gap of unknown length
* 43163
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* 46846
* 46945: gap of unknown length
*
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56808: gap of unknown length
60130: contig of 3322 bp in length
60131
62896: contig of 2666 bp in length
62966: gap of unknown length
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65384: gap of unknown length
68543: contig of 3159 bp in length
68644
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71705: gap of unknown length
73043: contig of 1338 bp in length
73143: gap of unknown length
75325: contig of 2182 bp in length
75425: gap of unknown length
77827: contig of 2402 bp in length
77927: gap of unknown length
79747: contig of 1820 bp in length
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82048: contig of 2201 bp in length
82148: gap of unknown length
84544: contig of 2396 bp in length
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91934: contig of 1852 bp in length
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108225
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109716: contig of 1392 bp in length
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109816: gap of unknown length
111020: contig of 1204 bp in length
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111120: gap of unknown length
113035: contig of 1915 bp in length
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113136
114902: contig of 1767 bp in length
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116304: contig of 1302 bp in length
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116404: gap of unknown length
117754: contig of 1350 bp in length
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117854: gap of unknown length
119553: contig of 1699 bp in length
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120688: contig of 1035 bp in length
120689
120788: gap of unknown length
121913: contig of 1125 bp in length
121914
122013: gap of unknown length
123345: contig of 1332 bp in length

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT


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primer_bind       67944..67962
                  /note="19-47-315.mis"
misc_feature      67951..67975
                  /note="19-47-315.probe"
variation         67963
                  /note="19-47-315 : polymorphic base C or T"
primer_bind       67964..67982
                  /note="19-47-315.mis complement"
primer_bind       68051..68070
                  /note="19-47.rp complement"
BASE COUNT      43057 a 36601 c 38189 g 42727 t 181 others
ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 160755;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
    |||||||
Db 63345 CCTTCTCGCCCTGTT 63359
```

Search completed: December 11, 2002, 18:06:59
Job time : 1834 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:29:02 ; Search time 213 Seconds
(without alignments)
158.591 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 ccttctgcctgtt 15

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :					N_Geneseq_101002:*				
Result No.	Score	Query Match %	Length	ID	Description				
1	15	100.0	15	22	AAH28084	1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*	15	100.0	160755
2	15	100.0	920	23	AAH88259	2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*	14	93.3	336
3	15	100.0	920	23	AAH88264	3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*	14	93.3	655
4	15	100.0	980	22	AAH28088	4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*	14	93.3	708
5	15	100.0	1044	23	AAH80746	5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*	14	93.3	2036
6	15	100.0	1854	22	AAH28082	6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*	14	93.3	2397
7	15	100.0	1854	22	AAH28086	7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*	14	93.3	2397
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						73: /SID22/gcgdata/geneseq/geneseq-emb1/NA2003X.DAT:*	23	86.7	2292
						74: /SID22/gcgdata/geneseq/geneseq-emb1/NA2003Y.DAT:*	23	86.7	2292
						75: /SID22/gcgdata/geneseq/geneseq-emb1/NA2003Z.DAT:*	23	86.7	2292
						76: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004A.DAT:*	23	86.7	2292
						77: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004B.DAT:*	23	86.7	2292
						78: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004C.DAT:*	23	86.7	2292
						79: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004D.DAT:*	23	86.7	2292
						80: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004E.DAT:*	23	86.7	2292
						81: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004F.DAT:*	23	86.7	2292
						82: /SID22/gcgdata/geneseq/geneseq-emb1/NA2004G.DAT:*	23	86.7	2292

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human DNA sequence
Human OREF polynuc
Human ovarian anti
C glutamic codin
Drosophila melanog
Tea gene (cDNA 20.
T-cell transmembra
Human T-cell early
Drosophila melanog
C glutamic codin
CSF-1 receptor PCR
Human polymorphic
SSP1 cDNA amplifi
Homo sapiens TSH r
Human OREF polynuc
Human immune/haema
Human immune/haema
Human TSH-receptor
Human prostate exp
Murine 7-transmemb
Bovine embryonic g
Drosophila melanog
Arabidopsis thalia
Arabidopsis thalia
Fusarium venenatum
Drosophila melanog
Arabidopsis thalia
Pasteurella multoc
Human N-proteinase
DNA encoding novel
Drosophila melanog
DNA encoding novel
Non-endogenous hum
Non-endogenous hum
Non-endogenous hum
Non-endogenous hum
Non-endogenous hum
Human TSH receptor
Homo sapiens TSH r
Human TSH-receptor
Human Thyroid Stim
Mouse thyroid stim
Polynucleotide seq
DNA encoding novel
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
A. chrysogenum gam
Drosophila melanog
Drosophila melanog
Drosophila melanog
Non-endogenous hum
Drosophila melanog
DNA encoding novel
Sequence encoding
Actin gene (incl.
Actin. Homo sapie
A. chrysogenum act
Drosophila melanog
Human immune/haema
DNA encoding novel
Human macrophage c
SSP1 protein encod
DNA encoding novel
Drosophila melanog

83	13	86.7	4374	22	AAK52302	Human polynucleoti	156	12	80.0	358	14	AAQ37959	Streptomyces ghana
84	13	86.7	4402	23	ABL03713	Drosophila melanog	157	12	80.0	380	24	ABL82646	Human ovarian canc
85	13	86.7	4455	22	AAK52301	Human polynucleoti	158	12	80.0	389	23	AS85414	DNA encoding novel
86	13	86.7	4495	22	AAK52301	Human polynucleoti	159	12	80.0	396	22	ABA44725	Human breast cell
87	13	86.7	4558	22	AAK52301	Human lung antigen	160	12	80.0	396	22	ABA55181	Human foetal liver
88	13	86.7	4558	22	AAK52301	Genomic sequence #	161	12	80.0	396	22	ABA24926	Probe #3392 for ge
89	13	86.7	4645	20	AAK20577	Polynucleotide seq	162	12	80.0	396	22	AAK03441	Human brain expres
90	13	86.7	4657	20	AAK20577	Nucleotide sequenc	163	12	80.0	396	22	AAK28895	Human bone marrow
91	13	86.7	4889	23	ABV23267	Human prostate exp	164	12	80.0	396	22	AAI13484	Probe #3417 for ge
92	13	86.7	5299	23	ABL07890	Drosophila melanog	165	12	80.0	396	22	AAI34839	Probe #3525 used t
93	13	86.7	5494	23	ABLI13956	Drosophila melanog	166	12	80.0	396	22	AAI03363	Probe #3354 used t
94	13	86.7	5828	21	AAAL4845	DNA encoding tolue	167	12	80.0	396	22	ABV16446	Human genome-deriv
95	13	86.7	5902	23	ABLI0962	Drosophila melanog	168	12	80.0	401	23	ABV16446	Human prostate exp
96	13	86.7	6390	23	AAK59665	DNA encoding novel	169	12	80.0	404	22	AAI17958	Human breast cance
97	13	86.7	6390	23	AAK59665	DNA encoding novel	170	12	80.0	413	22	AAI17958	Human polynucleoti
98	13	86.7	6689	23	ABLI19618	Drosophila melanog	171	12	80.0	414	24	ABL62037	Colon adenocarcino
99	13	86.7	6692	19	AAV06592	Human N-proteinase	172	12	80.0	414	24	ABL62037	Breast cancer rela
100	13	86.7	6916	23	ABLI19616	Drosophila melanog	173	12	80.0	425	21	AAK23904	Human secreted pro
101	13	86.7	7149	23	ABLI19614	Drosophila melanog	174	12	80.0	445	22	ABA52057	Human foetal liver
102	13	86.7	7430	23	AAK59509	Propionibacterium	175	12	80.0	445	22	ABA21871	Probe #337 for gen
103	13	86.7	7829	23	ABLI02642	Drosophila melanog	176	12	80.0	445	22	AAK00340	Human brain expres
104	13	86.7	8115	22	AAK52860	Human genomic DNA	177	12	80.0	445	22	AAK25783	Human bone marrow
105	13	86.7	8116	22	AAK52861	Human genomic DNA	178	12	80.0	445	22	AAI10412	Probe #345 for gen
106	13	86.7	9320	22	AAH45588	DNA encoding hydro	179	12	80.0	445	22	AAI31664	Probe #350 used to
107	13	86.7	9785	17	AAI44457	DNA encoding tolue	180	12	80.0	445	22	AAI00347	Probe #338 used to
108	13	86.7	10726	23	ABLI06616	Drosophila melanog	181	12	80.0	445	24	ABS00363	Human genome-deriv
109	13	86.7	11992	23	ABLI03712	Drosophila melanog	182	12	80.0	447	20	AAK27717	Human DNA marker c
110	13	86.7	12213	23	ABLI19644	Drosophila melanog	183	12	80.0	447	23	AAK583716	DNA encoding novel
111	13	86.7	35100	19	AAV20441	Human c-fms oncoge	184	12	80.0	451	21	AAK64576	Elmeria tenella PK
112	13	86.7	38258	24	AAK59663	DNA encoding colon	185	12	80.0	461	24	ABU63543	Breast cancer rela
113	13	86.7	349980	22	AAH41224	Pyrococcus abyssi	186	12	80.0	463	22	AAK79697	Human immune/haema
114	12	80.0	18	24	ABK87886	Midkine (MK) expre	187	12	80.0	475	22	AAI92355	Human polynucleoti
115	12	80.0	18	24	ABK87887	Midkine (MK) expre	188	12	80.0	478	23	ABV46244	Human prostate exp
116	12	80.0	19	21	AAK83529	cdk-we-hu ribozyme	189	12	80.0	485	21	AAK02660	Human colon cancer
117	12	80.0	19	21	AAK83530	cdk-we-hu ribozyme	190	12	80.0	486	24	ABL82663	Human ovarian canc
118	12	80.0	19	21	AAK83531	cdk-we-hu ribozyme	191	12	80.0	494	24	ABQ36572	Human colon cancer
119	12	80.0	19	21	AAH58691	cdk-we-hu ribozyme	192	12	80.0	503	22	AAK63333	Human immune/haema
120	12	80.0	19	22	AAH58692	cdk-we-hu ribozyme	193	12	80.0	509	22	AAH09380	Human cDNA clone (
121	12	80.0	19	22	AAH58693	cdk-we-hu ribozyme	194	12	80.0	522	23	AAK585412	DNA encoding novel
122	12	80.0	24	24	ABN86828	Human fructose-6-p	195	12	80.0	523	20	AAV86036	EST clone B227. H
123	12	80.0	30	24	AAK97855	Oligonucleotide ME	196	12	80.0	537	24	ABL83088	Human ovarian canc
124	12	80.0	49	22	AAK10683	PCR primer oOH011	197	12	80.0	539	22	AAH13272	Human cDNA clone (
125	12	80.0	51	22	AAK127462	Human SNP oligonuc	198	12	80.0	550	22	AAK505612	Mammalian gossypii AG
126	12	80.0	152	22	ABA46826	Human breast cell	199	12	80.0	576	24	AAK18065	Human colon cancer
127	12	80.0	152	22	ABA64706	Human foetal liver	200	12	80.0	607	24	ABQ57802	Human prostate exp
128	12	80.0	152	22	ABA31830	Probe #10296 for g	201	12	80.0	611	23	ABV46802	Oligonucleotide fo
129	12	80.0	152	22	AAK13141	Human brain expres	202	12	80.0	611	24	ABQ19264	Oligonucleotide fo
130	12	80.0	152	22	AAK38872	Human bone marrow	203	12	80.0	611	24	ABQ19265	Oligonucleotide fo
131	12	80.0	152	22	AAK19680	Probe #9613 for ge	204	12	80.0	612	24	ABQ15078	Oligonucleotide fo
132	12	80.0	152	22	AAI19680	Probe #13561 used	205	12	80.0	612	24	ABQ15079	Oligonucleotide fo
133	12	80.0	152	22	AAI44875	Probe #5390 used t	206	12	80.0	615	21	AAFI1528	Aspergillus niger
134	12	80.0	152	22	AAI05399	Human genome-deriv	207	12	80.0	619	24	ABQ44298	Oligonucleotide fo
135	12	80.0	152	24	ABK12953	Bacillus clausii g	208	12	80.0	619	24	ABQ44299	Oligonucleotide fo
136	12	80.0	173	24	ABK79902	Human immune/haema	209	12	80.0	626	21	AAK09531	Fusarium venenatum
137	12	80.0	180	22	AAK64796	Human secreted pro	210	12	80.0	631	21	AAFI3423	Aspergillus oryzae
138	12	80.0	187	21	AAK13925	Human secreted pro	211	12	80.0	657	21	AAK50247	Maize heat shock p
139	12	80.0	237	21	AAK31359	Human immune/haema	212	12	80.0	657	22	AAH26480	Maize heat shock p
140	12	80.0	245	22	AAK67522	Drosophila melanog	213	12	80.0	659	21	AAFI12907	Aspergillus oryzae
141	12	80.0	252	23	ABLI14549	Human l-alpha-OHas	214	12	80.0	660	21	AAK07969	Fusarium venenatum
142	12	80.0	257	20	AAK223310	Human secreted pro	215	12	80.0	662	21	AAK01928	Human colon cancer
143	12	80.0	261	21	AAK31684	Human secreted re	216	12	80.0	667	21	AAK9649	Eucalyptus grandis
144	12	80.0	279	22	AAI199217	Human kidney relat	217	12	80.0	667	24	ABK63167	Rat sequence diffe
145	12	80.0	285	16	AAI63567	Human gene signatu	218	12	80.0	674	24	ABQ13506	Oligonucleotide fo
146	12	80.0	294	22	AAI199215	Human kidney relat	219	12	80.0	674	24	ABQ13507	Oligonucleotide fo
147	12	80.0	294	22	AAI63565	Human kidney relat	220	12	80.0	681	23	ABL26035	Drosophila melanog
148	12	80.0	300	21	AAA002553	Human colon cancer	221	12	80.0	711	21	AAK294085	Haematopoietic ste
149	12	80.0	309	21	AAA42072	Human secreted exp	222	12	80.0	751	22	AAI94531	Human neuroblastom
150	12	80.0	334	24	ABN24354	Human ORFX polynuc	223	12	80.0	761	22	AAK20473	Human secreted pro
151	12	80.0	337	23	AAK586961	DNA encoding novel	224	12	80.0	762	21	AAK08886	Fusarium venenatum
152	12	80.0	350	22	AAK64318	Novel human polynu	225	12	80.0	768	23	ABL27737	Drosophila melanog
153	12	80.0	354	21	AAK03111	Human secreted pro	226	12	80.0	774	22	AAH68308	C glutamic codin
154	12	80.0	355	21	AAK28671	Human secreted pro	227	12	80.0	787	24	AAK33829	Human secreted pro
155	12	80.0	357	21	AAK242551	Human 5' EST isola	228	12	80.0	792	22	AAI97289	Human neuroblastom

c 229	12	80.0	797	22	AAI97288	Human neuroblastom	302	12	80.0	1671	20	AAZ30705	Rat neuronal immed
c 230	12	80.0	801	23	AAS80358	DNA encoding novel	c 303	12	80.0	1695	24	ABO40322	Oligonucleotide fo
c 231	12	80.0	809	24	ABQ33820	Oligonucleotide fo	304	12	80.0	1695	24	ABO40323	Oligonucleotide fo
c 232	12	80.0	809	24	ABQ33821	Oligonucleotide fo	305	12	80.0	1746	22	AAH23097	Osteoarthritis tis
c 233	12	80.0	824	24	AAS22636	Human cDNA encodin	306	12	80.0	1746	22	AAH23097	Osteoarthritis tis
c 234	12	80.0	829	21	AA50250	Maize heat shock p	307	12	80.0	1746	24	ABN95923	Human cDNA differe
c 235	12	80.0	829	22	AAH26478	Maize heat shock p	308	12	80.0	1746	24	ABN95923	Human cDNA differe
c 236	12	80.0	837	22	AAH68310	C glutamic codin	309	12	80.0	1746	24	ABK12141	Human benign prost
c 237	12	80.0	840	23	AAS88313	DNA encoding novel	310	12	80.0	1746	24	ABL69359	Human zinc finger
c 238	12	80.0	846	22	AAF54823	Corn glutamate 1-s	311	12	80.0	1764	23	ABL04855	Prostate cancer re
c 239	12	80.0	879	24	AD333862	Human secreted pro	312	12	80.0	1770	23	ABL22915	Drosophila melanog
c 240	12	80.0	902	22	AAI97794	Human secreted pro	313	12	80.0	1770	23	ABL22915	Drosophila melanog
c 241	12	80.0	903	23	ABL06853	Drosophila melanog	314	12	80.0	1797	23	AAS86812	DNA encoding novel
c 242	12	80.0	904	18	AAI64849	Myceliophthora the	315	12	80.0	1806	21	AAF18258	Lung cancer associ
c 243	12	80.0	960	22	AAI71350	Corynebacterium gl	c 316	12	80.0	1820	11	AAQ04731	cDNA sequence from
c 244	12	80.0	972	23	ABL28095	Drosophila melanog	c 317	12	80.0	1846	24	ABN59602	Novel human coding
c 245	12	80.0	974	21	AAF21745	Human breast and o	c 318	12	80.0	1878	22	AAH51962	Mycobacterium tube
c 246	12	80.0	981	24	ABR97002	Human ZFP36 coding	c 319	12	80.0	1878	22	AAH51962	Mycobacterium tube
c 247	12	80.0	984	19	AAV16105	Fusarium oxysporum	c 320	12	80.0	1879	22	AAH17119	M. tuberculosis he
c 248	12	80.0	987	19	AAV54011	Nucleotide sequenc	c 321	12	80.0	1954	22	ABA46112	Human breast cell
c 249	12	80.0	1011	22	AAH68290	C glutamic codin	c 322	12	80.0	1974	24	ABQ50596	Oligonucleotide fo
c 250	12	80.0	1014	21	AAC56329	Pinus radiata tran	c 323	12	80.0	1974	24	ABQ50597	Oligonucleotide fo
c 251	12	80.0	1020	21	AA940432	Mycobacterium auru	c 324	12	80.0	1992	23	ABL15361	Drosophila melanog
c 252	12	80.0	1020	21	AA940440	Mycobacterium auru	c 325	12	80.0	2013	24	ABN89466	Abeta42-hsp70 fusi
c 253	12	80.0	1022	24	ABQ40746	Oligonucleotide fo	c 326	12	80.0	2077	22	AAK94927	Human full-length
c 254	12	80.0	1022	24	ABQ40747	Oligonucleotide fo	c 327	12	80.0	2079	23	ABL24645	Drosophila melanog
c 255	12	80.0	1028	21	AA50251	Maize heat shock p	c 328	12	80.0	2085	24	ABK80509	Bacillus clausii g
c 256	12	80.0	1028	22	AAH26477	Maize heat shock p	c 329	12	80.0	2104	14	AAQ43722	Sequence of DNA cl
c 257	12	80.0	1038	24	ABL87981	DNA polymerase III	c 330	12	80.0	2109	24	ABA90378	Drosophila cell cy
c 258	12	80.0	1038	24	ABL87982	DNA polymerase III	c 331	12	80.0	2122	24	ABN95249	Gene #1747 used to
c 259	12	80.0	1080	24	ABN84013	Human oestrogen do	c 332	12	80.0	2136	22	AAF25028	Nucleotide sequenc
c 260	12	80.0	1116	23	ABN85415	DNA encoding novel	c 333	12	80.0	2172	22	AA502618	Chimeric immunogen
c 261	12	80.0	1116	23	AA591079	DNA encoding novel	c 334	12	80.0	2175	22	AAF25031	Nucleotide sequenc
c 262	12	80.0	1124	21	AA95776	Human immune syste	c 335	12	80.0	2178	22	AAH18098	Human cDNA sequenc
c 263	12	80.0	1128	24	ABQ90902	M. capsulatus gene	c 336	12	80.0	2199	19	AAV82778	Clone bp783_3 isol
c 264	12	80.0	1134	22	AAI71711	Corynebacterium gl	c 337	12	80.0	2199	24	ABQ92015	Human polynucleoti
c 265	12	80.0	1143	23	AA574919	DNA encoding novel	c 338	12	80.0	2220	23	AAS82863	DNA encoding novel
c 266	12	80.0	1145	22	AAH29291	Drosophila melanog	c 339	12	80.0	2225	23	AAS83717	Human DNA sequenc
c 267	12	80.0	1152	24	ABQ68857	Listeria monocytog	c 340	12	80.0	2247	20	AA595016	Human secreted pro
c 268	12	80.0	1161	19	AAV69538	Thymosin beta 4, Y	c 341	12	80.0	2249	20	AAV84511	Human secreted pro
c 269	12	80.0	1161	22	AAI63759	Drosophila gustato	c 342	12	80.0	2249	22	ABA83294	Human secreted pro
c 270	12	80.0	1163	21	AA50252	Maize heat shock p	c 343	12	80.0	2252	23	ABL14548	Drosophila melanog
c 271	12	80.0	1163	22	AAH26479	Maize heat shock p	c 344	12	80.0	2268	23	ABL24186	Drosophila melanog
c 272	12	80.0	1200	23	AA580309	DNA encoding novel	c 345	12	80.0	2280	21	AAC59224	Human secreted pro
c 273	12	80.0	1230	23	ABL20857	Drosophila melanog	c 346	12	80.0	2281	23	ABL07965	Drosophila melanog
c 274	12	80.0	1242	23	ABL25337	Drosophila melanog	c 347	12	80.0	2334	22	AAF81369	Quorum sensing con
c 275	12	80.0	1252	24	ABN86826	Human fructose-6-p	c 348	12	80.0	2349	24	ABQ90069	M. capsulatus gene
c 276	12	80.0	1260	22	AA510677	Mycobacterium tube	c 349	12	80.0	2349	24	ABQ90651	M. capsulatus gene
c 277	12	80.0	1263	23	AA585416	DNA encoding novel	c 350	12	80.0	2362	20	AAQ02929	Human 1-alpha-hydr
c 278	12	80.0	1393	23	ABL24629	Drosophila melanog	c 351	12	80.0	2375	17	AAF38233	Multiple drug resi
c 279	12	80.0	1401	23	ABL07745	Drosophila melanog	c 352	12	80.0	2383	21	AAF18298	Lung cancer associ
c 280	12	80.0	1473	12	AAQ14857	Fusarium oxysporum	c 353	12	80.0	2389	22	AAK51748	Human polynucleoti
c 281	12	80.0	1473	13	AAQ26407	Fusarium oxysporum	c 354	12	80.0	2403	23	ABL03183	Drosophila melanog
c 282	12	80.0	1473	13	AAQ26382	Endoglucanase #2.	c 355	12	80.0	2409	21	AAZ30341	Partial sequence o
c 283	12	80.0	1473	13	AAQ25933	Cellulase containe	c 356	12	80.0	2434	22	AAI36971	Human musculoskele
c 284	12	80.0	1473	13	AAQ29935	Endoglucanase gene	c 357	12	80.0	2446	22	AAS27610	DNA encoding novel
c 285	12	80.0	1473	14	AAQ41733	Dye transfer inhib	c 358	12	80.0	2446	22	AAS27747	DNA encoding novel
c 286	12	80.0	1473	14	AAQ49942	Endoglucanase enzy	c 359	12	80.0	2451	20	AAZ07543	Human lalpa hydro
c 287	12	80.0	1473	16	AAZ60179	F. oxysporum endog	c 360	12	80.0	2454	24	AAS94853	Human DNA sequenc
c 288	12	80.0	1473	19	AAV16103	Fusarium oxysporum	c 361	12	80.0	2456	23	ABL24188	Drosophila melanog
c 289	12	80.0	1506	22	AAH65250	C glutamic codin	c 362	12	80.0	2464	24	ABA95855	Human flavoprotein
c 290	12	80.0	1524	20	AAV82433	Human 25-hydroxyvi	c 363	12	80.0	2465	21	AAZ94203	Human transferrase
c 291	12	80.0	1524	22	AAH76977	Human 25-hydroxyvi	c 364	12	80.0	2465	23	ABL05921	Drosophila melanog
c 292	12	80.0	1527	20	AA59352	Human secreted pro	c 365	12	80.0	2468	22	AAH99132	Human ESP-derived
c 293	12	80.0	1527	22	AA592323	Human cDNA encodin	c 366	12	80.0	2469	20	AAV82438	Human 25-hydroxyvi
c 294	12	80.0	1527	24	ABR90902	Human polynucleoti	c 367	12	80.0	2469	22	AAF76979	Human 25-hydroxyvi
c 295	12	80.0	1543	24	ABN95910	Gene #2408 used to	c 368	12	80.0	2484	22	AAF80536	Receptor #24 parti
c 296	12	80.0	1590	24	ABA96173	Human immunoavidin	c 369	12	80.0	2484	23	AAS83500	DNA encoding novel
c 297	12	80.0	1603	22	AAI70989	C. glutamicum SRT	c 370	12	80.0	2520	21	AAH78420	Human secreted pro
c 298	12	80.0	1608	22	AAI88315	Human polynucleoti	c 371	12	80.0	2528	22	AAH99142	Human ESP-derived
c 299	12	80.0	1609	23	ABLI2379	Drosophila melanog	c 372	12	80.0	2543	23	ABL26038	Drosophila melanog
c 300	12	80.0	1647	23	ABV21334	Human prostate exp	c 373	12	80.0	2589	23	ABLI1069	Drosophila melanog
c 301	12	80.0	1647	23	ABV27153	Human prostate exp	c 374	12	80.0	2627	24	ABL64775	Lung cancer relate
										2627	24	ABL65409	Lung cancer relate

375	12	80.0	2627	24	ABL66513	Lung cancer relate	448	12	80.0	4417	12	AAQ12163	Sequence encoding
376	12	80.0	2627	24	ABL68130	Ovary cancer relat	c 449	12	80.0	4457	23	ABL15360	Drosophila melanog
377	12	80.0	2627	24	ABL69119	Kidney cancer rela	c 450	12	80.0	4462	23	ABL03182	Drosophila melanog
378	12	80.0	2638	11	AAQ03741	Human B-myb related	451	12	80.0	4531	22	AAI199538	Human polynucleoti
379	12	80.0	2638	19	RAV20468	Human B-myb oncoge	452	12	80.0	4566	23	ABL21404	Drosophila melanog
380	12	80.0	2641	22	AAI61175	Human polynucleoti	453	12	80.0	4600	23	ABL22914	Drosophila melanog
c 381	12	80.0	2652	22	AAH26468	Ancestral HIV-1 gr	c 454	12	80.0	4859	22	AA540336	DNA encoding human
c 382	12	80.0	2652	22	AAH26470	Semi-Optimised anc	c 455	12	80.0	4859	22	AA540336	Human reproductive
c 383	12	80.0	2652	22	AAH81451	Escherichia coli p	c 456	12	80.0	4916	23	ABL18373	Drosophila melanog
c 384	12	80.0	2656	24	AAH94947	Human DNA sequence	c 457	12	80.0	4925	23	ABL04854	Drosophila melanog
385	12	80.0	2661	22	AAI59389	Human polynucleoti	458	12	80.0	4967	22	AAK80212	Human immune/haema
386	12	80.0	2662	17	AAT08977	Actual shortened B	c 459	12	80.0	5140	23	ABL07744	Drosophila melanog
387	12	80.0	2735	23	AA585641	DNA encoding novel	c 460	12	80.0	5154	23	AA584859	DNA encoding novel
388	12	80.0	2749	22	AAK94479	Human full-length	c 461	12	80.0	5186	16	AAQ84967	E. coli PEPC gene
c 389	12	80.0	2793	24	ABK63722	Rat sequence diffe	c 462	12	80.0	5342	23	ABL24644	Drosophila melanog
c 390	12	80.0	2821	24	ABN80292	Human chemically m	c 463	12	80.0	5369	20	AAW78080	A. gossypii ADE4 D
c 391	12	80.0	2870	24	ABQ73050	Human GPR5B-like	c 464	12	80.0	5410	23	ABL11068	Drosophila melanog
c 392	12	80.0	2888	23	ABLI16825	Drosophila melanog	c 465	12	80.0	5535	24	ABL92216	Chemically treated
c 393	12	80.0	2902	22	AAQ90433	Murine Lymph node	c 466	12	80.0	5535	24	ABL49317	Human immune syste
c 394	12	80.0	2979	23	ABL06852	Drosophila melanog	c 467	12	80.0	5676	15	AAQ64556	Human collagen (Ty
c 395	12	80.0	2993	22	AAI29134	Mouse full length	c 468	12	80.0	5692	22	AAF32248	Streptomyces sp. c
c 396	12	80.0	3018	24	ABK15653	Rice lipoxigenase	c 469	12	80.0	5740	23	ABL21400	Drosophila melanog
c 397	12	80.0	3038	23	ABL13842	Drosophila melanog	470	12	80.0	5742	22	AAK85933	Human immune/haema
398	12	80.0	3149	22	AAI61108	Human polynucleoti	471	12	80.0	5815	22	AAK71205	Human exostosin-4
399	12	80.0	3210	23	ABL13846	Drosophila melanog	c 472	12	80.0	5854	20	AAV72378	Drosophila melanog
c 400	12	80.0	3254	23	ABL10587	Drosophila melanog	c 473	12	80.0	5944	23	ABL06781	Drosophila melanog
c 401	12	80.0	3266	23	ABL16043	Drosophila melanog	c 474	12	80.0	5972	23	ABL05920	Chemically treated
c 402	12	80.0	3306	22	AAF87438	Corynebacterium th	c 475	12	80.0	6040	24	ABL92301	Human polynucleoti
c 403	12	80.0	3362	21	AAK77294	Human ORFX Orf2849	c 476	12	80.0	6040	24	ABL49370	Genomic sequence #
c 404	12	80.0	3387	23	AA586456	DNA encoding novel	c 477	12	80.0	6134	22	AA528462	DNA encoding huma
c 405	12	80.0	3402	23	AA588406	DNA encoding novel	c 478	12	80.0	6172	21	AAAI2734	Human cDNA differe
c 406	12	80.0	3416	23	ABL20856	Drosophila melanog	c 479	12	80.0	6189	24	ABR83455	DNA encoding novel
c 407	12	80.0	3479	21	AAAI2733	cDNA encoding mous	c 480	12	80.0	6223	23	AA578879	Drosophila melanog
c 408	12	80.0	3496	24	ABK75331	Bacillus lichenifo	c 481	12	80.0	6349	23	ABL20858	Drosophila melanog
c 409	12	80.0	3522	23	AA54200	Pseudomonas aerugi	c 482	12	80.0	6412	23	ABL19284	Human cDNA differe
c 410	12	80.0	3535	22	AAH47802	Chimeric CBD-fused	c 483	12	80.0	6462	24	ABK83473	Drosophila melanog
c 411	12	80.0	3536	22	AAD03917	Human caspase-10 D	c 484	12	80.0	6594	23	ABL15639	Drosophila melanog
c 412	12	80.0	3565	24	ABK83577	Human cDNA differe	c 485	12	80.0	6690	23	ABL16769	Drosophila melanog
c 413	12	80.0	3590	21	AAZ94124	Haematopoietic ste	c 486	12	80.0	6871	22	AA532589	Human genomic DNA
c 414	12	80.0	3701	16	AAQ79914	Cytochrome-P450-ox	c 487	12	80.0	7045	23	ABL26034	Drosophila melanog
c 415	12	80.0	3761	23	ABL05157	Drosophila melanog	c 488	12	80.0	7053	23	ABL29767	Drosophila melanog
c 416	12	80.0	3779	22	AAK79402	Human immune/haema	c 489	12	80.0	7105	22	AAI37450	Human musculoskele
c 417	12	80.0	3786	22	AAH73323	Human cervical can	c 490	12	80.0	7507	22	AAK87178	Human immune/haema
c 418	12	80.0	3820	23	ABL12378	Drosophila melanog	c 491	12	80.0	7734	22	AA527657	DNA encoding novel
c 419	12	80.0	3821	15	AAQ56609	Human PGF-2/NT-3 5	c 492	12	80.0	7734	22	AAK72311	Human immune/haema
c 420	12	80.0	3821	20	AAQ34365	Human nerve growth	c 493	12	80.0	8284	22	AAI26526	Human breast cance
c 421	12	80.0	3821	24	AAD30143	Human nerve growth	c 494	12	80.0	8284	22	AAI26526	Human breast cance
c 422	12	80.0	3821	24	ABR92502	Human G-protein co	c 495	12	80.0	8284	22	AAI26600	Human breast cance
c 423	12	80.0	3852	20	AAZ20298	Human ZFP36 gene.	c 496	12	80.0	8450	22	AAK71204	Human immune/haema
c 424	12	80.0	3889	24	ABA97001	Human cancer agent	c 497	12	80.0	8467	23	ABL10586	Drosophila melanog
c 425	12	80.0	3901	22	AA561042	Human prostate exp	c 498	12	80.0	8588	22	AAH26896	Human androgen rec
c 426	12	80.0	3901	23	ABV22740	Human prostate exp	c 499	12	80.0	8601	13	AAQ24828	AFP-1. Homo sapie
c 427	12	80.0	3901	23	ABV28568	Human prostate exp	500	12	80.0	8601	13	AAQ24829	AFP-1 (C 7508 T).
c 428	12	80.0	3921	22	AAH18220	Human cDNA sequenc	501	12	80.0	9339	22	AAI02697	Human reproductive
c 429	12	80.0	3922	23	ABL28094	Drosophila melanog	502	12	80.0	9447	23	ABL29766	Drosophila melanog
c 430	12	80.0	3953	22	AAK85377	Human immune/haema	c 503	12	80.0	9450	23	ABL29766	Drosophila melanog
c 431	12	80.0	3973	20	AAV65326	Human neuronatin g	c 504	12	80.0	9905	24	AAK98324	Human purinergic-r
c 432	12	80.0	4031	18	AAH84485	Mouse alpha-1 coll	c 505	12	80.0	10036	23	ABL10488	Drosophila melanog
c 433	12	80.0	4117	22	AAK77276	Rat cDNA encoding	c 506	12	80.0	10117	22	AAK87179	Human immune/haema
c 434	12	80.0	4138	7	AA606683	Sequence of premel	c 507	12	80.0	10468	23	ABL05156	Drosophila melanog
c 435	12	80.0	4160	22	AA527609	DNA encoding novel	c 508	12	80.0	10514	23	ABL28624	Drosophila melanog
c 436	12	80.0	4160	22	AA527746	DNA encoding novel	c 509	12	80.0	10515	24	ABK10772	Human small induci
c 437	12	80.0	4160	22	AAK77304	Human immune/haema	510	12	80.0	11125	22	AAK66446	Human immune/haema
c 438	12	80.0	4163	23	ABL24628	Drosophila melanog	511	12	80.0	11244	22	AAK74606	Human immune/haema
c 439	12	80.0	4185	22	AA527611	DNA encoding novel	c 512	12	80.0	11893	24	ABL68924	Kidney cancer rela
c 440	12	80.0	4185	22	AA527748	DNA encoding novel	513	12	80.0	13549	23	ABL07964	Drosophila melanog
c 441	12	80.0	4185	22	AAK77305	Human immune/haema	514	12	80.0	13549	23	ABL07964	Drosophila melanog
c 442	12	80.0	4200	23	AA551542	Pseudomonas aerugi	c 515	12	80.0	14333	24	ABL28579	Mouse ischaemic co
c 443	12	80.0	4238	24	ABK84776	Human cDNA differe	516	12	80.0	14775	23	ABL99535	Human box-dependen
c 444	12	80.0	4238	24	ABL69127	Kidney cancer rela	517	12	80.0	14985	17	AAK43574	Human Bin1 gene.
c 445	12	80.0	4262	21	AA645577	E. tenella cGMP de	c 518	12	80.0	14985	22	AAV15693	Human immune/haema
c 446	12	80.0	4285	23	ABL25336	Drosophila melanog	c 519	12	80.0	15296	22	AAK74605	Drosophila melanog
c 447	12	80.0	4413	23	AA583715	DNA encoding novel	c 520	12	80.0	15606	23	ABL16881	Drosophila melanog

c 521	12	80.0	17269	23	ABL14506	Drosophila melanog	594	11	73.3	15	17	AAT49764	Human CETP HH ribo
c 522	12	80.0	17677	22	AAK70506	Human immune/haema	595	11	73.3	15	17	AAT49766	Human CETP HH ribo
c 523	12	80.0	17677	22	AAK84095	Human immune/haema	596	11	73.3	15	17	AAT49762	Human CETP HH ribo
c 524	12	80.0	17949	22	AAH89228	Human signal trans	597	11	73.3	24	16	AAT00183	Hepatitis GB virus
c 525	12	80.0	18132	22	AAH67033	Human immune/haema	598	11	73.3	24	21	AAH55451	Hepatitis GB virus
c 526	12	80.0	18132	22	AAK79622	Human immune/haema	c 599	11	73.3	30	22	AAD10246	Human fibrinogen (
c 527	12	80.0	18522	23	AAH59560	Propionibacterium	c 600	11	73.3	31	21	AAH78804	Human genomic DNA
c 528	12	80.0	18533	22	AAK75941	Human immune/haema	c 601	11	73.3	35	21	AAZ49995	Bacteriophage T7 p
c 529	12	80.0	18647	21	AAK21059	Human low adenosin	c 602	11	73.3	40	24	AAH48381	Cytohesin binding
c 530	12	80.0	18648	21	AAK34937	Human adenosin re	c 603	11	73.3	41	22	AAH49741	Human amylase 8 co
c 531	12	80.0	18648	24	ABL65840	Lung cancer relate	c 604	11	73.3	41	22	AAH49742	Human amylase 8 co
c 532	12	80.0	18648	24	ABL69114	Kidney cancer rela	c 605	11	73.3	50	19	AAV95556	Human c-fos hairpi
c 533	12	80.0	19861	22	AAK71206	Human immune/haema	c 606	11	73.3	50	22	AAI75275	Human silent SNP c
c 534	12	80.0	19942	22	AAK87416	Human immune/haema	c 607	11	73.3	51	18	AAI69953	PCR primer RG749
c 535	12	80.0	20015	22	ABA20740	Human nervous syst	c 608	11	73.3	51	22	AAI75274	Human silent SNP c
c 536	12	80.0	20097	22	AAH32695	Human genomic DNA	c 609	11	73.3	54	18	AAI69954	PCR primer RG750
c 537	12	80.0	20097	22	AAH42142	Genomic sequence #	c 610	11	73.3	60	20	AAH36609	Mammalian CETP imm
c 538	12	80.0	20366	23	ABL28578	Drosophila melanog	c 611	11	73.3	60	22	AAH54488	Nucleotide sequenc
c 539	12	80.0	20645	22	AAH05355	Human reproductive	c 612	11	73.3	60	24	ABN59243	Human spliced tran
c 540	12	80.0	20645	23	ABL98224	Human testicular a	c 613	11	73.3	60	24	ABN59339	Human spliced tran
c 541	12	80.0	21010	22	AAH05888	Human reproductive	c 614	11	73.3	60	24	ABN59548	Human spliced tran
c 542	12	80.0	21010	22	AAH89247	Human digestive sy	c 615	11	73.3	65	24	ABN55183	Mouse spliced tran
c 543	12	80.0	21010	23	ABL98452	Human testicular a	c 616	11	73.3	70	13	AAQ35815	Annealing oligonuc
c 544	12	80.0	21024	22	AAH05889	Human reproductive	c 617	11	73.3	70	13	AAQ35816	Annealing oligonuc
c 545	12	80.0	21024	22	AAH89248	Human digestive sy	c 618	11	73.3	70	24	ABH98923	Oligonucleotide RW
c 546	12	80.0	21024	23	ABL98453	Human testicular a	c 619	11	73.3	70	24	ABH98924	Oligonucleotide RW
c 547	12	80.0	21185	21	AAH63350	Streptomyces globi	c 620	11	73.3	91	24	ABL71090	Corn tassell-deri
c 548	12	80.0	21606	22	AAH36233	Human cardiovascular	c 621	11	73.3	94	24	AAH48339	Cytohesin binding
c 549	12	80.0	21606	23	ABL28639	Drosophila melanog	c 622	11	73.3	139	22	ABA50440	Human breast cell
c 550	12	80.0	22253	23	ABL16042	Drosophila melanog	c 623	11	73.3	139	22	ABA68390	Human foetal liver
c 551	12	80.0	22401	22	AAK71911	Human immune/haema	c 624	11	73.3	139	22	ABA35385	Probe #13951 for g
c 552	12	80.0	22402	22	AAK71912	Human immune/haema	c 625	11	73.3	139	22	AAK16763	Human brain expres
c 553	12	80.0	23452	22	AAH42122	Genomic sequence #	c 626	11	73.3	139	22	AAK42540	Human bone marrow
c 554	12	80.0	23457	22	AAH42121	Genomic sequence #	c 627	11	73.3	139	22	AAI23286	Probe #13219 for g
c 555	12	80.0	23458	22	AAH42120	Genomic sequence #	c 628	11	73.3	139	22	AAI23286	Probe #17292 used
c 556	12	80.0	23580	22	AAH28556	Genomic sequence #	c 629	11	73.3	139	22	AAI08927	Probe #8918 used t
c 557	12	80.0	23580	22	AAH87248	Human immune/haema	c 630	11	73.3	139	24	ABS16584	Human genome-deriv
c 558	12	80.0	23677	20	AAH16323	Partial human geno	c 631	11	73.3	150	22	AAK70658	Human immune/haema
c 559	12	80.0	24236	23	ABL16880	Drosophila melanog	c 632	11	73.3	151	22	AAK85943	Human immune/haema
c 560	12	80.0	24593	6	AAH50226	Sequence of opine	c 633	11	73.3	160	24	AAH27054	Plasmid pGN1 DNA f
c 561	12	80.0	24596	6	AAH50182	Complete nucleotid	c 634	11	73.3	161	21	AAH13763	Human secreted pro
c 562	12	80.0	25996	23	ABL28638	Drosophila melanog	c 635	11	73.3	162	21	AAH13766	Human secreted pro
c 563	12	80.0	32012	22	AAH05864	Human reproductive	c 636	11	73.3	164	21	AAH13344	Human secreted pro
c 564	12	80.0	32012	23	ABL98428	Human testicular a	c 637	11	73.3	169	22	AAH86934	Human immune/haema
c 565	12	80.0	32190	22	AAH36709	Human cardiovascular	c 638	11	73.3	170	21	AAH14237	Human secreted pro
c 566	12	80.0	36336	23	ABL08764	Drosophila melanog	c 639	11	73.3	183	21	AAH12186	Human secreted pro
c 567	12	80.0	41335	22	AAH86202	Human immune/haema	c 640	11	73.3	183	24	ABH18469	Human OREF polynuc
c 568	12	80.0	47670	23	ABL16824	Drosophila melanog	c 641	11	73.3	199	22	ABA16948	Human nervous syst
c 569	12	80.0	50368	23	ABL16768	Drosophila melanog	c 642	11	73.3	214	21	AAH13975	Human secreted pro
c 570	12	80.0	62944	24	ABL66947	Lung cancer relate	c 643	11	73.3	228	22	ABA50316	Human breast cell
c 571	12	80.0	62944	24	ABL66947	Kidney cancer rela	c 644	11	73.3	228	22	ABA35269	Probe #13735 for g
c 572	12	80.0	63164	21	AAH63348	Streptomyces globi	c 645	11	73.3	228	22	AAH16638	Human brain expres
c 573	12	80.0	73465	24	AAH88161	Human osteoblast d	c 646	11	73.3	228	22	AAH42397	Human bone marrow
c 574	12	80.0	86080	24	AAH88164	Human osteoblast d	c 647	11	73.3	228	22	AAH08815	Probe #8806 used t
c 575	12	80.0	86080	24	AAH83561	Human cDNA differe	c 648	11	73.3	230	24	AAD27060	Plasmid pGN1 DNA f
c 576	12	80.0	89328	24	ABL61995	Colon adenocarcino	c 649	11	73.3	234	22	ABA70545	Human foetal liver
c 577	12	80.0	97835	24	AAH84796	Human cDNA differe	c 650	11	73.3	234	22	ABA71408	Human foetal liver
c 578	12	80.0	110608	24	AAH83572	Human cDNA differe	c 651	11	73.3	234	22	ABA37148	Probe #15614 for g
c 579	12	80.0	129722	24	AAH88117	Human osteoblast d	c 652	11	73.3	234	22	ABA37629	Probe #16095 for g
c 580	12	80.0	149480	24	ABL61947	Colon adenocarcino	c 653	11	73.3	234	22	AAH18790	Human brain expres
c 581	12	80.0	149480	24	ABL61947	Colon adenocarcino	c 654	11	73.3	234	22	AAH19728	Human brain expres
c 582	12	80.0	149480	24	ABL61948	Colon adenocarcino	c 655	11	73.3	234	22	AAH44727	Human bone marrow
c 583	12	80.0	149480	24	ABL61948	Colon adenocarcino	c 656	11	73.3	234	22	AAH45748	Human bone marrow
c 584	12	80.0	149480	24	ABL68365	Kidney cancer rela	c 657	11	73.3	234	22	AAH24990	Probe #14923 for g
c 585	12	80.0	149480	24	ABL68365	Kidney cancer rela	c 658	11	73.3	234	22	AAH25381	Probe #15314 for g
c 586	12	80.0	167343	24	ABL64403	Stomach cancer rel	c 659	11	73.3	234	22	AAI50705	Probe #19391 used
c 587	12	80.0	167343	24	ABL67239	Thyroid cancer rel	c 660	11	73.3	234	22	AAI51674	Probe #20360 used
c 588	12	80.0	302250	24	ABL67703	Oesophagus cancer	c 661	11	73.3	234	22	ABH18965	Human genome-deriv
c 589	12	80.0	309400	22	AAH68534	C glutamicum codin	c 662	11	73.3	234	24	ABH20026	Human genome-deriv
c 590	12	80.0	309400	22	AAH68534	C glutamicum codin	c 663	11	73.3	243	22	AAH67346	Human immune/haema
c 591	12	80.0	325791	22	AAH43104	Human oestrogen re	c 664	11	73.3	243	22	AAH67348	Human immune/haema
c 592	12	80.0	349980	22	AAH41226	Pyrococcus abyssi	c 665	11	73.3	243	22	AAH67349	Human immune/haema
c 593	12	80.0	349980	22	AAH64966	C glutamicum codin	c 666	11	73.3	245	21	AAH27911	Human secreted pro

c 667	11	73.3	246	24	ABK74699	Bacillus lichenifo	c 740	11	73.3	389	21	AAC00960	Human secreted pro
c 668	11	73.3	248	21	AAA45247	Human secreted exp	c 741	11	73.3	390	22	AAS40332	DNA encoding human
c 669	11	73.3	251	21	AAC04345	Human secreted pro	c 742	11	73.3	390	22	AAQ03932	Human reproductive
c 670	11	73.3	263	22	ABA16947	Human nervous syst	c 743	11	73.3	390	24	ABK39017	cDNA encoding lung
671	11	73.3	267	24	ABN19830	Human OREX polynuc	c 744	11	73.3	391	22	AAI86822	Human polynucleoti
672	11	73.3	269	21	AAA31621	Plant microsatelli	745	11	73.3	393	21	AAC28592	Human secreted pro
673	11	73.3	274	16	AAT20999	Human gene signatu	c 746	11	73.3	393	22	AAS40330	DNA encoding human
674	11	73.3	276	21	AAC03087	Human secreted pro	c 747	11	73.3	393	22	AAQ03930	Human reproductive
675	11	73.3	280	21	AAC23009	Human secreted pro	c 748	11	73.3	393	24	ABK80520	Bacillus clausii g
c 676	11	73.3	283	24	ABL40182	Phanerochaete chry	749	11	73.3	396	22	ABK94968	Human ovarian cnc
c 677	11	73.3	284	21	AAC48086	Zea mays DNA fragm	750	11	73.3	396	22	ABT03235	Human ovarian carc
678	11	73.3	285	23	ABV55515	Human prostate exp	751	11	73.3	396	24	ABL48918	Ovarian carcinoma
679	11	73.3	286	14	AAQ60018	Human brain Expres	c 752	11	73.3	397	21	AAC02453	Novel human polynu
c 680	11	73.3	286	24	ABL73864	Corn tassal-derive	c 753	11	73.3	397	22	ABF65137	Human prostate exp
681	11	73.3	300	20	AAZ14730	Human gene express	754	11	73.3	397	23	ABV35913	Human prostate exp
682	11	73.3	301	24	ABK76169	Bacillus lichenifo	755	11	73.3	397	23	ABV44976	Human transport pr
683	11	73.3	308	22	AAS47033	Human breast cncce	756	11	73.3	405	24	ABN79264	DNA encoding a poi
684	11	73.3	308	22	AAFI7603	Human breast cncce	c 757	11	73.3	409	21	AAA63745	Human cancer agent
685	11	73.3	308	24	ABK95068	Human breast tumou	758	11	73.3	410	22	AAS60195	DNA encoding novel
686	11	73.3	312	22	ABAI8819	Human nervous syst	759	11	73.3	410	23	AAS64312	Novel human polynu
c 687	11	73.3	315	23	ABLI14057	Drosophila melanog	c 760	11	73.3	411	22	ABF64900	Lung cancer associ
c 688	11	73.3	319	24	ABL66236	Lung cancer relat	c 761	11	73.3	416	21	AAFI8000	Human secreted pro
c 689	11	73.3	322	22	AAI82727	Human polynucleoti	762	11	73.3	420	21	AAC01121	Human 5' EST isola
c 690	11	73.3	323	24	ABNI8578	Human OREX polynuc	763	11	73.3	420	21	AAZ42745	Human benign prost
691	11	73.3	324	16	AAT19143	Human gene signatu	c 764	11	73.3	420	24	ABK64308	Human novel protei
c 692	11	73.3	324	17	AAT13728	ACNPV ORF 149, res	765	11	73.3	422	22	ABD16610	DNA encoding novel
c 693	11	73.3	329	24	ABO56111	Human ovarian anti	766	11	73.3	422	23	ABK43938	Human immune/haema
694	11	73.3	330	24	ABN24989	Human OREX polynuc	767	11	73.3	424	22	AAK56301	Human prostate exp
c 695	11	73.3	335	23	ABV47908	Human prostate exp	c 768	11	73.3	424	23	ABV22622	Human prostate exp
c 696	11	73.3	336	20	AAK40691	Human secreted pro	c 769	11	73.3	424	23	ABV28444	Human secreted pro
c 697	11	73.3	338	22	AAS37594	Novel human diagno	770	11	73.3	426	21	AAC12329	Human breast cncce
698	11	73.3	340	20	AAK57202	Porcine Oct-4 exon	771	11	73.3	427	22	AAI20935	Human breast cncce
c 699	11	73.3	342	24	ABN24124	Human OREX polynuc	772	11	73.3	428	22	AAI12050	Human ovarian cnc
700	11	73.3	343	21	AAC36650	Eucalyptus grandis	c 773	11	73.3	428	24	ABL184237	Human prostate exp
701	11	73.3	345	21	AAC36063	Eucalyptus grandis	c 774	11	73.3	429	23	ABV46777	Human prostate exp
702	11	73.3	345	21	AAC56644	M. tuberculosis an	775	11	73.3	435	13	AAV03986	Human immune/haema
703	11	73.3	348	20	AAZ19425	M. tuberculosis re	c 776	11	73.3	438	22	AAK55779	M. capsulatus gene
704	11	73.3	348	20	AAZ19213	Human immune/haema	777	11	73.3	438	24	ABQ90685	Human prostate exp
705	11	73.3	349	22	AAK68365	Human immune/haema	c 778	11	73.3	439	23	ABV13206	Human prostate exp
706	11	73.3	349	22	AAK82408	Human prostate exp	779	11	73.3	441	22	ABA42616	Human foetal liver
707	11	73.3	349	23	ABV15112	Streptomyces sp. c	780	11	73.3	441	22	ABA53045	Probe #1285 for ge
708	11	73.3	350	24	ABN88915	Human polynucleoti	781	11	73.3	441	22	ABA22819	Human brain expres
c 709	11	73.3	351	22	AAI89605	Human nervous syst	782	11	73.3	441	22	AAK01293	Human bone marrow
710	11	73.3	354	22	ABAI9471	Human secreted pro	783	11	73.3	441	22	AAK26753	Probe #1314 for ge
711	11	73.3	358	21	AAC22938	Human secreted pro	784	11	73.3	441	22	AAI11381	Probe #1335 used t
c 712	11	73.3	358	22	AAK78857	Human immune/haema	785	11	73.3	441	22	AAI32649	Probe #1288 used t
c 713	11	73.3	358	22	AAK78858	Human immune/haema	786	11	73.3	441	22	AAI01297	Bacillus DNA encod
c 714	11	73.3	360	21	AAZ50397	Human interferon-i	c 787	11	73.3	441	24	ABK92846	Human genome-deriv
715	11	73.3	361	13	AAQ27208	PDGF-B7, Syntheti	788	11	73.3	441	24	ABS01348	Human ovarian cnc
716	11	73.3	361	20	AAK41031	Human secreted pro	789	11	73.3	441	24	ABL83271	DNA encoding novel
717	11	73.3	362	22	ABA45180	Human breast cell	790	11	73.3	442	23	AAS68611	Human cancer relat
718	11	73.3	362	22	ABA23357	Probe #3823 for ge	791	11	73.3	442	24	ABN64468	Human cancer relat
719	11	73.3	362	22	ABA03648	Human bone marrow	792	11	73.3	443	24	ABN62530	Fusarium venenatum
720	11	73.3	362	22	AAK03688	Human brain expres	c 793	11	73.3	446	21	AAF08137	Human polynucleoti
721	11	73.3	362	22	AAK29357	Human bone marrow	c 794	11	73.3	447	22	AAI93786	Human cancer agent
722	11	73.3	362	22	AAI03812	Probe #3803 used t	795	11	73.3	450	22	AAS60194	Fusarium venenatum
c 723	11	73.3	369	22	AAK59183	Human cancer relat	796	11	73.3	451	21	AAF08070	Human prostate exp
724	11	73.3	370	22	ABA45307	Human breast cell	c 797	11	73.3	451	23	ABV04037	DNA encoding nove
725	11	73.3	370	22	ABA55796	Human foetal liver	798	11	73.3	454	22	AAK41644	Human OREX ORF531
726	11	73.3	370	22	ABA25477	Probe #3943 for ge	c 799	11	73.3	456	21	AAK74976	Human prostate exp
727	11	73.3	370	22	ABA04017	Human brain expres	c 800	11	73.3	458	23	ABV34325	Human prostate exp
728	11	73.3	370	22	AAK29504	Human bone marrow	c 801	11	73.3	458	23	ABV43186	Human genome-deriv
729	11	73.3	370	22	AAI14074	Probe #4007 for ge	802	11	73.3	458	24	ABV23895	Human prostate exp
730	11	73.3	370	22	AAI35454	Probe #4140 used t	c 803	11	73.3	459	23	ABV52949	Human cancer relat
731	11	73.3	370	22	AAI03927	Probe #3918 used t	c 804	11	73.3	459	24	ABN65832	Human brain expres
732	11	73.3	370	22	ABS04052	Human genome-deriv	c 805	11	73.3	461	22	AAK01575	Human immune/haema
c 733	11	73.3	373	22	AAS59182	Human cancer relat	c 806	11	73.3	461	22	AAK61455	Human prostate exp
c 734	11	73.3	375	22	ABAI1654	Human nervous syst	c 807	11	73.3	461	22	AAI01547	Probe #1538 used t
735	11	73.3	379	22	AAK60648	Human cancer agent	c 808	11	73.3	461	23	ABV09422	Human prostate exp
c 736	11	73.3	381	21	AAK97347	Helicobacter pylor	c 809	11	73.3	462	20	AAV84302	Wheat geminivirus
c 737	11	73.3	383	22	AAF64677	Novel human polynu	810	11	73.3	462	23	AAK74211	DNA encoding novel
c 738	11	73.3	384	22	AAI91239	Human polynucleoti	c 811	11	73.3	464	22	AAH99201	Human protein enco
c 739	11	73.3	386	22	AAF64412	Novel human polynu	c 812	11	73.3	467	24	ABL87387	Human ovarian cnc

c 813	11	73.3	470	21	AAC53876	Arabidopsis thalia	886	11	73.3	547	24	ABQ19219	Oligonucleotide fo
814	11	73.3	471	22	ABA57882	Human foetal liver	c 887	11	73.3	550	23	ABV57531	Human prostate exp
815	11	73.3	471	22	ABA27213	Probe #5679 for ge	c 888	11	73.3	552	24	ABQ16336	Oligonucleotide fo
816	11	73.3	471	22	AKO05955	Human brain expres	c 889	11	73.3	552	24	ABQ16337	Oligonucleotide fo
817	11	73.3	471	22	AAK31596	Human bone marrow	c 890	11	73.3	553	22	ABA63348	Human foetal liver
818	11	73.3	471	22	AAI15744	Probe #5677 for ge	c 891	11	73.3	553	22	ABA30552	Probe #9018 for ge
819	11	73.3	471	22	AAI37475	Probe #6161 used t	c 892	11	73.3	553	22	AAK37590	Human bone marrow
820	11	73.3	471	24	ABQ06350	Human genome-deriv	c 893	11	73.3	553	22	AAI18347	Probe #8280 for ge
821	11	73.3	474	24	ABQ91381	M. capsulatus gene	c 894	11	73.3	553	22	AAI43462	Probe #12148 used
822	11	73.3	474	24	ABI99634	Mouse ischaemic co	c 895	11	73.3	553	22	AAI1576	Human genome-deriv
c 823	11	73.3	476	22	AAI93440	Human polynucleoti	c 896	11	73.3	555	21	AAK39473	Human RBP 11 DNA.
824	11	73.3	478	24	ABM94180	Gene #678 used to	c 897	11	73.3	555	24	ABQ56320	Human colon cancer
825	11	73.3	478	24	ABL63371	Breast cancer rela	c 898	11	73.3	559	22	ABA60540	Human foetal liver
826	11	73.3	478	24	ABL63783	Breast cancer rela	c 899	11	73.3	559	22	AAK08821	Human brain expres
c 827	11	73.3	479	21	AAQ41321	Zea mays DNA fragm	c 900	11	73.3	559	22	AAK34708	Human bone marrow
c 828	11	73.3	480	20	AAK24459	Human SR-BI gene e	c 901	11	73.3	559	22	AAI40429	Probe #9115 used t
c 829	11	73.3	480	20	AAK24591	Human SR-BI gene e	c 902	11	73.3	560	24	ABQ34672	Oligonucleotide fo
c 830	11	73.3	483	22	AAI86667	Human polynucleoti	c 903	11	73.3	560	24	ABQ34673	Oligonucleotide fo
c 831	11	73.3	483	22	AAK30682	Human bone marrow	c 904	11	73.3	561	21	AAK76986	Human ORFX ORF2541
c 832	11	73.3	483	24	ABL91792	Human polynucleoti	c 905	11	73.3	562	23	ABV59302	Human prostate exp
c 833	11	73.3	484	23	ABV00253	Human prostate exp	c 906	11	73.3	568	21	AAK76527	Human ORFX ORF2082
c 834	11	73.3	484	22	ABA20246	Human nervous syst	c 907	11	73.3	572	21	AAK10180	Fusarium venenatum
c 835	11	73.3	488	22	AAI10200	Human breast cance	c 908	11	73.3	572	22	AAH13292	Human CDNA clone (
c 836	11	73.3	488	22	AAI19780	Human breast cance	c 909	11	73.3	573	23	ABV16982	Human prostate exp
c 837	11	73.3	488	22	AAI181857	Human polynucleoti	c 910	11	73.3	574	22	ABA88607	Escherichia coli p
c 838	11	73.3	489	22	ABA43763	Human breast cell	c 911	11	73.3	575	22	ABA61146	Human foetal liver
c 839	11	73.3	489	22	ABA54220	Human foetal liver	c 912	11	73.3	575	22	AAK09441	Human brain expres
c 840	11	73.3	489	22	ABA57936	Human foetal liver	c 913	11	73.3	575	22	AAK35333	Human bone marrow
c 841	11	73.3	489	22	ABA23968	Probe #2434 for ge	c 914	11	73.3	575	22	AAI41046	Probe #9732 used t
c 842	11	73.3	489	22	ABA27240	Probe #5706 for ge	c 915	11	73.3	575	22	AAH09628	Human CDNA clone (
c 843	11	73.3	489	22	AAK02497	Human brain expres	c 916	11	73.3	577	24	ABQ46256	Oligonucleotide fo
c 844	11	73.3	489	22	AAK06009	Human brain expres	c 917	11	73.3	577	24	ABQ46257	Oligonucleotide fo
c 845	11	73.3	489	22	AAK31653	Human bone marrow	c 918	11	73.3	578	24	ABQ38468	Oligonucleotide fo
c 846	11	73.3	489	22	AAI15771	Probe #5704 for ge	c 919	11	73.3	578	24	ABQ38469	Oligonucleotide fo
c 847	11	73.3	489	22	AAI37530	Probe #6216 used t	c 920	11	73.3	581	24	ABQ46608	Oligonucleotide fo
c 848	11	73.3	489	22	AAI02422	Probe #2413 used t	c 921	11	73.3	581	24	ABQ46609	Oligonucleotide fo
c 849	11	73.3	489	24	ABQ02394	Human genome-deriv	c 922	11	73.3	582	24	AAK42487	Human CDNA encodin
c 850	11	73.3	489	24	ABQ06408	Human genome-deriv	c 923	11	73.3	582	24	ABQ49072	Oligonucleotide fo
c 851	11	73.3	494	24	ABQ060169	Human colon cancer	c 924	11	73.3	582	24	ABQ49073	Oligonucleotide fo
852	11	73.3	500	24	ABQ73194	C. glutanicum tran	c 925	11	73.3	584	24	ABQ25760	Oligonucleotide fo
c 853	11	73.3	502	21	ABQ79486	Human lung tumour-	c 926	11	73.3	584	24	ABQ25761	Oligonucleotide fo
c 854	11	73.3	502	23	AAI23362	Human lung tumour-	c 927	11	73.3	588	21	AAK09369	Fusarium venenatum
c 855	11	73.3	507	22	ABA60120	Human foetal liver	c 928	11	73.3	590	22	AAI15299	Human breast cance
c 856	11	73.3	507	22	ABA28478	Probe #6944 for ge	c 929	11	73.3	595	22	AAK08504	Human secreted pro
c 857	11	73.3	507	22	AAK08396	Human brain expres	c 930	11	73.3	599	23	AAK83950	DNA encoding novel
c 858	11	73.3	507	22	AAK34276	Human bone marrow	c 931	11	73.3	606	23	ABK50586	Human prostate exp
c 859	11	73.3	507	22	AAI39999	Probe #8685 used t	c 932	11	73.3	607	24	ABK83886	Human CDNA differe
c 860	11	73.3	507	24	ABQ09003	Human genome-deriv	c 933	11	73.3	612	21	AAK07825	Fusarium venenatum
c 861	11	73.3	507	24	ABQ56838	Human colon cancer	c 934	11	73.3	612	21	AAK077160	Human ORFX ORF2715
c 862	11	73.3	508	22	ABA13728	Human nervous syst	c 935	11	73.3	612	22	AAK08528	Human secreted pro
863	11	73.3	508	22	AAK62580	Human immune/haema	c 936	11	73.3	617	22	AAK82842	Human immune/haema
864	11	73.3	508	24	ABL79848	Human ovarian canc	c 937	11	73.3	617	22	AAK82843	Human immune/haema
865	11	73.3	510	22	AAK60609	Human cancer agent	c 938	11	73.3	618	23	AAK84878	DNA encoding novel
866	11	73.3	510	22	AAK92676	Human CDNA 3'-end	c 939	11	73.3	619	24	ABN61608	Human cancer relat
867	11	73.3	514	13	AAQ27204	Synthetic PDGF-B g	c 940	11	73.3	625	22	ABA08653	Human zn finger pr
868	11	73.3	514	13	AAQ27205	Synthetic PDGF-B g	c 941	11	73.3	625	22	ABQ41922	Oligonucleotide fo
c 869	11	73.3	515	24	ABQ44524	Oligonucleotide fo	c 942	11	73.3	625	24	ABQ41923	Oligonucleotide fo
c 870	11	73.3	515	24	ABQ44525	Oligonucleotide fo	c 943	11	73.3	625	24	ABQ47864	Oligonucleotide fo
871	11	73.3	516	24	ABN62480	Human cancer relat	c 944	11	73.3	625	24	ABQ47865	Oligonucleotide fo
c 872	11	73.3	519	22	AAK85226	Nucleotide sequenc	c 945	11	73.3	627	23	AAK87080	DNA encoding novel
c 873	11	73.3	519	22	AAH29605	Drosophila melanog	c 946	11	73.3	629	23	AAK81635	N. meningitidis pa
874	11	73.3	520	24	ABK54836	Human colon cancer	c 947	11	73.3	633	23	ABL04069	Drosophila melanog
c 875	11	73.3	528	24	ABL87359	Human ovarian canc	c 948	11	73.3	634	24	ABQ57032	Human colon cancer
c 876	11	73.3	538	24	ABN59715	Novel human coding	c 949	11	73.3	638	21	AAI14136	Aspergillus oryzae
c 877	11	73.3	539	22	AAH11837	Human CDNA clone (c 950	11	73.3	639	22	AAH65877	c glutamicum codin
878	11	73.3	540	22	AAH10637	Human CDNA clone (c 951	11	73.3	641	24	ABQ33134	Oligonucleotide fo
c 879	11	73.3	541	23	ABV52199	Human prostate exp	c 952	11	73.3	641	24	ABQ33135	Oligonucleotide fo
880	11	73.3	543	24	ABV511537	Human genome-deriv	c 953	11	73.3	646	24	ABQ42450	Oligonucleotide fo
881	11	73.3	544	19	AAV69687	Human glial cell l	c 954	11	73.3	646	24	ABQ42451	Oligonucleotide fo
c 882	11	73.3	546	23	ABV30598	Human prostate exp	c 955	11	73.3	647	22	AAH07347	Human CDNA clone (
c 883	11	73.3	546	23	ABV39567	Human prostate exp	c 956	11	73.3	650	24	ABK36109	cDNA sequence #500
c 884	11	73.3	546	24	ABK63776	Rat sequence diffe	c 957	11	73.3	654	24	ABQ44552	Oligonucleotide fo
c 885	11	73.3	547	24	ABQ19218	Oligonucleotide fo	c 958	11	73.3	654	24	ABQ44553	Oligonucleotide fo

c 959 11 73.3 656 24 ABQ22194
c 960 11 73.3 656 24 ABQ22195
c 961 11 73.3 659 24 AAS62648
c 962 11 73.3 661 22 AAL24145
c 963 11 73.3 662 13 AAQ32354
c 964 11 73.3 662 15 AAQ72479
c 965 11 73.3 662 20 AAX84115
c 966 11 73.3 669 24 ABQ41786
c 967 11 73.3 669 24 ABQ41787
c 968 11 73.3 671 24 ABN73729
c 969 11 73.3 673 19 AAV42305
c 970 11 73.3 673 22 AAF25492
c 971 11 73.3 690 24 ABQ21698
c 972 11 73.3 690 24 ABQ21699
c 973 11 73.3 692 22 AAH04686
c 974 11 73.3 693 17 AAT08703
c 975 11 73.3 697 21 AAC03865
c 976 11 73.3 705 24 ABQ36860
c 977 11 73.3 705 24 ABQ36861
c 978 11 73.3 707 22 AAK58487
c 979 11 73.3 711 20 AAX34231
c 980 11 73.3 714 21 AAF13004
c 981 11 73.3 714 22 AAH98816
c 982 11 73.3 720 22 AAK91837
c 983 11 73.3 720 22 AAK93239
c 984 11 73.3 720 24 ABK77214
c 985 11 73.3 724 24 ABQ88914
c 986 11 73.3 724 24 RAD31158
c 987 11 73.3 724 24 ABQ43744
c 988 11 73.3 724 24 ABQ43745
c 989 11 73.3 725 24 ABK34436
c 990 11 73.3 730 24 ABN87190
c 991 11 73.3 736 21 AAF21773
c 992 11 73.3 738 24 ABQ43318
c 993 11 73.3 738 24 ABQ43319
c 994 11 73.3 739 20 AAZ24832
c 995 11 73.3 739 22 AAF44795
c 996 11 73.3 740 24 ABQ41086
c 997 11 73.3 740 24 ABQ41087
c 998 11 73.3 741 21 AAC03863
c 999 11 73.3 741 22 AAH68357
c1000 11 73.3 747 24 ABQ25166

ALIGNMENTS

RESULT 1
AAH28084 standard; DNA; 15 BP.
XX
AC AAH28084;
XX
DT 05-SEP-2001 (first entry)
XX
DE Probe for human norepinephrine transporter gene wild type allele.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.

Oligonucleotide fo
Oligonucleotide fo
cDNA sequence #435
Human breast cance
MAGE-21 gene. Hom
Tumour rejection a
MAGE-21 gene. Hom
Oligonucleotide fo
Oligonucleotide fo
Bovine embryonic g
HCV core protein c
Nucleotide sequenc
Oligonucleotide fo
Oligonucleotide fo
Human cDNA clone (
Partial human OCT-
Human secreted pro
Oligonucleotide fo
Oligonucleotide fo
Human immune/haema
Mycobacterium spec
Aspergillus oryzae
Human EST-derived
Human cDNA 5'-end
Human cDNA clone r
Bacillus clausii g
Human prostate exp
Human Alzheimer's
Oligonucleotide fo
Oligonucleotide fo
Human cDNA for nov
Lolium perenne LpO
Human breast and o
Oligonucleotide fo
Oligonucleotide fo
Human secreted pro
Cysteine protease
Oligonucleotide fo
Oligonucleotide fo
Human secreted pro
C. glutamicum codin
Oligonucleotide fo

XX Robertson D, Blakely RD;
PI
XX WPI; 2001-425681/45.
DR
XX
XX Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
XX Claim 15; Page 69; 133pp; English.
PS
XX The present sequence represents a probe for the wild type allele of
CC a human norepinephrine transporter gene. The specification a method
CC for screening for susceptibility to sub-optimal norepinephrine transport
CC in a subject. The method comprises obtaining a biological sample from
CC the subject and detecting a polymorphism of a norepinephrine transporter
CC gene in the sample from the subject, the presence of the polymorphism
CC indicating the susceptibility of the subject to sub-optimal
CC norepinephrine transport. The method is useful for screening for
CC susceptibility of a subject to orthostatic intolerance. Norepinephrine
CC transporter genes are useful for gene therapy for modulating
CC norepinephrine transport in a target cell and treating susceptibility
CC to impaired norepinephrine transporter function, orthostatic intolerance
CC or other relevant diseases in humans and animals such as mental illness,
CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
CC amphetamine abuse.
XX
SQ Sequence 15 BP; 0 A; 7 C; 2 G; 6 T; 0 other;
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCTGTT 15
Db | | | | | | | | | | | | | | | |
1 CCTTCTCGCCTGTT 15
RESULT 2
AAH88259
ID AAH88259 standard; DNA; 920 BP.
XX
XX AAH88259;
XX
DT 26-FEB-2002 (first entry)
XX
DE CNS disorder-related biallelic marker #10 from NET gene.
XX
KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;
KW central nervous system disorder; CNS; NET; norepinephrine transporter.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 95
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200151659-A2.
XX
PD 19-JUL-2001.
XX
XX 11-JAN-2001; 2001WO-IB00116.
XX
XX 13-JAN-2000; 2000US-0175854.
XX
XX (GEST) GENSET.
XX
PI Chu T, Blumenfeld M, Cohen D;
XX
DR WPI; 2001-483085/52.
XX
PT Isolated polynucleotides, useful for genotyping nucleic acids for

PT biallelic markers for the diagnosis of depression, comprises central
XX nervous system disorder related biallelic marker -
XX
PS Claim 1; Page 248; 519pp; English.
XX
CC The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders. The present
CC sequence is one such biallelic marker derived from human norepinephrine
CC transporter (NET) gene. This marker has a single nucleotide polymorphism
CC (SNP) and is useful in determining the genetic predisposition of
CC individuals to CNS disorders, by identifying the nucleotides at a set of
CC genetic markers in a biological sample, where the markers comprise at
CC least one CNS disorder related marker.
XX
SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;

Query Match 100.0%; Score 15; DB 23; Length 920;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
IIIIIIIIIIIIIIII
Db 170 CCTTCTCGCCCTGTT 184

RESULT 3
AAH88264
ID AAH88264 standard; DNA; 920 BP.
XX
AC AAH88264;
XX
DT 26-FEB-2002 (first entry)
XX
DE CNS disorder-related biallelic marker #15 from NET gene.
XX
KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;
KW central nervous system disorder; CNS; NET; norepinephrine transporter.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 206
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200151659-A2.
XX
PD 19-JUL-2001.
XX
PF 11-JAN-2001; 2001WO-IB00116.
XX
PR 13-JAN-2000; 2000US-0175854.
XX
PA (GEST) GENSET.
XX
PI Chu T, Blumenfeld M, Cohen D;
XX
DR WPI; 2001-483085/52.
XX
PT Isolated polynucleotides, useful for genotyping nucleic acids for
PT biallelic markers for the diagnosis of depression, comprises central
PT nervous system disorder related biallelic marker -
XX
PS Claim 1; Pages 251-252; 519pp; English.
XX
CC The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders. The present
CC sequence is one such biallelic marker derived from human norepinephrine
CC transporter (NET) gene. This marker has a single nucleotide polymorphism
CC (SNP) and is useful in determining the genetic predisposition of
CC individuals to CNS disorders, by identifying the nucleotides at a set of
CC genetic markers in a biological sample, where the markers comprise at
CC least one CNS disorder related marker.

XX
SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;

Query Match 100.0%; Score 15; DB 23; Length 920;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
IIIIIIIIIIIIIIII
Db 170 CCTTCTCGCCCTGTT 184

RESULT 4
AAH28088
ID AAH28088 standard; DNA; 980 BP.
XX
AC AAH28088;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a exon 9 of norepinephrine transporter gene.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 129..257
FT /*tag= a
FT intron 257..700
FT /*tag= b
FT exon 701..802
FT /*tag= c
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
PS Disclosure; Page 125; 133pp; English.
XX
CC The present sequence represents exon 9 of the human norepinephrine
CC transporter gene. The specification a method for screening for
CC susceptibility to sub-optimal norepinephrine (NE) transport in a
CC subject. The method comprises obtaining a biological sample from the
CC subject and detecting a polymorphism of a norepinephrine transporter
CC gene in the sample from the subject, the presence of the polymorphism
CC indicating the susceptibility of the subject to sub-optimal
CC norepinephrine transport. The method is useful for screening for
CC susceptibility of a subject to orthostatic intolerance. Norepinephrine
CC transporter genes are useful for gene therapy for modulating
CC norepinephrine transport in a target cell and treating susceptibility
CC to impaired norepinephrine transporter function, orthostatic intolerance
CC or other relevant diseases in humans and animals such as mental illness,
CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
CC amphetamine abuse.
XX

SQ Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 238 T; 3 other;

Query Match 100.0%; Score 15; DB 22; Length 980;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 230 CCTTCTCGCCCTGTT 244

RESULT 5
AAS80746/c
ID AAS80746 standard; cDNA; 1044 BP.

XX AC AAS80746;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #16550.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX FN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
DR P-PSDB; ABG16559.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID No 16550; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS84197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 1044;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 97 CCTTCTCGCCCTGTT 83

RESULT 6
AAH28082
ID AAH28082 standard; DNA; 1854 BP.

XX AC AAH28082;
XX DT 05-SEP-2001 (first entry)
XX DE Nucleotide sequence of a human norepinephrine transporter.
XX KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX OS Homo sapiens.
XX FN Key Location/Qualifiers
FT 1..1854
FT CDS /*tag= a
FT /*product= "norepinephrine transporter"
XX PN WO200148246-A1.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US35491.
XX PR 29-DEC-1999; 99US-0173682.
XX PR 11-JAN-2000; 2000US-0175456.
XX PA (UYVA-) UNIV VANDERBILT.
XX PI Robertson D, Blakely RD;
XX DR WPI; 2001-425681/45.
DR P-PSDB; AAB84532.
XX
XX Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
XX Claim 75; Page 98-101; 133pp; English.

CC The present sequence encodes a human norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
XX Sequence 1854 BP; 356 A; 554 C; 494 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 CCTTCTCGCCCTGTT 15
Db 1362 CCTTCTCGCCCTGTT 1376

RESULT 7
AAH28086
ID AAH28086 standard; DNA; 1854 BP.
XX
AC
XX AAH28086;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a human norepinephrine transporter.
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1854
FT /*tag= a
FT /product= "norepinephrine transporter"
XX
PN WO200148246-A1.
XX
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI: 2001-425681/45.
DR P-PSDB; AAB84534.
XX
XX Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene
XX
PS Claim 75; Page 112-115; 133pp; English.
XX
XX The present sequence encodes a human norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 357 A; 553 C; 494 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCGCCCTGTT 15
Db 1362 CCTTCTCGCCCTGTT 1376
```

```
RESULT 8
AAQ28118
ID AAQ28118 standard; cDNA; 1983 BP.
XX
AC AAQ28118;
XX
DT 15-MAR-1993 (first entry)
XX
DE Human norepinephrine transporter protein cDNA clone.
XX
KW NT; noradrenaline; neuroblastoma; neurotransmitter; antidepressant;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..1914
FT /*tag= a
XX
PN WO9217568-A.
XX
PD 15-OCT-1992.
XX
PF 20-FEB-1992; 92WO-US01376.
XX
PR 28-MAR-1991; 91US-0676980.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Amara SG, Blakely RD, Pacholczyk T;
XX
DR WPI: 1992-366242/44.
DR P-PSDB; AAR26416.
XX
XX Complementary DNA clone encoding human norepinephrine transporter
PT protein - isolated from human neuroblastoma cells and useful for
PT determining action of e.g. antidepressant drugs
XX
PS Claim 3; Fig 1; 37pp; English.
XX
XX Pools of clones from a human SK-N-SH cell (a human neuroblastoma
CC cell line) cDNA library were transfected into COS-1 cells. The
CC transfected clones were in the form of expression vectors (pXM)
CC having an SV-40 replication origin to enable amplification.
CC Transfectants of these cells expressing the norepinephrine
CC transporter were identified by employing an assay exploiting the
CC fact that the norepinephrine analogue m-iodobenzylguanidine (m-IBG)
CC is accumulated intracellularly by SK-N-SH cells expressing the
CC intact NT. The accumulated radiolabelled m-IBG allows direct
CC autoradiographic visualisation of transporter expressing
CC transfectants. DNA was rescued from positive colonies and the
CC resulting plasmid pools rescreened and subdivided until a single
CC clone was obtd. Transfected cells become capable of norepinephrine
CC uptake, which may be inhibited by various drugs, e.g. cocaine, to
CC a degree similar to the effect of such drugs on noradrenergic
CC neurons. The cloned cDNA makes possible well-controlled studies
CC of neurotransmitter transporter function in non-neuronal cells
CC without the abfuscating influence of other transporters in the
CC same cell. Such studies include the relative effects of various
CC (psychotropic) drugs such as antidepressants.
XX
SQ Sequence 1983 BP; 384 A; 602 C; 529 G; 468 T; 0 other;

Query Match 100.0%; Score 15; DB 13; Length 1983;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCGCCCTGTT 15
Db 1422 CCTTCTCGCCCTGTT 1436
```

RESULT 9
ABK8362/c
ID ABK8362 standard; cDNA; 5161 BP.
XX
AC ABK8362;
DT
XX 14-AUG-2002 (first entry)
DE Human cDNA differentially expressed in granulocytic cells #433.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
XX WO200228999-A2.
PN
XX
PD
XX
XX 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
XX 03-OCT-2000; 2000US-237189P.
PR
XX
PA (GENE-) GENE LOGIC INC.
XX
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
DR
XX WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 433; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection, and M5 is
CC useful for treating one of the above conditions. The present

CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;
Query Match 100.0%; Score 15; DB 24; Length 5161;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 2673 CCTTCTCGCCCTGTT 2659
|||||
RESULT 10
AAH88704
ID AAH88704 standard; DNA; 160755 BP.
XX
AC AAH88704;
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Human DNA sequence SEQ ID 544.
DE
XX
KW Single nucleotide polymorphism; SNP; biallelic marker; human;
KW central nervous system disorder; CNS; ds.
XX
OS Homo sapiens.
XX
XX WO200151659-A2.
PN
XX
PD 19-JUL-2001.
XX
XX 11-JAN-2001; 2001WO-IB00116.
PF
XX
XX 13-JAN-2000; 2000US-0175854.
PR
XX
XX (GEST) GENSET.
XX
XX Chu T, Blumenfeld M, Cohen D;
PI
XX WPI; 2001-483085/52.
DR
XX Isolated polynucleotides, useful for genotyping nucleic acids for
PT biallelic markers for the diagnosis of depression, comprises central
PT nervous system disorder related biallelic marker -
XX
PS Disclosure; Page 476-519; 519pp; English.
XX
XX The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders (see
CC AAH88161-AAH88702). The markers have a single nucleotide polymorphism
CC (SNP) and are useful in determining the genetic predisposition of
CC individuals to CNS disorders, by identifying the nucleotides at a set of
CC genetic markers in a biological sample, where the markers comprise at
CC least one CNS disorder related marker. The present sequence was used
CC to illustrate the invention.
XX
SQ Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;
Query Match 100.0%; Score 15; DB 23; Length 160755;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 63345 CCTTCTCGCCCTGTT 63359
|||||
RESULT 11

ABN18096
ID ABN18096 standard; cDNA; 336 BP.
AC ABN18096;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX polynucleotide sequence SEQ ID NO:4669.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US10836.
XX
PR 30-MAY-2000; 2000US-206132P.
PR 29-AUG-2000; 2000US-228716P.
XX
XX (CURA-) CURAGEN CORP.
PA
PI Shimkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
DR P-PSDB; ABP02344.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders
XX
XX Disclosure; SEQ ID 4669; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;

Query Match 93.3%; Score 14; DB 24; Length 336;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15
|||||
Db 82 CTTCTCGCCCTGTT 95
RESULT 12
ABQ56203/c
ID ABQ56203 standard; cDNA; 655 BP.
XX
AC ABQ56203;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HVVAV26 cDNA, SEQ ID NO:2083.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR P-PSDB; ABP43126.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases
XX
PS Claim 1; SEQ ID NO 2083; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 655 BP; 182 A; 168 C; 177 G; 116 T; 12 other;

Query Match 93.3%; Score 14; DB 24; Length 655;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTCTCGCCCTGTT 15
DB 556 CCTCTCGCCCTGTT 543
|||||

RESULT 13
AAH65499/c
ID AAH65499 standard; DNA; 708 BP.
XX
AC AAH65499;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 534.
XX
KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG90280.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
PS Claim 8; SEQ ID NO: 534; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.

XX
SQ Sequence 708 BP; 152 A; 212 C; 196 G; 148 T; 0 other;

Query Match 93.3%; Score 14; DB 22; Length 708;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGT 14
DB 250 CCTTCTCGCCCTGT 237
|||||

RESULT 14
ABL11823/c
ID ABL11823 standard; cDNA; 2036 BP.
XX
AC ABL11823;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29951.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB67720.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 29951; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2036 BP; 552 A; 513 C; 553 G; 418 T; 0 other;

Query Match 93.3%; Score 14; DB 23; Length 2036;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGT 14
DB 326 CCTTCTCGCCCTGT 313
|||||

RESULT 15

AAQ14533
ID AAQ14533 standard; DNA; 2397 BP.
XX
AC AAQ14533;
XX
DT 29-JAN-1992 (first entry)
XX
DE Tea gene (cDNA 20.5).
XX
KW Multiple membrane spanning protein; T cell; development; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 410..1767
FT /*tag= a
XX
PN W09116430-A.
XX
PD 31-OCT-1991.
XX
PF 12-APR-1990; 90WO-U002518.
XX
PR 13-APR-1990; 90US-0509684.
XX
PA (REDE-) RES DEV FOUND.
XX
PI Macleod CL;
XX
WPI; 1991-339818/46.
DR P-PSDB; AAR14645.
XX
PT New recombinant polypeptide comprising a T-cell protein - used to
PT regulate T-cell development and tumorigenic phenotype and to
PT block T-cell activation in auto-immune disease
XX
PS Disclosure; Fig 13; 98pp; English.
XX
CC The 23 Ns in the sequence represent bases illegible in the
CC specification.
CC The 20.5 gene, also referred to as Tea, identifies transcripts
CC found in only a limited number of tissues. Tea transcripts are
CC induced in splenocytes activated with the T cell mitogen ConA.
CC Unlike other known genes expressed in activated T cells, the Tea gene
CC appears to encode a protein which traverses the membrane multiple times,
CC whereas the large number of known integral membrane protein which are
CC induced in T cell activation are single membrane spanning proteins.
CC See also AAQ14530-34.
XX
SQ Sequence 2397 BP; 541 A; 570 C; 579 G; 684 T; 23 other;
Query Match 93.3%; Score 14; DB 12; Length 2397;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTCTCGCCCTGTT 15
| | | | | | | | | |
Db 1379 CTTCTCGCCCTGTT 1392

Search completed: December 11, 2002, 17:09:29
Job time : 262 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-750-609-9

Perfect score: 15

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	14	93.3	2397	1 US-08-002-999-5	Sequence 5, Appli
3	14	93.3	2397	2 US-08-132-990A-5	Sequence 5, Appli
4	14	93.3	2397	5 PCT-US92-09382-5	Sequence 5, Appli
5	13	86.7	485	4 US-09-400-208B-22	Sequence 22, Appl
6	13	86.7	491	4 US-09-400-208B-23	Sequence 23, Appl
7	13	86.7	497	4 US-09-400-208B-24	Sequence 24, Appl
8	13	86.7	2001	4 US-09-400-208B-4	Sequence 4, Appli
9	13	86.7	2023	4 US-09-491-522-6	Sequence 6, Appli
10	13	86.7	2450	4 US-09-491-522-2	Sequence 2, Appli
11	13	86.7	3240	4 US-09-171-337A-4	Sequence 4, Appli
12	13	86.7	3748	1 US-08-261-206A-76	Sequence 76, Appl
13	13	86.7	4657	3 US-09-254-325-1	Sequence 1, Appli
14	13	86.7	6692	4 US-09-491-522-1	Sequence 1, Appli
15	13	86.7	9785	1 US-08-319-387-1	Sequence 1, Appli
16	13	86.7	35100	1 US-08-306-691B-19	Sequence 19, Appl
17	13	86.7	35100	5 PCT-US93-06251-19	Sequence 19, Appl
18	12	80.0	257	3 US-08-906-791-4	Sequence 4, Appli
19	12	80.0	358	1 US-07-925-920-1	Sequence 1, Appli
20	12	80.0	447	4 US-09-018-584A-17	Sequence 17, Appl
21	12	80.0	476	4 US-09-625-188-15	Sequence 15, Appl
22	12	80.0	576	4 US-09-249-180-7	Sequence 7, Appli
23	12	80.0	657	4 US-09-249-180-4	Sequence 4, Appli
24	12	80.0	829	4 US-09-230-665-7	Sequence 7, Appli
25	12	80.0	984	4 US-09-527-522-2	Sequence 2, Appli
26	12	80.0	1020	4 US-09-249-180-1	Sequence 1, Appli
27	12	80.0	1161	3 US-09-058-489-26	Sequence 26, Appl

1163	4	80.0	1163	4	US-09-249-180-5	Sequence 5, Appli
1173	6	80.0	1173	6	5248670-6	Patent No. 5248670
1292	1	80.0	1292	1	US-08-503-133A-7	Sequence 7, Appli
1292	2	80.0	1292	2	US-08-576-775A-7	Sequence 7, Appli
1292	3	80.0	1292	3	US-08-972-498-7	Sequence 7, Appli
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1473	1	80.0	1473	1	US-08-090-013-3	Sequence 3, Appli
1473	1	80.0	1473	1	US-08-081-328-3	Sequence 3, Appli
1473	1	80.0	1473	1	US-08-232-249-3	Sequence 3, Appli
1473	1	80.0	1473	1	US-08-833-642A-3	Sequence 3, Appli
1473	2	80.0	1473	2	US-08-389-423-3	Sequence 3, Appli
1473	4	80.0	1473	4	US-09-230-665-3	Sequence 3, Appli
1473	4	80.0	1473	4	US-09-189-028-3	Sequence 3, Appli
1524	4	80.0	1524	4	US-09-111-730-4	Sequence 4, Appli
2310	2	80.0	2310	2	US-08-476-062A-41	Sequence 41, Appli
2310	5	80.0	2310	5	PCT-US96-01314-41	Sequence 41, Appli
2376	1	80.0	2376	1	US-08-394-880B-1	Sequence 1, Appli
2409	4	80.0	2409	4	US-09-293-322C-8	Sequence 8, Appli
2469	4	80.0	2469	4	US-09-111-730-6	Sequence 6, Appli
2484	4	80.0	2484	4	US-09-276-531-46	Sequence 46, Appli
2638	1	80.0	2638	1	US-08-306-691B-46	Sequence 46, Appli
2662	3	80.0	2662	3	US-08-750-357-8	Sequence 8, Appli
2976	4	80.0	2976	4	US-09-221-017B-36	Sequence 36, Appli
3535	2	80.0	3535	2	US-08-618-408B-1	Sequence 1, Appli
3701	1	80.0	3701	1	US-08-553-279-1	Sequence 1, Appli
3973	2	80.0	3973	2	US-08-602-093-6	Sequence 6, Appli
4031	1	80.0	4031	1	US-08-159-784-1	Sequence 1, Appli
4417	4	80.0	4417	4	US-07-741-453A-57	Sequence 57, Appli
5186	2	80.0	5186	2	US-08-596-366-1	Sequence 1, Appli
5186	2	80.0	5186	2	US-08-967-104-1	Sequence 1, Appli
5369	3	80.0	5369	3	US-09-212-247C-3	Sequence 3, Appli
8078	3	80.0	8078	3	US-08-870-126-12	Sequence 12, Appli
8078	4	80.0	8078	4	US-09-445-247-12	Sequence 12, Appli
14985	1	80.0	14985	1	US-08-652-972A-6	Sequence 6, Appli
14985	5	80.0	14985	5	PCT-US96-06231A-6	Sequence 6, Appli
17656	4	80.0	17656	4	US-09-433-579-3	Sequence 3, Appli
17949	4	80.0	17949	4	US-09-087-465-3	Sequence 3, Appli
24595	6	80.0	24595	6	5428147-1	Patent No. 5428147
112132	4	80.0	112132	4	US-09-741-150-3	Sequence 3, Appli
15	1	73.3	15	1	US-08-363-240A-119	Sequence 119, App
15	1	73.3	15	1	US-08-363-240A-120	Sequence 120, App
15	1	73.3	15	1	US-08-363-240A-121	Sequence 121, App
24	4	73.3	24	4	US-08-459-260A-677	Sequence 677, App
321	8	73.3	321	8	US-09-321-831-8	Sequence 8, Appli
50	3	73.3	50	3	US-08-998-099-296	Sequence 296, App
51	2	73.3	51	2	US-08-566-398-6	Sequence 6, Appli
54	2	73.3	54	2	US-08-566-398-7	Sequence 7, Appli
70	1	73.3	70	1	US-08-105-483-406	Sequence 406, App
70	1	73.3	70	1	US-08-105-483-407	Sequence 407, App
70	1	73.3	70	1	US-08-105-483-407	Sequence 407, App
70	1	73.3	70	1	US-08-224-657-89	Sequence 89, Appl
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70	1	73.3	70	1	US-08-709-209-406	Sequence 406, App
70	1	73.3	70	1	US-08-709-209-407	Sequence 407, App
70	1	73.3	70	1	US-08-257-073-44	Sequence 44, Appl
70	1	73.3	70	1	US-08-257-073-45	Sequence 45, Appl
70	1	73.3	70	1	US-08-303-275-112	Sequence 112, App
70	1	73.3	70	1	US-08-303-275-113	Sequence 113, App
70	1	73.3	70	1	US-08-458-101-406	Sequence 406, App
70	1	73.3	70	1	US-08-458-101-407	Sequence 407, App
70	2	73.3	70	2	US-08-658-665-129	Sequence 129, App
70	2	73.3	70	2	US-08-658-665-130	Sequence 130, App
70	3	73.3	70	3	US-08-675-566-71	Sequence 71, Appl
70	3	73.3	70	3	US-08-675-566-72	Sequence 72, Appl
70	4	73.3	70	4	US-08-796-101-105	Sequence 105, App
70	4	73.3	70	4	US-08-796-101-106	Sequence 106, App
70	4	73.3	70	4	US-09-085-273-129	Sequence 129, App
70	4	73.3	70	4	US-09-085-273-130	Sequence 130, App
70	4	73.3	70	4	US-09-354-138-89	Sequence 89, Appl
70	4	73.3	70	4	US-09-354-138-90	Sequence 90, Appl
70	5	73.3	70	5	PCT-US96-00547-42	Sequence 42, Appl
71	2	73.3	71	2	PCT-US96-00547-43	Sequence 43, Appl
71	2	73.3	71	2	US-08-184-009-100	Sequence 100, App
71	2	73.3	71	2	US-08-458-356-100	Sequence 100, App

c 101	11	73.3	71	4	US-08-460-736-100	Sequence 100, App	c 174	11	73.3	1700	3	US-09-078-596-1	Sequence 1, Appl
102	11	73.3	306	2	US-08-634-797-10	Sequence 10, Appl	175	11	73.3	1723	4	US-09-199-637A-135	Sequence 135, App
103	11	73.3	308	4	US-09-222-575-88	Sequence 88, Appl	176	11	73.3	1777	4	US-09-064-411A-5	Sequence 5, Appl
104	11	73.3	348	4	US-09-072-596-308	Sequence 308, App	177	11	73.3	1839	4	US-09-516-914-6	Sequence 6, Appl
105	11	73.3	361	1	US-08-094-079-12	Sequence 12, Appl	178	11	73.3	1879	3	US-08-403-8520-5	Sequence 5, Appl
106	11	73.3	361	1	US-08-094-079-18	Sequence 18, Appl	179	11	73.3	1879	3	US-08-510-646B-5	Sequence 5, Appl
107	11	73.3	361	1	US-08-094-079-20	Sequence 20, Appl	180	11	73.3	1879	4	US-09-231-818-5	Sequence 5, Appl
108	11	73.3	361	1	US-08-094-079-22	Sequence 22, Appl	181	11	73.3	1882	4	US-08-540-650B-11	Sequence 11, Appl
c 109	11	73.3	479	3	US-08-890-980-6	Sequence 6, Appl	182	11	73.3	1885	3	US-08-501-572-5	Sequence 5, Appl
c 110	11	73.3	479	3	US-08-890-979-6	Sequence 6, Appl	183	11	73.3	1885	3	US-09-040-444-5	Sequence 5, Appl
c 111	11	73.3	479	3	US-09-032-894-6	Sequence 6, Appl	184	11	73.3	1892	5	PCI-US96-00547-41	Sequence 41, Appl
c 112	11	73.3	479	4	US-09-031-626-6	Sequence 6, Appl	185	11	73.3	1954	3	US-08-922-635-2	Sequence 2, Appl
113	11	73.3	514	1	US-08-094-079-6	Sequence 6, Appl	186	11	73.3	1981	3	US-08-747-574-1	Sequence 1, Appl
114	11	73.3	514	1	US-08-094-079-10	Sequence 10, Appl	187	11	73.3	2020	2	US-08-417-210A-138	Sequence 138, App
c 115	11	73.3	555	3	US-08-705-771-4	Sequence 4, Appl	188	11	73.3	2028	2	US-08-417-210A-138	Sequence 138, App
116	11	73.3	662	1	US-07-807-043B-10	Sequence 10, Appl	189	11	73.3	2060	2	US-08-417-210A-141	Sequence 141, App
117	11	73.3	662	1	US-08-299-849B-10	Sequence 10, Appl	190	11	73.3	2073	4	US-09-221-017B-404	Sequence 404, App
118	11	73.3	662	2	US-08-142-368A-10	Sequence 10, Appl	191	11	73.3	2179	2	US-08-551-356-3	Sequence 3, Appl
119	11	73.3	662	3	US-08-967-727-10	Sequence 10, Appl	192	11	73.3	2179	5	PCI-US93-12687-3	Sequence 3, Appl
120	11	73.3	662	4	US-08-037-230D-10	Sequence 10, Appl	193	11	73.3	2242	3	US-09-400-742-1	Sequence 1, Appl
c 121	11	73.3	739	4	US-09-325-932A-100	Sequence 100, App	194	11	73.3	2242	3	US-08-618-651A-1	Sequence 1, Appl
122	11	73.3	759	1	US-08-685-660A-4	Sequence 4, Appl	195	11	73.3	2242	4	US-09-215-252-1	Sequence 1, Appl
123	11	73.3	759	2	US-08-974-196-4	Sequence 4, Appl	196	11	73.3	2257	4	US-09-605-785-332	Sequence 332, App
c 124	11	73.3	796	1	US-08-104-073-2	Sequence 2, Appl	197	11	73.3	2507	4	US-09-439-313-332	Sequence 332, App
125	11	73.3	847	1	US-08-998-416-545	Sequence 545, App	198	11	73.3	2507	4	US-09-352-616A-332	Sequence 332, App
126	11	73.3	867	1	US-08-181-471-3	Sequence 3, Appl	199	11	73.3	2507	4	US-09-232-149A-332	Sequence 332, App
127	11	73.3	897	2	US-08-486-663A-19	Sequence 19, Appl	200	11	73.3	2511	2	US-08-680-326-116	Sequence 116, App
128	11	73.3	897	3	US-08-767-942A-24	Sequence 24, Appl	201	11	73.3	2565	1	US-08-619-554-5	Sequence 5, Appl
c 129	11	73.3	905	2	US-08-158-009-79	Sequence 79, Appl	202	11	73.3	2566	4	US-09-270-542-124	Sequence 124, App
c 130	11	73.3	965	2	US-08-458-356-79	Sequence 79, Appl	203	11	73.3	2568	6	5196526-3	Patent No. 5196526
c 131	11	73.3	965	4	US-08-460-736-79	Sequence 79, Appl	204	11	73.3	2605	2	US-08-680-395-4	Sequence 4, Appl
c 132	11	73.3	1001	4	US-09-641-638-319	Sequence 319, App	205	11	73.3	2630	2	US-08-890-980-1	Sequence 1, Appl
c 133	11	73.3	1086	1	US-08-464-400-1	Sequence 1, Appl	206	11	73.3	2630	3	US-08-890-979-1	Sequence 1, Appl
c 134	11	73.3	1086	3	US-08-875-273A-1	Sequence 1, Appl	207	11	73.3	2630	3	US-09-032-894-1	Sequence 1, Appl
c 135	11	73.3	1086	4	US-09-123-386-1	Sequence 1, Appl	208	11	73.3	2630	4	US-09-031-626-1	Sequence 1, Appl
c 136	11	73.3	1086	5	PCI-US95-01827A-1	Sequence 1, Appl	209	11	73.3	2648	4	US-09-373-157-5	Sequence 5, Appl
c 137	11	73.3	1094	2	US-08-184-009-109	Sequence 109, App	210	11	73.3	2681	4	US-08-928-213B-7	Sequence 7, Appl
c 138	11	73.3	1094	2	US-08-458-356-109	Sequence 109, App	211	11	73.3	2700	3	US-08-815-809-4	Sequence 4, Appl
c 139	11	73.3	1094	4	US-08-460-736-109	Sequence 109, App	212	11	73.3	2749	3	US-07-717-331B-4	Sequence 4, Appl
c 140	11	73.3	1139	3	US-09-124-758-5	Sequence 5, Appl	213	11	73.3	2750	2	US-08-136-277-1	Sequence 1, Appl
c 141	11	73.3	1257	3	US-08-487-748A-11	Sequence 11, Appl	214	11	73.3	2750	2	US-08-479-403-1	Sequence 1, Appl
c 142	11	73.3	1257	3	US-08-480-070C-11	Sequence 11, Appl	215	11	73.3	2750	3	US-08-835-734-1	Sequence 1, Appl
c 143	11	73.3	1257	3	US-08-829-525-11	Sequence 11, Appl	216	11	73.3	2784	1	US-08-104-073-3	Sequence 3, Appl
c 144	11	73.3	1257	4	US-08-609-583A-11	Sequence 11, Appl	217	11	73.3	2784	1	US-08-351-413-10	Sequence 10, Appl
c 145	11	73.3	1257	4	US-08-937-399-11	Sequence 11, Appl	218	11	73.3	2784	2	US-09-025-583-10	Sequence 10, Appl
c 146	11	73.3	1257	4	US-09-310-367-11	Sequence 11, Appl	219	11	73.3	2868	4	US-09-228-986-4	Sequence 4, Appl
c 147	11	73.3	1257	4	US-09-032-337-11	Sequence 11, Appl	220	11	73.3	2935	1	US-09-041-075A-13	Sequence 13, Appl
c 148	11	73.3	1313	1	US-08-138-446B-7	Sequence 7, Appl	221	11	73.3	2935	4	US-08-716-873-12	Sequence 12, Appl
c 149	11	73.3	1313	2	US-08-870-693-7	Sequence 7, Appl	222	11	73.3	2935	4	US-09-368-431-12	Sequence 12, Appl
c 150	11	73.3	1394	4	US-09-504-445-3	Sequence 3, Appl	223	11	73.3	2945	6	5196526-2	Patent No. 5196526
c 151	11	73.3	1413	4	US-09-504-445-1	Sequence 1, Appl	224	11	73.3	2959	1	US-09-041-075A-15	Sequence 15, Appl
152	11	73.3	1419	3	US-09-354-129-1	Sequence 1, Appl	225	11	73.3	2989	2	US-08-566-398-9	Sequence 9, Appl
153	11	73.3	1419	4	US-09-504-357-1	Sequence 1, Appl	226	11	73.3	3043	4	US-09-008-271A-14	Sequence 14, Appl
154	11	73.3	1428	4	US-09-171-969-3	Sequence 3, Appl	227	11	73.3	3083	4	US-08-693-308-1	Sequence 1, Appl
c 155	11	73.3	1428	4	US-09-171-969-3	Sequence 3, Appl	228	11	73.3	3176	2	US-08-425-299A-3	Sequence 3, Appl
156	11	73.3	1441	1	US-08-136-277-18	Sequence 18, Appl	229	11	73.3	3176	2	US-08-486-663A-14	Sequence 14, Appl
157	11	73.3	1441	3	US-08-479-403-18	Sequence 18, Appl	230	11	73.3	3176	2	US-08-247-904B-13	Sequence 13, Appl
158	11	73.3	1441	3	US-08-835-734-18	Sequence 18, Appl	231	11	73.3	3176	2	US-08-767-942A-14	Sequence 14, Appl
159	11	73.3	1458	4	US-09-105-537-9	Sequence 9, Appl	232	11	73.3	3177	2	US-09-070-060-10	Sequence 10, Appl
c 160	11	73.3	1483	4	US-08-796-101-44	Sequence 44, Appl	233	11	73.3	3177	3	US-09-357-746-10	Sequence 10, Appl
c 161	11	73.3	1484	2	US-08-184-009-103	Sequence 103, App	234	11	73.3	3250	3	US-08-617-860B-1	Sequence 1, Appl
c 162	11	73.3	1484	2	US-08-458-356-103	Sequence 103, App	235	11	73.3	3318	3	US-08-650-766-3	Sequence 3, Appl
c 163	11	73.3	1484	4	US-08-460-736-103	Sequence 103, App	236	11	73.3	3318	3	US-08-922-635-3	Sequence 3, Appl
c 164	11	73.3	1511	4	US-08-796-101-168	Sequence 168, App	237	11	73.3	3323	2	US-07-624-299-14	Sequence 14, Appl
c 165	11	73.3	1512	2	US-08-184-009-99	Sequence 99, Appl	238	11	73.3	3385	3	US-08-650-766-1	Sequence 1, Appl
c 166	11	73.3	1512	2	US-08-458-356-99	Sequence 99, Appl	239	11	73.3	3385	3	US-08-922-635-1	Sequence 1, Appl
c 167	11	73.3	1512	4	US-08-460-736-99	Sequence 99, Appl	240	11	73.3	3460	2	US-08-658-665-57	Sequence 57, Appl
c 168	11	73.3	1565	3	US-09-320-878-24	Sequence 24, Appl	241	11	73.3	3460	4	US-08-796-101-21	Sequence 21, Appl
c 169	11	73.3	1600	4	US-09-325-932A-98	Sequence 98, Appl	242	11	73.3	3460	4	US-09-085-273-57	Sequence 57, Appl
c 170	11	73.3	1610	4	US-09-013-896A-1	Sequence 1, Appl	243	11	73.3	3579	3	US-08-674-168-15	Sequence 15, Appl
c 171	11	73.3	1678	2	US-08-650-766-2	Sequence 2, Appl	244	11	73.3	3579	3	US-08-985-908-18	Sequence 18, Appl
c 172	11	73.3	1700	2	US-08-428-131-1	Sequence 1, Appl	245	11	73.3	3579	3	US-08-852-730-3	Sequence 3, Appl
c 173	11	73.3	1700	2	US-08-602-846-1	Sequence 1, Appl	246	11	73.3	3579	4	US-08-985-916-10	Sequence 10, Appl

c 247	11	73.3	3622	2	US-08-658-665-60	Sequence 60, Appl	c 320	11	73.3	8147	4	US-09-514-247A-9	Sequence 9, Appl
c 248	11	73.3	3622	4	US-08-796-101-24	Sequence 24, Appl	c 321	11	73.3	9034	4	US-08-469-260A-397	Sequence 397, Appl
c 249	11	73.3	3622	4	US-09-085-273-60	Sequence 60, Appl	c 322	11	73.3	9122	2	US-08-417-629B-1	Sequence 1, Appl
c 250	11	73.3	3668	2	US-08-792-055-2	Sequence 2, Appl	c 323	11	73.3	9126	1	US-08-580-038-26	Sequence 26, Appl
c 251	11	73.3	3695	1	US-08-091-569-1	Sequence 1, Appl	c 324	11	73.3	9126	2	US-08-639-857-3	Sequence 3, Appl
c 252	11	73.3	3695	1	US-08-203-676-1	Sequence 1, Appl	c 325	11	73.3	10962	2	US-08-816-155B-6	Sequence 6, Appl
c 253	11	73.3	3695	2	US-08-822-238-1	Sequence 1, Appl	c 326	11	73.3	10962	3	US-09-079-587-6	Sequence 6, Appl
c 254	11	73.3	3770	4	US-09-221-017B-807	Sequence 807, App	c 327	11	73.3	11492	4	US-08-991-840A-1	Sequence 1, Appl
c 255	11	73.3	3825	4	US-09-332-295-1	Sequence 1, Appl	c 328	11	73.3	11531	1	US-08-068-945A-1	Sequence 1, Appl
c 256	11	73.3	3825	4	US-09-709-979-1	Sequence 1, Appl	c 329	11	73.3	11531	1	US-08-442-806-1	Sequence 1, Appl
c 257	11	73.3	4002	2	US-08-996-545-1	Sequence 1, Appl	c 330	11	73.3	11672	4	US-09-441-340-2	Sequence 2, Appl
c 258	11	73.3	4002	2	US-08-996-545-1	Sequence 1, Appl	c 331	11	73.3	13613	4	US-09-105-537-3	Sequence 3, Appl
c 259	11	73.3	4002	2	US-09-328-320-1	Sequence 3, Appl	c 332	11	73.3	13613	4	US-09-738-884-3	Sequence 3, Appl
c 260	11	73.3	4002	4	US-09-328-320-3	Sequence 3, Appl	c 333	11	73.3	14272	4	US-09-516-914-23	Sequence 23, Appl
c 261	11	73.3	4027	4	US-08-551-356-5	Sequence 5, Appl	c 334	11	73.3	15202	3	US-08-922-635-21	Sequence 21, Appl
c 262	11	73.3	4027	5	PCT-US93-12687-5	Sequence 5, Appl	c 335	11	73.3	15602	4	US-09-844-634-17	Sequence 17, Appl
c 263	11	73.3	4047	2	US-08-612-734B-1	Sequence 1, Appl	c 336	11	73.3	16595	4	US-09-146-053-7	Sequence 7, Appl
c 264	11	73.3	4157	1	US-07-807-043B-9	Sequence 9, Appl	c 337	11	73.3	16595	2	US-08-816-155B-8	Sequence 8, Appl
c 265	11	73.3	4157	1	US-08-299-849B-9	Sequence 9, Appl	c 338	11	73.3	19877	3	US-09-079-587-8	Sequence 8, Appl
c 266	11	73.3	4157	2	US-08-142-369A-9	Sequence 9, Appl	c 339	11	73.3	25165	4	US-09-453-702B-39	Sequence 39, Appl
c 267	11	73.3	4157	3	US-08-967-727-9	Sequence 9, Appl	c 340	11	73.3	30001	1	US-08-125-468-1	Sequence 1, Appl
c 268	11	73.3	4157	4	US-08-037-230D-9	Sequence 9, Appl	c 341	11	73.3	30001	2	US-08-474-933-1	Sequence 1, Appl
c 269	11	73.3	4162	4	US-09-453-702B-259	Sequence 259, App	c 342	11	73.3	35081	2	US-08-752-760A-1	Sequence 1, Appl
c 270	11	73.3	4204	2	US-08-928-615-1	Sequence 1, Appl	c 343	11	73.3	35100	2	US-08-770-379-17	Sequence 17, Appl
c 271	11	73.3	4204	4	US-09-056-105-6	Sequence 6, Appl	c 344	11	73.3	35100	4	US-08-757-669A-17	Sequence 17, Appl
c 272	11	73.3	4204	4	US-09-166-448-1	Sequence 1, Appl	c 345	11	73.3	35100	4	US-09-230-371A-17	Sequence 17, Appl
c 273	11	73.3	4204	4	US-09-348-933-1	Sequence 1, Appl	c 346	11	73.3	35100	2	US-08-804-227C-1	Sequence 1, Appl
c 274	11	73.3	4204	4	US-09-697-884-1	Sequence 1, Appl	c 347	11	73.3	36899	1	US-08-471-119A-1	Sequence 1, Appl
c 275	11	73.3	4343	1	US-08-224-657-93	Sequence 93, Appl	c 348	11	73.3	36899	4	US-09-797-906-3	Sequence 3, Appl
c 276	11	73.3	4343	4	US-09-354-138-93	Sequence 93, Appl	c 349	11	73.3	84495	4	US-08-781-891-79	Sequence 79, Appl
c 277	11	73.3	4427	2	US-08-658-665-48	Sequence 48, Appl	c 350	11	73.3	87350	3	US-09-791-211-3	Sequence 3, Appl
c 278	11	73.3	4427	4	US-08-796-101-12	Sequence 12, Appl	c 351	11	73.3	87543	4	US-09-754-250-3	Sequence 3, Appl
c 279	11	73.3	4427	4	US-09-085-273-48	Sequence 48, Appl	c 352	11	73.3	11282	4	US-09-426-230-1	Sequence 1, Appl
c 280	11	73.3	4463	2	US-08-760-489-1	Sequence 1, Appl	c 353	11	73.3	168575	4	US-09-676-610B-24	Sequence 24, Appl
c 281	11	73.3	4463	2	US-08-760-489-1	Sequence 1, Appl	c 354	11	73.3	169998	4	US-09-103-840A-2	Sequence 2, Appl
c 282	11	73.3	4463	4	US-09-185-373-1	Sequence 3, Appl	c 355	11	73.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl
c 283	11	73.3	4463	4	US-09-185-373-1	Sequence 3, Appl	c 356	11	73.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl
c 284	11	73.3	4559	4	US-09-056-105-5	Sequence 5, Appl	c 357	11	73.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl
c 285	11	73.3	4584	2	US-08-901-200A-15	Sequence 15, Appl	c 358	11	66.7	17	6	5202428-6	Patent No. 5202428
c 286	11	73.3	4584	3	US-09-219-391-15	Sequence 15, Appl	c 359	10	66.7	18	2	US-08-359-705B-38	Sequence 38, Appl
c 287	11	73.3	4604	1	US-08-224-657-96	Sequence 96, Appl	c 360	10	66.7	18	2	US-08-286-846A-38	Sequence 38, Appl
c 288	11	73.3	4604	4	US-09-354-138-96	Sequence 96, Appl	c 361	10	66.7	18	2	US-08-457-880A-38	Sequence 38, Appl
c 289	11	73.3	4635	2	US-08-404-531B-27	Sequence 27, Appl	c 362	10	66.7	18	3	US-09-255-911-20	Sequence 20, Appl
c 290	11	73.3	4635	3	US-08-476-900A-27	Sequence 27, Appl	c 363	10	66.7	18	3	US-08-444-622A-38	Sequence 38, Appl
c 291	11	73.3	4635	3	US-08-488-546A-27	Sequence 27, Appl	c 364	10	66.7	18	3	US-09-156-923-38	Sequence 38, Appl
c 292	11	73.3	4800	2	US-08-612-734B-3	Sequence 3, Appl	c 365	10	66.7	19	4	US-08-815-795-2	Sequence 2, Appl
c 293	11	73.3	4857	2	US-08-566-398-16	Sequence 16, Appl	c 366	10	66.7	20	4	US-09-517-467B-107	Sequence 107, App
c 294	11	73.3	4931	4	US-08-726-320-2	Sequence 2, Appl	c 367	10	66.7	21	5	PCT-US94-06331A-29	Sequence 29, Appl
c 295	11	73.3	4931	4	US-09-208-715-2	Sequence 2, Appl	c 368	10	66.7	27	2	US-08-937-102-5	Sequence 5, Appl
c 296	11	73.3	5091	4	US-08-469-260A-668	Sequence 668, App	c 369	10	66.7	27	4	US-09-439-616-8	Sequence 8, Appl
c 297	11	73.3	5110	2	US-08-404-531B-4	Sequence 4, Appl	c 370	10	66.7	27	4	US-08-584-040-4829	Sequence 4829, Ap
c 298	11	73.3	5110	2	US-08-404-531B-5	Sequence 5, Appl	c 371	10	66.7	29	3	US-09-006-597-9	Sequence 9, Appl
c 299	11	73.3	5110	3	US-08-476-900A-4	Sequence 4, Appl	c 372	10	66.7	35	4	US-09-475-460A-12	Sequence 12, Appl
c 300	11	73.3	5110	3	US-08-476-900A-5	Sequence 5, Appl	c 373	10	66.7	35	4	US-09-748-061A-12	Sequence 12, Appl
c 301	11	73.3	5110	3	US-08-488-546A-4	Sequence 4, Appl	c 374	10	66.7	36	2	US-08-988-128-11	Sequence 11, Appl
c 302	11	73.3	5110	3	US-08-488-546A-5	Sequence 5, Appl	c 375	10	66.7	36	3	US-09-124-758-30	Sequence 30, Appl
c 303	11	73.3	5630	2	US-08-937-931-1	Sequence 1, Appl	c 376	10	66.7	39	1	US-08-324-977-27	Sequence 27, Appl
c 304	11	73.3	5630	4	US-09-285-502-1	Sequence 1, Appl	c 377	10	66.7	39	2	US-08-384-616-27	Sequence 27, Appl
c 305	11	73.3	5630	4	US-09-709-126-1	Sequence 1, Appl	c 378	10	66.7	39	2	US-08-904-886A-27	Sequence 27, Appl
c 306	11	73.3	5630	4	US-09-871-385A-1	Sequence 1, Appl	c 379	10	66.7	39	4	US-09-315-850-27	Sequence 27, Appl
c 307	11	73.3	5943	1	US-08-206-176-1	Sequence 1, Appl	c 380	10	66.7	41	2	US-08-464-257-8	Sequence 8, Appl
c 308	11	73.3	6344	1	US-08-843-417-1	Sequence 1, Appl	c 381	10	66.7	41	2	US-09-062-375-8	Sequence 8, Appl
c 309	11	73.3	6418	1	US-08-480-528A-11	Sequence 11, Appl	c 382	10	66.7	41	3	US-09-203-796A-8	Sequence 8, Appl
c 310	11	73.3	6418	1	US-08-479-666-11	Sequence 11, Appl	c 383	10	66.7	45	2	US-08-937-102-3	Sequence 3, Appl
c 311	11	73.3	6418	5	PCT-US93-10520-11	Sequence 11, Appl	c 384	10	66.7	47	4	US-08-849-602C-4	Sequence 4, Appl
c 312	11	73.3	6524	4	US-08-669-656A-1	Sequence 1, Appl	c 385	10	66.7	54	1	US-08-373-124A-2182	Sequence 2182, Ap
c 313	11	73.3	6527	4	US-08-669-656A-7	Sequence 7, Appl	c 386	10	66.7	54	1	US-08-363-240A-1039	Sequence 1039, Ap
c 314	11	73.3	6678	3	US-08-816-617A-1	Sequence 1, Appl	c 387	10	66.7	54	1	US-08-363-240A-1162	Sequence 1162, Ap
c 315	11	73.3	7052	4	US-09-194-905-7	Sequence 7, Appl	c 388	10	66.7	54	1	US-08-435-628-2182	Sequence 2182, Ap
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c 317	11	73.3	7326	4	US-08-194-468-1	Sequence 1, Appl	c 390	10	66.7	54	4	US-08-584-040-8256	Sequence 8256, Ap
c 318	11	73.3	7326	4	US-09-514-247A-7	Sequence 7, Appl	c 391	10	66.7	54	4	US-08-679-645-594	Sequence 594, App
c 319	11	73.3	7344	3	US-08-961-739-1	Sequence 1, Appl	c 392	10	66.7	68	1	US-08-095-481-1	Sequence 1, Appl

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C 411	10	66.7	247	3	US-08-934-946A-2	Sequence 2, Appl	c 485	10	66.7	537	4	US-08-984-919A-40	Sequence 40, Appl
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C 437	10	66.7	411	4	US-08-828-323-39	Sequence 39, Appl	511	10	66.7	576	2	US-08-468-570-21	Sequence 21, Appl
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C 452	10	66.7	445	4	US-09-173-300-12	Sequence 12, Appl	526	10	66.7	576	5	PCT-US95-10398-13	Sequence 13, Appl
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C 458	10	66.7	470	2	US-08-592-541-99	Sequence 99, Appl	532	10	66.7	576	5	PCT-US95-10398-42	Sequence 42, Appl
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C 461	10	66.7	470	4	US-09-127-480-99	Sequence 99, Appl	535	10	66.7	594	1	US-08-324-977-21	Sequence 21, Appl
C 462	10	66.7	470	4	US-08-496-841C-99	Sequence 99, Appl	536	10	66.7	594	2	US-08-384-616-21	Sequence 21, Appl
C 463	10	66.7	470	4	US-09-124-523-99	Sequence 99, Appl	537	10	66.7	594	2	US-08-904-686A-21	Sequence 21, Appl
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599	10	66.7	797	1	US-08-515-903A-3	Sequence 3, Appli	672	10	66.7	989	4	US-09-123-492A-2	Sequence 2, Appli
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603	10	66.7	803	5	PCT-US95-12840-7	Sequence 7, Appli	676	10	66.7	1001	4	US-09-641-638-464	Sequence 464, App
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605	10	66.7	812	4	US-09-439-313-471	Sequence 471, App	678	10	66.7	1005	3	US-09-134-591-4	Sequence 4, Appli
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607	10	66.7	812	4	US-09-352-616A-471	Sequence 471, App	680	10	66.7	1007	4	US-09-247-373B-3	Sequence 3, Appli
608	10	66.7	818	4	US-09-420-592A-3	Sequence 3, Appli	681	10	66.7	1007	4	US-09-296-715-3	Sequence 3, Appli
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686	10	66.7	1037	2	US-08-636-883-1	Sequence 1, Appli	759	10	66.7	1334	4	US-09-296-284-52	Sequence 52, Appli
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702	10	66.7	1107	4	US-08-191-160-19	Sequence 19, Appl	c 775	10	66.7	1371	1	US-08-454-876-43	Sequence 43, Appl
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714	10	66.7	1167	2	US-08-904-686A-9	Sequence 9, Appli	c 787	10	66.7	1418	4	US-09-111-470-7	Sequence 7, Appli
715	10	66.7	1167	4	US-09-315-850-9	Sequence 9, Appli	c 788	10	66.7	1422	4	US-08-979-608A-13	Sequence 13, Appl
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c 720	10	66.7	1204	4	US-08-257-179-26	Sequence 87, Appl	c 791	10	66.7	1434	2	US-09-055-097-2	Sequence 2, Appli
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c 723	10	66.7	1248	4	US-09-232-197-54	Sequence 54, Appl	c 794	10	66.7	1440	3	US-09-687-594-17	Sequence 17, Appl
c 724	10	66.7	1248	4	US-09-232-201-54	Sequence 54, Appl	c 795	10	66.7	1446	4	US-09-149-476-139	Sequence 139, App
c 725	10	66.7	1263	2	US-08-860-882A-56	Sequence 56, Appl	c 796	10	66.7	1460	2	US-08-392-338A-18	Sequence 18, Appl
c 726	10	66.7	1263	4	US-09-011-769A-38	Sequence 38, Appl	c 797	10	66.7	1460	3	US-09-166-750-18	Sequence 18, Appl
c 727	10	66.7	1263	4	US-09-221-017B-566	Sequence 566, App	c 798	10	66.7	1460	3	US-09-172-019-18	Sequence 18, Appl
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c 731	10	66.7	1278	4	US-09-232-191-18	Sequence 18, Appl	c 802	10	66.7	1470	2	US-08-353-485-3	Sequence 3, Appli
c 732	10	66.7	1278	4	US-09-232-200-18	Sequence 18, Appl	c 803	10	66.7	1471	4	US-09-492-985-11	Sequence 11, Appl
c 733	10	66.7	1278	4	US-09-232-197-18	Sequence 18, Appl	c 804	10	66.7	1474	5	PCT-US94-00545-19	Sequence 19, Appl
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c 738	10	66.7	1280	4	US-09-283-471A-38	Sequence 38, Appl	c 809	10	66.7	1499	2	US-08-324-977-3	Sequence 3, Appli
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745	10	66.7	1300	4	US-08-483-533-39	Sequence 39, Appl	c 816	10	66.7	1521	2	US-08-815-667-10	Sequence 10, Appl
746	10	66.7	1300	4	US-09-283-471A-39	Sequence 39, Appl	c 817	10	66.7	1524	2	US-08-716-942-24	Sequence 24, Appl
c 747	10	66.7	1308	4	US-09-029-755C-6	Sequence 6, Appli	c 818	10	66.7	1524	4	US-09-130-337A-24	Sequence 24, Appl
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756	10	66.7	1327	4	US-09-283-471A-36	Sequence 36, Appl	c 827	10	66.7	1576	3	US-09-556-877-188	Sequence 188, App
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833	10	66.7	1617	4	US-08-979-608A-11	Sequence 11, Appl	906	10	66.7	1920	1	US-08-087-772A-1	Sequence 1, Appl
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836	10	66.7	1618	1	US-08-298-687A-22	Sequence 22, Appl	c 909	10	66.7	1931	4	US-09-431-470-3	Sequence 3, Appl
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c 845	10	66.7	1642	2	US-08-666-067-1	Sequence 1, Appl	918	10	66.7	1994	3	US-09-234-613-58	Sequence 58, Appl
c 846	10	66.7	1642	2	US-08-732-870-1	Sequence 1, Appl	919	10	66.7	2003	2	US-08-942-423-1	Sequence 1, Appl
c 847	10	68.7	1645	4	US-09-310-842-2	Sequence 2, Appl	920	10	66.7	2003	4	US-08-630-915A-25	Sequence 25, Appl
c 848	10	66.7	1654	4	US-08-487-596-3	Sequence 3, Appl	921	10	66.7	2004	4	US-09-094-557-2	Sequence 2, Appl
c 849	10	66.7	1665	3	US-08-766-354A-29	Sequence 29, Appl	c 922	10	66.7	2007	4	US-09-232-191-22	Sequence 22, Appl
c 850	10	66.7	1674	1	US-08-889-402-7	Sequence 7, Appl	c 923	10	66.7	2007	4	US-09-232-200-22	Sequence 22, Appl
c 851	10	66.7	1683	1	US-07-945-283-3	Sequence 3, Appl	c 924	10	66.7	2007	4	US-09-232-197-22	Sequence 22, Appl
c 852	10	66.7	1694	5	PCT-US95-04910-9	Sequence 9, Appl	c 925	10	66.7	2007	4	US-09-232-201-22	Sequence 22, Appl
853	10	66.7	1703	4	US-09-851-520-10	Sequence 10, Appl	926	10	66.7	2015	1	US-07-912-015-1	Sequence 1, Appl
854	10	66.7	1707	1	US-08-790-309-1	Sequence 1, Appl	927	10	66.7	2018	4	US-09-484-970B-128	Sequence 128, App
855	10	66.7	1707	4	US-09-250-585A-1	Sequence 1, Appl	928	10	66.7	2036	3	US-08-923-454A-17	Sequence 17, Appl
856	10	66.7	1710	2	US-08-912-794-1	Sequence 1, Appl	c 929	10	66.7	2037	4	US-08-840-767-9	Sequence 9, Appl
857	10	66.7	1734	6	5352575-8	Patent No. 5352575	930	10	66.7	2040	3	US-08-581-148C-21	Sequence 21, Appl
858	10	66.7	1738	2	US-08-932-376A-1	Sequence 1, Appl	c 931	10	66.7	2046	1	US-07-688-299-12	Sequence 12, Appl
859	10	66.7	1740	4	US-09-125-642C-2	Sequence 2, Appl	c 932	10	66.7	2046	1	US-07-688-299-12	Sequence 12, Appl
860	10	66.7	1742	4	US-09-125-642C-13	Sequence 13, Appl	933	10	66.7	2049	1	US-08-268-797-1	Sequence 1, Appl
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862	10	66.7	1751	4	US-08-491-944-1	Sequence 1, Appl	c 935	10	66.7	2073	4	US-09-134-001C-2101	Sequence 2101, Ap
863	10	66.7	1766	4	US-09-227-357-135	Sequence 135, App	c 936	10	66.7	2087	4	US-09-257-894-9	Sequence 9, Appl
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c 865	10	66.7	1776	1	US-08-889-402-5	Sequence 5, Appl	938	10	66.7	2089	1	US-07-977-630-82	Sequence 82, Appl
c 866	10	66.7	1780	3	US-08-813-150-3	Sequence 3, Appl	c 939	10	66.7	2096	1	US-08-458-084-1	Sequence 1, Appl
c 867	10	66.7	1794	4	US-09-232-191-36	Sequence 36, Appl	c 940	10	66.7	2096	1	US-08-205-508-1	Sequence 1, Appl
c 868	10	66.7	1794	4	US-09-232-200-90	Sequence 90, Appl	c 941	10	66.7	2096	5	US-08-278-630A-10	Sequence 10, Appl
c 869	10	66.7	1794	4	US-09-232-197-90	Sequence 90, Appl	c 942	10	66.7	2096	5	PCT-US95-02945-1	Sequence 1, Appl
c 870	10	66.7	1794	4	US-09-232-201-90	Sequence 90, Appl	c 943	10	66.7	2116	1	US-07-811-048-9	Sequence 9, Appl
c 871	10	66.7	1802	3	US-09-289-377-1	Sequence 1, Appl	944	10	66.7	2116	4	US-08-191-160-21	Sequence 21, Appl
c 872	10	66.7	1815	4	US-09-042-788A-24	Sequence 24, Appl	945	10	66.7	2132	2	US-09-159-385-3	Sequence 3, Appl
c 873	10	66.7	1818	1	US-08-889-402-4	Sequence 4, Appl	946	10	66.7	2132	4	US-09-552-322-1	Sequence 1, Appl
c 874	10	66.7	1818	1	US-08-889-402-6	Sequence 6, Appl	c 947	10	66.7	2132	4	US-09-552-322-1	Sequence 1, Appl
875	10	66.7	1821	3	US-09-056-105-23	Sequence 23, Appl	c 948	10	66.7	2154	2	US-09-171-945-124	Sequence 124, App
876	10	66.7	1831	6	5215881-1	Sequence 6, Appl	c 949	10	66.7	2165	2	US-08-263-911-6	Sequence 6, Appl
877	10	66.7	1831	6	5215881-3	Sequence 3, Appl	c 950	10	66.7	2165	2	US-08-263-911-8	Sequence 8, Appl
c 878	10	66.7	1841	1	US-08-570-311-5	Sequence 5, Appl	951	10	66.7	2165	4	US-09-257-894-8	Sequence 8, Appl
c 879	10	66.7	1841	2	US-08-353-485-5	Sequence 5, Appl	952	10	66.7	2167	2	US-09-067-351-5	Sequence 5, Appl
c 880	10	66.7	1848	4	US-09-475-460A-31	Sequence 31, Appl	953	10	66.7	2167	4	US-09-360-490-5	Sequence 5, Appl
c 881	10	66.7	1848	4	US-09-748-061A-31	Sequence 31, Appl	c 954	10	66.7	2186	3	US-08-959-382-1	Sequence 1, Appl
882	10	66.7	1860	3	US-09-071-434-2	Sequence 2, Appl	c 955	10	66.7	2187	4	US-09-302-769-7	Sequence 7, Appl
883	10	66.7	1863	2	US-08-470-426B-14	Sequence 14, Appl	956	10	66.7	2205	3	US-08-888-077A-41	Sequence 41, Appl
884	10	68.7	1872	1	US-08-153-848-39	Sequence 39, Appl	957	10	66.7	2207	6	5216203-3	Patent No. 5216203
885	10	66.7	1872	3	US-09-299-843A-39	Sequence 39, Appl	c 958	10	66.7	2219	1	US-08-606-322-1	Sequence 1, Appl
886	10	66.7	1872	4	US-09-088-337B-39	Sequence 39, Appl	c 959	10	66.7	2219	5	PCT-US93-07213-4	Sequence 4, Appl
887	10	66.7	1872	5	PCT-US93-11153-39	Sequence 39, Appl	960	10	66.7	2220	2	US-08-932-376A-3	Sequence 3, Appl
c 888	10	66.7	1873	3	US-09-329-418-1	Sequence 1, Appl	c 961	10	66.7	2221	4	US-09-232-191-24	Sequence 24, Appl
c 889	10	66.7	1873	4	US-09-531-914-1	Sequence 1, Appl	c 962	10	66.7	2221	4	US-09-232-200-74	Sequence 74, Appl
c 890	10	66.7	1878	2	US-08-435-149-17	Sequence 17, Appl	c 963	10	66.7	2221	4	US-09-232-197-74	Sequence 74, Appl
c 891	10	66.7	1893	4	US-09-363-970-34	Sequence 34, Appl	c 964	10	66.7	2221	4	US-09-232-201-74	Sequence 74, Appl
c 892	10	66.7	1897	2	US-08-532-547-6	Sequence 6, Appl	c 965	10	66.7	2222	1	US-07-828-790B-5	Sequence 5, Appl
c 893	10	66.7	1897	2	US-08-532-547-8	Sequence 8, Appl	c 966	10	66.7	2229	4	US-09-605-785-469	Sequence 469, App
c 894	10	66.7	1897	3	US-09-019-809-6	Sequence 6, Appl	c 967	10	66.7	2229	4	US-09-439-313-469	Sequence 469, App
c 895	10	66.7	1897	3	US-09-019-809-8	Sequence 8, Appl	c 968	10	66.7	2229	4	US-03-352-616A-469	Sequence 469, App
c 896	10	66.7	1897	4	US-09-471-177-6	Sequence 6, Appl	969	10	66.7	2231	4	US-08-961-527-265	Sequence 265, App
c 897	10	66.7	1897	4	US-09-471-177-8	Sequence 8, Appl	c 970	10	66.7	2234	1	US-07-811-048-10	Sequence 10, Appl
898	10	66.7	1899	3	US-09-354-129-7	Sequence 7, Appl	971	10	66.7	2251	4	US-09-221-017B-674	Sequence 674, App
899	10	66.7	1899	4	US-09-504-357-7	Sequence 7, Appl	c 972	10	66.7	2271	4	US-09-052-521C-3	Sequence 3, Appl
900	10	66.7	1904	2	US-08-933-750C-95	Sequence 95, Appl	c 973	10	66.7	2271	1	US-08-676-967-5	Sequence 5, Appl
901	10	66.7	1904	3	US-09-234-613-95	Sequence 95, Appl	c 974	10	66.7	2277	1	US-08-676-974-5	Sequence 5, Appl
c 902	10	66.7	1908	2	US-08-909-965C-17	Sequence 17, Appl	c 975	10	66.7	2277	2	US-09-098-487-5	Sequence 5, Appl
c 903	10	66.7	1908	4	US-08-999-774A-9	Sequence 9, Appl	c 976	10	66.7	2329	1	US-08-253-785-2	Sequence 2, Appl

977 10 66.7 2369 4 US-09-302-769-20
c 978 10 66.7 2372 4 US-09-145-391-1
c 979 10 66.7 2408 1 US-08-608-241-1
c 980 10 66.7 2408 1 US-08-922-182-1
c 981 10 66.7 2408 2 US-08-919-953-1
c 982 10 66.7 2408 4 US-09-192-983-1
c 983 10 66.7 2414 6 5248599-1
c 984 10 66.7 2419 4 US-09-624-693A-12
c 985 10 66.7 2426 4 US-09-605-785-470
c 986 10 66.7 2426 4 US-09-439-313-470
c 987 10 66.7 2426 4 US-09-352-616A-470
c 988 10 66.7 2440 1 US-08-160-861-2
c 989 10 66.7 2440 4 US-09-513-007-1
c 990 10 66.7 2442 1 US-08-542-363-3
c 991 10 66.7 2442 4 US-09-100-089-3
c 992 10 66.7 2442 4 US-09-670-827-3
c 993 10 66.7 2508 4 US-08-981-392-1
c 994 10 66.7 2537 6 5168051-1
c 995 10 66.7 2539 3 US-08-581-148C-20
c 996 10 66.7 2543 1 US-08-555-669-11
c 997 10 66.7 2543 3 US-09-073-663-11
c 998 10 66.7 2544 4 US-09-302-769-17
c 999 10 66.7 2559 2 US-08-886-152-4
c1000 10 66.7 2559 4 US-09-196-222-4

ALIGNMENTS

RESULT 1
US-07-686-322A-5
; Sequence 5, Application US/07686322A
; Patent No. 5312733
; GENERAL INFORMATION:
; APPLICANT: MacLeod Dr., Carol L.
; TITLE OF INVENTION: NO. 5312733el T-cell Lymphoma cDNA Clones
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department, Fulbright & Jaworski
; STREET: 1301 McKinney, Suit 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/686.322A
; FILING DATE: 19910411
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/509684
; FILING DATE: 13-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Launer, Charlene A.
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: D-5232-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 651-3634
; TELEFAX: (713) 651-5246
; TELEX: Western Union 762829
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORGANISM: Mouse

; STRAIN: AKRI Jackson
; INDIVIDUAL ISOLATE: SL12 cell line
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4
; IMMEDIATE SOURCE:
; CLONE: 20.5
US-07-686-322A-5
Query Match 93.3%; Score 14; DB 1; Length 2397;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTCTCGCCCTGTT 15
|||||
Db 1379 CTCTCGCCCTGTT 1392
RESULT 2
US-08-002-999-5
; Sequence 5, Application US/08002999
; Patent No. 5440017
; GENERAL INFORMATION:
; APPLICANT: MacLeod Dr., Carol L.
; TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department, Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,999
; FILING DATE: 19930111
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/686,322
; FILING DATE: 11-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D-5232-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 651-5587
; TELEFAX: (713) 651-5246
; TELEX: Western Union 762829
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORGANISM: Mouse
; STRAIN: AKRI Jackson
; INDIVIDUAL ISOLATE: SL12 cell line
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4
; IMMEDIATE SOURCE:
; CLONE: 20.5
US-08-002-999-5
Query Match 93.3%; Score 14; DB 1; Length 2397;
Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTGTT 15
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 3

US-08-132-990A-5
; Sequence 5, Application US/08132990A
; Patent No. 5834589
; GENERAL INFORMATION:
; APPLICANT: MERUELO, DANIEL
; APPLICANT: YOSHIMOTO, TAKAYUKI
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/132,990A
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/084,729
; FILING DATE: 29-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05569
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/899,075
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/806,178
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/627,950
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8105-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 410..1768
US-08-132-990A-5

Query Match 93.3%; Score 14; DB 2; Length 2397;

Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTGTT 15
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 4

PCT-US92-09382-5
; Sequence 5, Application PC/TUS9209382
; GENERAL INFORMATION:
; APPLICANT: MERUELO, DANIEL
; APPLICANT: YOSHIMOTO, TAKAYUKI
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09382
; FILING DATE: 19921213
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Livnat, Shmuel
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: MERUELO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 628-5197
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 410..1768
PCT-US92-09382-5

Query Match 93.3%; Score 14; DB 5; Length 2397;

Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTGTT 15

|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 5

US-09-400-208B-22/c
; Sequence 22, Application US/09400208B
; Patent No. 6271011
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neureminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-400-208B-22

Query Match 86.7%; Score 13; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14
|||||
Db 414 CTTCTCGCCCTGT 402

RESULT 6

US-09-400-208B-23/c
; Sequence 23, Application US/09400208B
; Patent No. 6271011

; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-400-208B-23

Query Match 86.7%; Score 13; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14
|||||
Db 414 CTTCTCGCCCTGT 402

RESULT 7

US-09-400-208B-24/c
; Sequence 24, Application US/09400208B
; Patent No. 6271011

; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-400-208B-24

Query Match 86.7%; Score 13; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14
|||||
Db 464 CTTCTCGCCCTGT 452

RESULT 8

US-09-400-208B-4/c
; Sequence 4, Application US/09400208B
; Patent No. 6271011

; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (188)..(1486)
; NAME/KEY: mat.peptide
; LOCATION: (251)..(1486)
US-09-400-208B-4

Query Match 86.7%; Score 13; DB 4; Length 2001;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14
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Db 1064 CTTCTCGCCCTGT 1052

RESULT 9

US-09-491-522-6/c
; Sequence 6, Application US/09491522
; Patent No. 6428998

; GENERAL INFORMATION:
; APPLICANT: Colige, Alain
; APPLICANT: Lapiere, Charles M.
; APPLICANT: Prockop, Darwin J.
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
; TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

```

; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/491,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,333
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8389-0060-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-491-522-6

Query Match      86.7%; Score 13; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTG 13
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Db 511 CCTTCTCGCCCTG 499

RESULT 10
US-09-491-522-2/c
; Sequence 2, Application US/09491522
; Patent No. 6428998
; GENERAL INFORMATION:
; APPLICANT: Colige, Alain
; APPLICANT: Lapiere, Charles M.
; APPLICANT: Prockop, Darwin J.
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
; TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/491,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,333
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8389-0060-999

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-491-522-2

Query Match      86.7%; Score 13; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTG 13
   |||||
Db 511 CCTTCTCGCCCTG 499

RESULT 11
US-09-171-337A-4/c
; Sequence 4, Application US/09171337A
; Patent No. 6300095
; GENERAL INFORMATION:
; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE, Migueal Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, Bruno
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
; AND -ACTIN AND THEIR USE IN FILAMENTOUS
; FUNGI EXPRESSION, SECRETION AND ANTISENSE

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: WordPerfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,337A
; FILING DATE: 14-May-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ES98/00056
; FILING DATE: 5-MAR-1998
; APPLICATION NUMBER: ES9700482
; FILING DATE: 5-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 233288
; INFORMATION FOR SEQ ID NO: 4
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleotides
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Penicillium chrysogenum
; IMMEDIATE SOURCE:
; CLONE: <Unknown>
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; NAME/KEY: intron
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; NAME/KEY: intron
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; FEATURE:
; NAME/KEY: intron
; LOCATION: 1180...1289
; FEATURE:
; NAME/KEY: intron
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; FEATURE:
; NAME/KEY: intron
; LOCATION: 2183...2249
; OTHER INFORMATION: act gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-171-337A-4

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Best Local Similarity 100.0%; Pred. No. 14;
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RESULT 12
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; Sequence 76, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 76:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3748 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Acremonium chrysogenum
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; OTHER INFORMATION: /note= "Nucleotide sequence of region B in Figure
; OTHER INFORMATION: 60. Sequence corresponds to Figure 62."
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; NAME/KEY: exon
; LOCATION: 1428..1458
; FEATURE:
; NAME/KEY: exon
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; LOCATION: 1918..2689
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; LOCATION: ..1827, 1918..2689, 2757..2984)
US-08-261-206A-76

Query Match      86.7%; Score 13; DB 1; Length 3748;
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; Sequence 1, Application US/09254325
; Patent No. 6050607
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ENHANCED EXPRESSION OF
; TITLE OF INVENTION: PROTEOLYTIC ENZYMES IN KOJI MOLDS
; NUMBER OF SEQUENCES: 17
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,325
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4657 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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OTHER INFORMATION: A DNA BINDING DOMAIN"
US-09-254-325-1

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 1, Application US/09491522
; Patent No. 6428998
; GENERAL INFORMATION:
; APPLICANT: Colige, Alain
; APPLICANT: Lapierre, Charles M.
; APPLICANT: Prockop, Darwin J.
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
; AND THE PRODUCTION, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/491,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,333
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8389-0060-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-491-522-1

Query Match 86.7%; Score 13; DB 4; Length 6692;

Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTG 13
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DB 511 CCTTCTCGCCCTG 499

RESULT 15
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; Sequence 1, Application US/08319387
; Patent No. 5543317
; GENERAL INFORMATION:
; APPLICANT: Shields, Malcolm S.
; APPLICANT: Francesconi, Stephen C.
; TITLE OF INVENTION: Microbial Degradation of Trichloroethylene,
; TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,387
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/167,457
; FILING DATE: 15-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UMF-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-319-387-1

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4408 CCTTCTCGCCCTG 4396

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Perfect score: 15

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	13	86.7	4558	10 US-09-764-878-258	Sequence 258, App
3	13	86.7	4558	10 US-09-764-860-937	Sequence 937, App
4	13	86.7	5828	9 US-09-430-029-1	Sequence 1, Appli
5	12	80.0	49	10 US-09-761-534A-17	Sequence 17, Appl
6	12	80.0	152	10 US-09-864-761-17150	Sequence 17150, A
7	12	80.0	173	10 US-09-974-300-7193	Sequence 7193, Ap
8	12	80.0	235	10 US-09-923-876-97	Sequence 97, Appl
9	12	80.0	356	10 US-09-983-965-5128	Sequence 5128, Ap
10	12	80.0	380	10 US-09-867-701-5624	Sequence 5624, Ap
11	12	80.0	396	10 US-09-864-761-3392	Sequence 3392, Ap
12	12	80.0	414	9 US-09-954-531-880	Sequence 880, App
13	12	80.0	445	10 US-09-864-761-337	Sequence 337, App
14	12	80.0	447	10 US-09-784-423-17	Sequence 17, Appl
15	12	80.0	461	9 US-09-954-531-813	Sequence 813, App
16	12	80.0	471	10 US-09-867-550-723	Sequence 723, App
17	12	80.0	486	10 US-09-867-701-5641	Sequence 5641, Ap
18	12	80.0	537	10 US-09-867-701-6066	Sequence 6066, Ap
19	12	80.0	657	10 US-09-742-137-7	Sequence 7, Appli

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Sequence 2, Appli	10	US-10-067-291-2	1020	80.0	12
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c 99	11	73.3	296	10	US-09-960-352-14240	Sequence 14240, A	c 172	11	73.3	957	12	US-10-042-417-41	Sequence 41, Appl
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c 104	11	73.3	309	10	US-09-878-574-14539	Sequence 14539, A	c 177	11	73.3	1077	10	US-09-815-242-7973	Sequence 7973, Ap
c 105	11	73.3	319	10	US-09-954-456-1546	Sequence 1546, Ap	c 178	11	73.3	1086	12	US-10-021-002-1	Sequence 1, Appli
c 106	11	73.3	336	10	US-09-983-965-2012	Sequence 2012, Ap	c 179	11	73.3	1142	9	US-09-981-876-47	Sequence 47, Appl
c 107	11	73.3	362	10	US-09-864-761-3823	Sequence 3823, Ap	c 180	11	73.3	1150	12	US-10-052-586-519	Sequence 519, App
c 108	11	73.3	370	10	US-09-864-761-3943	Sequence 3943, Ap	c 181	11	73.3	1164	10	US-09-815-242-7696	Sequence 7696, App
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c 117	11	73.3	398	10	US-09-878-574-1655	Sequence 1655, Ap	c 190	11	73.3	1410	10	US-09-954-456-2274	Sequence 5, Appli
c 118	11	73.3	398	10	US-09-878-574-2360	Sequence 2360, Ap	c 191	11	73.3	1428	10	US-09-943-548-5	Sequence 5, Appli
c 119	11	73.3	398	10	US-09-983-965-4236	Sequence 4236, Ap	c 192	11	73.3	1428	10	US-09-943-548-5	Sequence 15, Appli
c 120	11	73.3	399	10	US-09-878-574-2347	Sequence 2347, Ap	c 193	11	73.3	1435	9	US-09-732-618-15	Sequence 9, Appli
c 121	11	73.3	399	10	US-09-878-574-5038	Sequence 5038, Ap	c 194	11	73.3	1435	10	US-09-860-846-9	Sequence 9, Appli
c 122	11	73.3	402	10	US-09-960-352-624	Sequence 624, App	c 195	11	73.3	1458	10	US-09-861-289-9	Sequence 9, Appli
c 123	11	73.3	403	10	US-09-878-574-3940	Sequence 1626, Ap	c 196	11	73.3	1458	10	US-09-925-301-63	Sequence 63, Appl
c 124	11	73.3	408	10	US-09-878-574-196	Sequence 3940, Ap	c 197	11	73.3	1503	10	US-09-974-300-1681	Sequence 1681, Ap
c 125	11	73.3	410	10	US-09-834-975-196	Sequence 196, App	c 198	11	73.3	1527	10	US-09-822-830A-95	Sequence 95, Appl
c 126	11	73.3	416	10	US-09-925-302-19	Sequence 19, Appl	c 199	11	73.3	1544	10	US-09-880-107-3429	Sequence 3429, Ap
c 127	11	73.3	418	10	US-09-960-352-6075	Sequence 6075, Ap	c 200	11	73.3	1610	10	US-09-827-948-1	Sequence 1, Appli
c 128	11	73.3	428	10	US-09-837-381-794	Sequence 794, App	c 201	11	73.3	1610	10	US-09-925-301-424	Sequence 424, App
c 129	11	73.3	428	10	US-09-867-701-7215	Sequence 7215, Ap	c 202	11	73.3	1680	9	US-09-815-242-7806	Sequence 7806, Ap
c 130	11	73.3	437	10	US-09-983-965-5289	Sequence 5289, Ap	c 203	11	73.3	1728	9	US-09-906-514-3	Sequence 3, Appli
c 131	11	73.3	441	10	US-09-864-761-1285	Sequence 1285, Ap	c 204	11	73.3	1770	9	US-09-906-514-1	Sequence 1, Appli
c 132	11	73.3	441	10	US-09-867-701-6249	Sequence 6249, Ap	c 205	11	73.3	1787	10	US-09-880-107-2321	Sequence 2321, Ap
c 133	11	73.3	450	10	US-09-834-975-195	Sequence 195, App	c 206	11	73.3	1800	10	US-09-880-107-2321	Sequence 1, Appli
c 134	11	73.3	458	10	US-09-864-761-32413	Sequence 32413, A	c 207	11	73.3	1800	10	US-09-975-901-1	Sequence 13, Appl
c 135	11	73.3	461	10	US-09-864-761-10060	Sequence 10060, A	c 208	11	73.3	1815	10	US-09-758-269-13	Sequence 6, Appli
c 136	11	73.3	467	10	US-09-867-701-10365	Sequence 10365, A	c 209	11	73.3	1836	9	US-09-938-842A-1222	Sequence 1222, Ap
c 137	11	73.3	471	10	US-09-864-761-5679	Sequence 5679, Ap	c 210	11	73.3	1839	10	US-09-870-162A-6	Sequence 3832, Ap
c 138	11	73.3	478	9	US-09-954-531-641	Sequence 641, App	c 211	11	73.3	1936	10	US-09-880-107-3832	Sequence 15, Appl
c 139	11	73.3	478	9	US-09-954-531-1053	Sequence 1053, Ap	c 212	11	73.3	1958	10	US-09-975-901-15	Sequence 4107, Ap
c 140	11	73.3	483	10	US-09-880-107-678	Sequence 678, App	c 213	11	73.3	2000	9	US-09-938-842A-4107	Sequence 6020, Ap
c 141	11	73.3	483	10	US-09-864-761-16053	Sequence 16053, A	c 214	11	73.3	2109	10	US-09-815-242-6020	Sequence 19, Appl
c 142	11	73.3	489	10	US-09-864-761-2434	Sequence 2434, Ap	c 215	11	73.3	2176	9	US-10-032-159A-19	Sequence 6215, Ap
c 143	11	73.3	489	10	US-09-864-761-5706	Sequence 5706, Ap	c 216	11	73.3	2205	10	US-09-815-242-6215	Sequence 1, Appli
c 144	11	73.3	502	10	US-09-738-973-328	Sequence 328, App	c 217	11	73.3	2242	9	US-09-970-989-1	Sequence 52, Appl
c 145	11	73.3	507	10	US-09-864-761-6944	Sequence 6944, Ap	c 218	11	73.3	2254	10	US-09-800-729-52	Sequence 368, App
c 146	11	73.3	508	10	US-09-867-701-2826	Sequence 2826, Ap	c 219	11	73.3	2281	9	US-09-989-293A-368	Sequence 368, App
c 147	11	73.3	508	10	US-09-998-598-2597	Sequence 2597, Ap	c 220	11	73.3	2281	9	US-09-989-722-368	Sequence 368, App
c 148	11	73.3	510	10	US-09-834-975-610	Sequence 610, App	c 221	11	73.3	2281	10	US-09-989-723-368	Sequence 368, App
c 149	11	73.3	512	10	US-09-783-590-7859	Sequence 7859, Ap	c 222	11	73.3	2281	10	US-09-989-279-368	Sequence 368, App
c 150	11	73.3	520	10	US-09-919-580-306	Sequence 306, App	c 223	11	73.3	2281	10	US-09-989-727-368	Sequence 368, App
c 151	11	73.3	528	10	US-09-867-701-159037	Sequence 10337, A	c 224	11	73.3	2281	10	US-09-989-731-368	Sequence 368, App
c 152	11	73.3	543	10	US-09-864-761-15909	Sequence 15909, A	c 225	11	73.3	2281	10	US-09-989-732-368	Sequence 368, App
c 153	11	73.3	546	10	US-09-917-800A-1683	Sequence 1683, Ap	c 226	11	73.3	2281	10	US-09-991-073-368	Sequence 368, App
c 154	11	73.3	553	10	US-09-864-761-9018	Sequence 9018, Ap	c 227	11	73.3	2281	10	US-09-990-442-368	Sequence 368, App
c 155	11	73.3	553	10	US-09-734-017A-77	Sequence 77, Appl	c 228	11	73.3	2281	10	US-09-991-163-368	Sequence 368, App
c 156	11	73.3	559	10	US-09-864-761-12322	Sequence 12322, A	c 229	11	73.3	2281	10	US-09-991-163-368	Sequence 368, App
c 157	11	73.3	560	10	US-09-887-576-804	Sequence 804, App	c 230	11	73.3	2281	10	US-09-990-456-368	Sequence 368, App
c 158	11	73.3	575	10	US-09-864-761-12618	Sequence 12618, A	c 231	11	73.3	2281	10	US-09-989-721-368	Sequence 368, App
c 159	11	73.3	650	10	US-09-867-550-1597	Sequence 1507, Ap	c 232	11	73.3	2281	12	US-10-052-586-253	Sequence 253, App
c 160	11	73.3	659	10	US-09-822-830A-435	Sequence 435, App	c 233	11	73.3	2294	12	US-10-052-586-283	Sequence 283, App
c 161	11	73.3	720	10	US-09-974-300-4505	Sequence 4505, Ap	c 234	11	73.3	2295	10	US-09-764-864-1767	Sequence 1767, Ap
c 162	11	73.3	744	10	US-09-833-381-293	Sequence 293, App	c 235	11	73.3	2354	10	US-09-967-768A-300	Sequence 300, App
c 163	11	73.3	757	10	US-09-861-893-71	Sequence 71, Appl	c 236	11	73.3	2406	10	US-09-974-300-1529	Sequence 1529, Ap
c 164	11	73.3	758	10	US-09-867-550-1385	Sequence 1385, Ap	c 237	11	73.3	2412	9	US-09-801-220-3	Sequence 3, Appli
c 165	11	73.3	772	10	US-09-770-445-908	Sequence 908, App	c 238	11	73.3				

c 239	11	73.3	2415	10	US-09-974-300-1159	Sequence 1159, Ap	c 312	11	73.3	25950	10	US-09-764-870-597	Sequence 597, App
c 240	11	73.3	2507	10	US-09-759-143-332	Sequence 332, App	c 313	11	73.3	26928	10	US-09-880-107-2278	Sequence 2278, Ap
c 241	11	73.3	2507	10	US-09-780-669-332	Sequence 332, App	314	11	73.3	32170	10	US-09-764-860-1108	Sequence 1108, Ap
c 242	11	73.3	2507	10	US-09-822-827-332	Sequence 332, App	315	11	73.3	32188	10	US-09-764-860-799	Sequence 799, App
c 243	11	73.3	2604	10	US-09-801-368-97	Sequence 97, Appl	c 316	11	73.3	35100	10	US-09-782-378A-26	Sequence 26, Appl
c 244	11	73.3	2648	9	US-10-112-527-5	Sequence 5, Appl	317	11	73.3	42432	9	US-10-027-806-2	Sequence 2, Appl
c 245	11	73.3	2662	9	US-09-764-868-1388	Sequence 1388, Ap	318	11	73.3	45845	10	US-09-927-091-6	Sequence 6, Appl
c 246	11	73.3	2754	10	US-09-861-801-3	Sequence 3, Appl	319	11	73.3	46718	10	US-09-816-093-3	Sequence 3, Appl
c 247	11	73.3	2760	9	US-09-991-496-126	Sequence 126, App	320	11	73.3	57130	10	US-09-835-081-3	Sequence 3, Appl
c 248	11	73.3	2781	9	US-09-991-496-125	Sequence 125, App	321	11	73.3	58837	10	US-09-982-091A-5	Sequence 5, Appl
c 249	11	73.3	2810	10	US-09-833-381-873	Sequence 873, App	322	11	73.3	62944	10	US-09-954-456-2257	Sequence 2257, Ap
c 250	11	73.3	2844	12	US-10-044-090-813	Sequence 813, App	c 323	11	73.3	110096	10	US-09-880-107-1542	Sequence 1542, Ap
c 251	11	73.3	2875	9	US-09-801-220-1	Sequence 1, Appl	c 324	11	73.3	111282	12	US-10-094-989-3	Sequence 3, Appl
c 252	11	73.3	2894	10	US-09-954-456-691	Sequence 691, App	c 325	11	73.3	116592	10	US-09-818-512-3	Sequence 3, Appl
c 253	11	73.3	2935	10	US-09-742-582-13	Sequence 13, Appl	c 326	11	73.3	126512	10	US-09-804-474A-3	Sequence 3, Appl
c 254	11	73.3	2959	10	US-09-742-582-15	Sequence 15, Appl	c 327	11	73.3	145831	10	US-09-969-708-79	Sequence 79, Appl
c 255	11	73.3	3287	10	US-09-925-297-128	Sequence 128, App	c 328	11	73.3	145831	10	US-09-954-456-2116	Sequence 2116, Ap
c 256	11	73.3	3320	9	US-09-981-876-66	Sequence 66, Appl	c 329	11	73.3	170834	10	US-09-835-232-7	Sequence 7, Appl
c 257	11	73.3	3398	9	US-10-108-605-192	Sequence 192, App	c 330	11	73.3	172637	10	US-09-805-458A-3	Sequence 3, Appl
c 258	11	73.3	3472	10	US-09-925-299-96	Sequence 96, Appl	331	11	73.3	302250	10	US-09-962-832-154	Sequence 154, App
c 259	11	73.3	3669	10	US-09-861-801-1	Sequence 1, Appl	332	11	73.3	397658	10	US-09-813-320-3	Sequence 3, Appl
c 260	11	73.3	3744	10	US-09-815-242-6048	Sequence 6048, Ap	c 333	11	73.3	397658	10	US-09-946-807-1	Sequence 1, Appl
c 261	11	73.3	3825	12	US-10-147-268-1	Sequence 1, Appl	c 334	11	73.3	1503841	9	US-09-795-668-1	Sequence 1, Appl
c 262	11	73.3	3826	10	US-09-927-091-3	Sequence 3, Appl	c 335	11	73.3	1503841	10	US-09-795-668-1	Sequence 1, Appl
c 263	11	73.3	3915	10	US-09-954-456-507	Sequence 507, App	336	11	66.7	15	10	US-09-504-231A-589	Sequence 589, App
c 264	11	73.3	4002	9	US-09-758-828-1	Sequence 1, Appl	337	10	66.7	15	10	US-09-504-231A-591	Sequence 591, App
c 265	11	73.3	4002	9	US-09-758-828-1	Sequence 1, Appl	338	10	66.7	15	10	US-09-504-231A-591	Sequence 591, App
c 266	11	73.3	4119	10	US-09-954-456-729	Sequence 729, App	339	10	66.7	15	10	US-09-274-553D-589	Sequence 589, App
c 267	11	73.3	4139	10	US-09-880-107-2279	Sequence 2279, Ap	340	10	66.7	15	10	US-09-274-553D-591	Sequence 591, App
c 268	11	73.3	4162	10	US-09-861-881-1	Sequence 1, Appl	341	10	66.7	15	10	US-09-866-108-186	Sequence 186, App
c 269	11	73.3	4204	9	US-09-784-199-1	Sequence 1, Appl	342	10	66.7	17	10	US-09-866-108-187	Sequence 187, App
c 270	11	73.3	4204	10	US-09-954-456-747	Sequence 747, App	343	10	66.7	17	10	US-09-866-108-188	Sequence 188, App
c 271	11	73.3	4330	10	US-09-880-107-2361	Sequence 2361, Ap	344	10	66.7	17	10	US-09-866-108-188	Sequence 188, App
c 272	11	73.3	4393	10	US-09-861-881-2	Sequence 2, Appl	345	10	66.7	17	10	US-09-866-108-189	Sequence 189, App
c 273	11	73.3	4744	10	US-09-880-107-3459	Sequence 3459, Ap	346	10	66.7	17	10	US-09-866-108-190	Sequence 190, App
c 274	11	73.3	5091	8	US-08-424-5508-668	Sequence 668, App	347	10	66.7	17	10	US-09-866-108-191	Sequence 191, App
c 275	11	73.3	5512	10	US-09-764-887-522	Sequence 522, App	348	10	66.7	17	10	US-09-866-108-192	Sequence 192, App
c 276	11	73.3	5630	10	US-09-871-388-1	Sequence 1, Appl	349	10	66.7	17	10	US-09-866-108-193	Sequence 193, App
c 277	11	73.3	6336	10	US-09-964-824A-114	Sequence 114, App	350	10	66.7	18	10	US-09-966-147-38	Sequence 38, Appl
c 278	11	73.3	6336	9	US-09-880-107-1537	Sequence 1537, Ap	c 351	10	66.7	20	9	US-09-963-875-35	Sequence 35, Appl
c 279	11	73.3	6560	9	US-09-808-602-76	Sequence 76, Appl	c 352	10	66.7	23	9	US-09-931-007A-10	Sequence 10, Appl
c 280	11	73.3	6651	10	US-09-954-456-178	Sequence 178, App	353	10	66.7	25	10	US-09-866-108-3115	Sequence 3115, Ap
c 281	11	73.3	6651	10	US-09-954-456-1217	Sequence 1217, Ap	354	10	66.7	25	10	US-09-866-108-3116	Sequence 3116, Ap
c 282	11	73.3	6800	10	US-09-764-869-2142	Sequence 2142, Ap	355	10	66.7	25	10	US-09-866-108-3117	Sequence 3117, Ap
c 283	11	73.3	6892	10	US-09-764-877-3770	Sequence 3770, Ap	356	10	66.7	25	10	US-09-866-108-3118	Sequence 3118, Ap
c 284	11	73.3	7326	12	US-10-109-886-7	Sequence 7, Appl	357	10	66.7	25	10	US-09-866-108-3119	Sequence 3119, Ap
c 285	11	73.3	8145	10	US-09-070-927A-386	Sequence 386, App	358	10	66.7	25	10	US-09-866-108-3120	Sequence 3120, Ap
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c 287	11	73.3	8663	10	US-09-764-878-397	Sequence 397, App	360	10	66.7	25	10	US-09-866-108-3122	Sequence 3122, Ap
c 288	11	73.3	8689	9	US-09-808-602-74	Sequence 74, Appl	361	10	66.7	25	10	US-09-866-108-3123	Sequence 3123, Ap
c 289	11	73.3	8797	9	US-09-808-602-77	Sequence 77, Appl	362	10	66.7	25	10	US-09-866-108-3124	Sequence 3124, Ap
c 290	11	73.3	8797	9	US-09-808-602-77	Sequence 77, Appl	363	10	66.7	25	10	US-09-866-108-3125	Sequence 3125, Ap
c 291	11	73.3	8911	10	US-09-764-853-895	Sequence 895, App	364	10	66.7	25	10	US-09-866-108-3126	Sequence 3126, Ap
c 292	11	73.3	9034	8	US-08-424-5508-397	Sequence 397, App	365	10	66.7	25	10	US-09-866-108-3127	Sequence 3127, Ap
c 293	11	73.3	9729	9	US-09-808-602-12	Sequence 12, Appl	366	10	66.7	25	10	US-09-866-108-3128	Sequence 3128, Ap
c 294	11	73.3	9815	10	US-09-764-847-1601	Sequence 1601, Ap	367	10	66.7	25	10	US-09-866-108-3129	Sequence 3129, Ap
c 295	11	73.3	9826	9	US-09-808-602-7	Sequence 7, Appl	368	10	66.7	25	10	US-09-866-108-3130	Sequence 3130, Ap
c 296	11	73.3	10419	9	US-10-027-806-3	Sequence 3, Appl	c 369	10	66.7	27	10	US-09-928-796A-8	Sequence 8, Appl
c 297	11	73.3	10953	10	US-09-764-846-313	Sequence 313, App	c 370	10	66.7	31	10	US-09-801-274-1765	Sequence 1765, Ap
c 298	11	73.3	12928	10	US-09-764-847-1343	Sequence 1343, Ap	371	10	66.7	38	9	US-09-864-785-744	Sequence 744, App
c 299	11	73.3	12822	10	US-09-764-847-1579	Sequence 1579, Ap	c 372	10	66.7	50	10	US-09-504-231A-2980	Sequence 2980, Ap
c 300	11	73.3	13272	10	US-09-764-846-312	Sequence 312, App	c 373	10	66.7	50	10	US-09-504-231A-3097	Sequence 3097, Ap
c 301	11	73.3	13337	10	US-09-764-846-3129	Sequence 1629, Ap	c 374	10	66.7	50	10	US-09-274-553D-2980	Sequence 2980, Ap
c 302	11	73.3	13613	9	US-09-860-846-3	Sequence 3, Appl	c 375	10	66.7	50	10	US-09-274-553D-3097	Sequence 3097, Ap
c 303	11	73.3	13613	9	US-09-861-289-3	Sequence 3, Appl	376	10	66.7	81	10	US-09-398-473-2	Sequence 2, Appl
c 304	11	73.3	13953	9	US-10-096-961-3	Sequence 3, Appl	377	10	66.7	113	10	US-09-878-574-939	Sequence 2, Appl
c 305	11	73.3	14272	10	US-09-870-162A-23	Sequence 23, Appl	378	10	66.7	114	9	US-09-768-827-19	Sequence 19, Appl
c 306	11	73.3	15425	10	US-09-764-869-1654	Sequence 1654, Ap	379	10	66.7	120	8	US-08-902-572-15	Sequence 15, Appl
c 307	11	73.3	15515	10	US-09-822-860-3	Sequence 3, Appl	380	10	66.7	120	10	US-09-862-179A-42	Sequence 42, Appl
c 308	11	73.3	15843	10	US-09-764-869-2396	Sequence 2396, Ap	381	10	66.7	127	10	US-09-864-761-29696	Sequence 29696, A
c 309	11	73.3	16774	10	US-09-764-869-2395	Sequence 2395, Ap	382	10	66.7	128	10	US-09-294-093B-1263	Sequence 1263, Ap
c 310	11	73.3	16774	10	US-09-764-869-2398	Sequence 2398, Ap	383	10	66.7	128	10	US-09-923-876-1504	Sequence 1504, Ap
c 311	11	73.3	24533	9	US-09-764-868-1349	Sequence 1349, Ap	384	10	66.7	137	10	US-09-864-761-31703	Sequence 31703, A

c 531	10	66.7	385	10	US-09-878-574-2420	Sequence 2420, Ap	604	10	66.7	480	9	US-09-878-178-1959	Sequence 1959, Ap
c 532	10	66.7	386	10	US-09-881-752A-1115	Sequence 115, App	c 605	10	66.7	480	10	US-09-878-574-4688	Sequence 4688, Ap
c 533	10	66.7	387	10	US-09-216-393-61	Sequence 61, Appl	c 606	10	66.7	480	10	US-09-974-300-4502	Sequence 4502, Ap
c 534	10	66.7	389	10	US-09-960-352-220	Sequence 220, App	c 607	10	66.7	486	10	US-09-878-574-4269	Sequence 4269, Ap
c 535	10	66.7	389	10	US-09-960-352-6086	Sequence 6086, Ap	c 608	10	66.7	487	10	US-09-747-153-147	Sequence 147, App
c 536	10	66.7	390	10	US-09-783-590-10785	Sequence 10785, A	c 609	10	66.7	487	10	US-09-747-155-159	Sequence 159, App
c 537	10	66.7	392	10	US-09-878-574-106	Sequence 106, App	c 610	10	66.7	487	10	US-09-747-155-228	Sequence 228, App
c 538	10	66.7	392	10	US-09-960-352-9126	Sequence 9126, Ap	c 611	10	66.7	487	10	US-09-747-155-287	Sequence 287, App
c 539	10	66.7	394	10	US-09-960-352-6266	Sequence 6266, Ap	c 612	10	66.7	488	10	US-09-867-701-3971	Sequence 3971, Ap
c 540	10	66.7	396	10	US-09-974-300-2211	Sequence 2211, Ap	c 613	10	66.7	491	10	US-09-833-381-24	Sequence 24, Appl
c 541	10	66.7	398	10	US-09-878-574-2520	Sequence 2520, Ap	c 614	10	66.7	493	10	US-09-833-381-24	Sequence 24, Appl
c 542	10	66.7	398	10	US-09-783-590-4352	Sequence 4352, Ap	c 615	10	66.7	495	9	US-09-783-295A-191	Sequence 8994, Ap
c 543	10	66.7	399	10	US-09-974-300-3251	Sequence 3251, Ap	c 616	10	66.7	495	9	US-09-978-697-191	Sequence 191, App
c 544	10	66.7	403	10	US-09-878-574-3926	Sequence 3926, Ap	c 617	10	66.7	495	9	US-09-978-697-191	Sequence 191, App
c 545	10	66.7	406	10	US-09-878-574-3848	Sequence 3848, Ap	c 618	10	66.7	496	10	US-09-978-192A-191	Sequence 181, App
c 546	10	66.7	406	10	US-09-974-300-1971	Sequence 1971, Ap	c 619	10	66.7	499	10	US-09-783-590-8183	Sequence 8183, Ap
c 547	10	66.7	407	10	US-09-925-302-390	Sequence 390, App	c 620	10	66.7	500	9	US-09-880-107-3569	Sequence 3569, Ap
c 548	10	66.7	407	10	US-09-922-217-175	Sequence 175, App	c 621	10	66.7	500	9	US-10-047-542-33	Sequence 33, Appl
c 549	10	66.7	407	10	US-09-833-263-175	Sequence 175, App	c 622	10	66.7	500	10	US-09-866-108-15709	Sequence 15709, A
c 550	10	66.7	407	10	US-09-960-352-10916	Sequence 10916, A	c 623	10	66.7	505	10	US-09-864-761-7619	Sequence 7619, Ap
c 551	10	66.7	408	10	US-09-764-877-3715	Sequence 3715, Ap	c 624	10	66.7	511	10	US-09-814-122-18	Sequence 18, Appl
c 552	10	66.7	408	10	US-09-764-877-3716	Sequence 3716, Ap	c 625	10	66.7	511	10	US-09-917-800A-220	Sequence 220, App
c 553	10	66.7	409	10	US-09-864-761-1024	Sequence 1024, Ap	c 626	10	66.7	512	10	US-09-828-313-2	Sequence 2, Appl
c 554	10	66.7	409	10	US-09-960-352-8974	Sequence 8974, Ap	c 627	10	66.7	513	9	US-09-991-496-136	Sequence 136, App
c 555	10	66.7	413	10	US-09-960-352-7288	Sequence 7288, Ap	c 628	10	66.7	514	9	US-09-736-457-1656	Sequence 1656, Ap
c 556	10	66.7	414	10	US-09-974-300-5024	Sequence 5024, Ap	c 629	10	66.7	514	9	US-09-902-941-1656	Sequence 1656, Ap
c 557	10	66.7	416	10	US-09-867-550-607	Sequence 607, App	c 630	10	66.7	515	10	US-09-917-800A-73	Sequence 73, Appl
c 558	10	66.7	417	10	US-09-216-393-63	Sequence 63, Appl	c 631	10	66.7	515	10	US-09-867-701-4756	Sequence 4756, Ap
c 559	10	66.7	417	10	US-09-864-761-13856	Sequence 13856, A	c 632	10	66.7	518	10	US-09-908-711-43	Sequence 43, Appl
c 560	10	66.7	421	10	US-09-960-352-9855	Sequence 9855, Ap	c 633	10	66.7	519	9	US-10-040-733-939	Sequence 939, App
c 561	10	66.7	422	10	US-09-960-352-9158	Sequence 9158, Ap	c 634	10	66.7	519	10	US-09-887-576-780	Sequence 780, App
c 562	10	66.7	424	10	US-09-960-352-9340	Sequence 9340, Ap	c 635	10	66.7	519	12	US-10-095-492-12	Sequence 12, Appl
c 563	10	66.7	425	10	US-09-960-352-6049	Sequence 6049, Ap	c 636	10	66.7	525	10	US-09-833-381-27	Sequence 27, Appl
c 564	10	66.7	425	10	US-09-960-352-7427	Sequence 7427, Ap	c 637	10	66.7	526	10	US-09-917-800A-1156	Sequence 1156, Ap
c 565	10	66.7	425	10	US-09-960-352-8301	Sequence 8301, Ap	c 638	10	66.7	527	10	US-09-925-299-684	Sequence 684, App
c 566	10	66.7	426	9	US-10-125-815-6	Sequence 6, Appl	c 639	10	66.7	527	10	US-09-443-704-1	Sequence 1, Appl
c 567	10	66.7	427	10	US-09-864-761-4063	Sequence 4063, Ap	c 640	10	66.7	534	10	US-09-801-115-1	Sequence 1, Appl
c 568	10	66.7	427	10	US-09-764-847-266	Sequence 266, App	c 641	10	66.7	536	10	US-09-764-855-30	Sequence 30, Appl
c 569	10	66.7	427	10	US-09-960-352-11827	Sequence 11827, A	c 642	10	66.7	537	10	US-09-765-111A-36	Sequence 36, Appl
c 570	10	66.7	428	10	US-09-864-761-18340	Sequence 18340, A	c 643	10	66.7	538	10	US-09-922-217-928	Sequence 928, App
c 571	10	66.7	429	10	US-09-783-590-12378	Sequence 12378, A	c 644	10	66.7	538	10	US-09-833-263-928	Sequence 928, App
c 572	10	66.7	431	10	US-09-867-550-23	Sequence 23, Appl	c 645	10	66.7	540	10	US-09-815-242-7725	Sequence 7725, Ap
c 573	10	66.7	431	10	US-09-924-035A-333	Sequence 333, App	c 646	10	66.7	540	10	US-09-922-217-964	Sequence 964, App
c 574	10	66.7	433	10	US-09-956-004-116	Sequence 116, App	c 647	10	66.7	540	10	US-09-833-263-964	Sequence 964, App
c 575	10	66.7	433	10	US-09-960-352-818	Sequence 818, App	c 648	10	66.7	540	10	US-09-887-576-796	Sequence 796, App
c 576	10	66.7	434	9	US-10-079-623-245	Sequence 245, App	c 649	10	66.7	543	10	US-09-864-761-14939	Sequence 14939, A
c 577	10	66.7	436	10	US-09-960-352-12415	Sequence 12415, A	c 650	10	66.7	543	10	US-09-970-532-3	Sequence 3, Appl
c 578	10	66.7	438	9	US-09-938-842A-899	Sequence 899, App	c 651	10	66.7	546	9	US-09-938-842A-1339	Sequence 1339, Ap
c 579	10	66.7	440	10	US-09-960-352-12870	Sequence 12870, A	c 652	10	66.7	549	10	US-09-867-701-4856	Sequence 4856, Ap
c 580	10	66.7	441	10	US-09-880-107-1057	Sequence 1057, Ap	c 653	10	66.7	549	10	US-09-734-017A-45	Sequence 45, Appl
c 581	10	66.7	442	10	US-09-867-701-5221	Sequence 5221, Ap	c 654	10	66.7	550	10	US-09-919-580-307	Sequence 307, App
c 582	10	66.7	445	10	US-09-783-590-3731	Sequence 3731, Ap	c 655	10	66.7	551	10	US-09-969-708-592	Sequence 592, App
c 583	10	66.7	445	12	US-10-027-450-12	Sequence 12, Appl	c 656	10	66.7	552	10	US-09-917-800A-1272	Sequence 1272, Ap
c 584	10	66.7	447	10	US-09-998-598-884	Sequence 884, App	c 657	10	66.7	554	10	US-09-974-300-95	Sequence 655, App
c 585	10	66.7	449	10	US-09-864-761-13829	Sequence 13829, A	c 658	10	66.7	555	10	US-09-919-580-327	Sequence 95, Appl
c 586	10	66.7	450	10	US-09-974-300-3110	Sequence 3110, Ap	c 659	10	66.7	566	10	US-09-864-761-25808	Sequence 25808, A
c 587	10	66.7	451	9	US-09-954-531-460	Sequence 460, App	c 660	10	66.7	567	10	US-09-864-761-31880	Sequence 31880, A
c 588	10	66.7	451	10	US-09-960-352-8378	Sequence 8378, Ap	c 661	10	66.7	567	10	US-09-864-761-31880	Sequence 31880, A
c 589	10	66.7	453	10	US-09-960-352-6118	Sequence 6118, Ap	c 662	10	66.7	568	10	US-09-974-300-2876	Sequence 2876, Ap
c 590	10	66.7	456	10	US-09-974-300-6234	Sequence 6234, Ap	c 663	10	66.7	569	10	US-09-864-761-13135	Sequence 13135, A
c 591	10	66.7	460	10	US-09-864-761-15176	Sequence 15176, A	c 664	10	66.7	571	10	US-09-833-790-344	Sequence 344, App
c 592	10	66.7	461	10	US-09-864-761-11233	Sequence 11233, A	c 665	10	66.7	572	10	US-09-974-300-1878	Sequence 1878, Ap
c 593	10	66.7	462	10	US-09-735-705-289	Sequence 289, App	c 666	10	66.7	573	10	US-09-764-869-1483	Sequence 1483, Ap
c 594	10	66.7	462	10	US-09-850-716A-289	Sequence 289, App	c 667	10	66.7	573	10	US-09-764-869-1484	Sequence 1484, Ap
c 595	10	66.7	462	10	US-09-897-778-289	Sequence 289, App	c 668	10	66.7	574	10	US-09-864-761-18330	Sequence 18330, A
c 596	10	66.7	465	10	US-09-864-761-10105	Sequence 10105, A	c 669	10	66.7	574	10	US-09-864-761-20532	Sequence 20532, A
c 597	10	66.7	467	10	US-09-864-761-2463	Sequence 2463, Ap	c 670	10	66.7	574	10	US-09-922-217-840	Sequence 840, App
c 598	10	66.7	468	10	US-09-864-761-672	Sequence 672, App	c 671	10	66.7	578	10	US-09-833-263-840	Sequence 840, App
c 599	10	66.7	472	10	US-09-880-107-2556	Sequence 2556, Ap	c 672	10	66.7	579	10	US-09-764-853-411	Sequence 411, App
c 600	10	66.7	474	10	US-09-833-790-285	Sequence 285, App	c 673	10	66.7	579	10	US-09-864-761-9907	Sequence 9907, Ap
c 601	10	66.7	476	10	US-09-867-701-4771	Sequence 4771, Ap	c 674	10	66.7	579	10	US-09-873-880-5	Sequence 5, Appl
c 602	10	66.7	476	10	US-09-867-701-7285	Sequence 7285, Ap	c 675	10	66.7	588	10	US-09-864-761-9158	Sequence 9158, Ap
c 603	10	66.7	480	9	US-10-046-935-1959	Sequence 1959, Ap	c 676	10	66.7	590	10	US-09-919-580-612	Sequence 612, App
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c 677	10	66.7	590	10	US-09-878-574-4342	Sequence 4342, Ap	c 750	10	66.7	812	10	US-09-822-827-471	Sequence 471, App
c 678	10	66.7	592	10	US-09-878-574-541	Sequence 541, App	c 751	10	66.7	813	10	US-09-974-300-5032	Sequence 5032, Ap
c 679	10	66.7	597	10	US-09-974-300-4947	Sequence 4947, Ap	c 752	10	66.7	818	9	US-09-985-442-3	Sequence 3, Appli
c 680	10	66.7	597	10	US-09-974-300-4977	Sequence 4977, Ap	c 753	10	66.7	818	10	US-09-878-574-4624	Sequence 4624, Ap
c 681	10	66.7	598	10	US-09-770-149-992	Sequence 992, App	c 754	10	66.7	818	10	US-09-983-580-3	Sequence 3, Appli
c 682	10	66.7	599	10	US-09-842-552-21	Sequence 21, Appl	c 755	10	66.7	824	10	US-09-816-828-2	Sequence 2, Appli
c 683	10	66.7	599	10	US-09-925-300-100	Sequence 100, App	c 756	10	66.7	831	9	US-10-001-887-58	Sequence 58, Appl
c 684	10	66.7	601	10	US-09-867-701-10472	Sequence 10472, A	c 757	10	66.7	846	10	US-09-974-300-5070	Sequence 5070, Ap
c 685	10	66.7	606	10	US-09-917-800A-162	Sequence 162, App	c 758	10	66.7	850	12	US-09-964-238-8	Sequence 8, Appli
c 686	10	66.7	607	10	US-09-922-217-951	Sequence 951, App	c 759	10	66.7	852	12	US-10-024-579-9	Sequence 9, Appli
c 687	10	66.7	607	10	US-09-833-263-951	Sequence 951, App	c 760	10	66.7	858	10	US-09-815-242-4013	Sequence 4013, Ap
c 688	10	66.7	608	10	US-09-770-149-892	Sequence 892, App	c 761	10	66.7	858	10	US-09-815-242-7815	Sequence 7815, Ap
c 689	10	66.7	609	10	US-09-974-300-2569	Sequence 2569, Ap	c 762	10	66.7	861	10	US-09-925-297-286	Sequence 286, App
c 690	10	66.7	616	10	US-09-764-877-2564	Sequence 2564, Ap	c 763	10	66.7	864	10	US-09-764-864-156	Sequence 156, App
c 691	10	66.7	619	10	US-09-879-536-815	Sequence 815, App	c 764	10	66.7	871	10	US-09-956-999-7	Sequence 7, Appli
c 692	10	66.7	624	10	US-09-770-149-759	Sequence 759, App	c 765	10	66.7	871	10	US-09-962-832-101	Sequence 101, App
c 693	10	66.7	624	10	US-09-880-107-309	Sequence 309, App	c 766	10	66.7	871	10	US-09-880-107-2307	Sequence 2307, Ap
c 694	10	66.7	630	10	US-09-925-299-293	Sequence 293, App	c 767	10	66.7	873	10	US-09-815-242-7800	Sequence 7800, Ap
c 695	10	66.7	633	10	US-09-867-550-777	Sequence 777, App	c 768	10	66.7	882	10	US-09-974-300-2352	Sequence 2352, Ap
c 696	10	66.7	633	10	US-09-974-300-6076	Sequence 6076, Ap	c 769	10	66.7	882	10	US-09-764-864-642	Sequence 642, App
c 697	10	66.7	633	10	US-09-974-300-6076	Sequence 6076, Ap	c 770	10	66.7	885	10	US-09-815-242-9236	Sequence 9236, Ap
c 698	10	66.7	641	10	US-09-833-381-1326	Sequence 1326, Ap	c 771	10	66.7	896	10	US-09-884-441-22	Sequence 22, Appl
c 699	10	66.7	642	10	US-09-974-300-1333	Sequence 1333, Ap	c 772	10	66.7	900	10	US-09-764-864-211	Sequence 211, App
c 700	10	66.7	644	10	US-09-886-404-1	Sequence 1, Appli	c 773	10	66.7	903	10	US-09-764-877-2956	Sequence 2956, Ap
c 701	10	66.7	644	12	US-10-001-843-114	Sequence 114, App	c 774	10	66.7	905	10	US-09-748-033-5	Sequence 5, Appli
c 702	10	66.7	657	10	US-09-974-300-5602	Sequence 5602, Ap	c 775	10	66.7	905	10	US-09-969-708-88	Sequence 88, Appl
c 703	10	66.7	663	9	US-09-978-295A-189	Sequence 189, App	c 776	10	66.7	905	10	US-09-969-708-88	Sequence 88, Appl
c 704	10	66.7	663	9	US-09-978-697-189	Sequence 189, App	c 777	10	66.7	912	8	US-08-902-572-13	Sequence 13, Appl
c 705	10	66.7	663	9	US-09-978-192A-189	Sequence 189, App	c 778	10	66.7	912	10	US-09-862-179A-40	Sequence 40, Appl
c 706	10	66.7	675	10	US-09-764-864-678	Sequence 678, App	c 779	10	66.7	918	10	US-09-815-242-7705	Sequence 7705, Ap
c 707	10	66.7	678	10	US-09-815-242-7612	Sequence 7612, Ap	c 780	10	66.7	918	10	US-09-886-055-300	Sequence 300, App
c 708	10	66.7	680	10	US-09-974-300-5462	Sequence 5462, Ap	c 781	10	66.7	928	12	US-10-001-843-115	Sequence 115, App
c 709	10	66.7	683	10	US-09-867-701-6261	Sequence 6261, Ap	c 782	10	66.7	930	10	US-09-771-161A-49	Sequence 49, Appl
c 710	10	66.7	686	10	US-09-910-943-313	Sequence 313, App	c 783	10	66.7	938	10	US-09-770-445-367	Sequence 367, App
c 711	10	66.7	693	10	US-09-974-300-1576	Sequence 1576, Ap	c 784	10	66.7	949	10	US-09-833-381-1064	Sequence 1064, Ap
c 712	10	66.7	714	12	US-10-078-929-85	Sequence 85, Appl	c 785	10	66.7	949	10	US-09-791-171-11	Sequence 11, Appl
c 713	10	66.7	717	10	US-09-815-242-7765	Sequence 7765, Ap	c 786	10	66.7	951	10	US-09-974-300-5212	Sequence 5212, Ap
c 714	10	66.7	717	12	US-10-024-579-15	Sequence 15, App	c 787	10	66.7	954	9	US-09-877-650-12	Sequence 12, Appl
c 715	10	66.7	718	10	US-09-759-143-313	Sequence 313, App	c 788	10	66.7	954	10	US-09-871-856-12	Sequence 12, Appl
c 716	10	66.7	718	10	US-09-780-669-313	Sequence 313, App	c 789	10	66.7	957	10	US-09-974-300-7292	Sequence 7292, Ap
c 717	10	66.7	718	10	US-09-822-827-313	Sequence 313, App	c 790	10	66.7	958	10	US-09-864-761-15366	Sequence 15366, A
c 718	10	66.7	719	10	US-09-920-345-28	Sequence 28, Appl	c 791	10	66.7	960	10	US-09-741-669-186	Sequence 186, App
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c 720	10	66.7	723	10	US-09-791-578-5	Sequence 5, Appli	c 793	10	66.7	961	10	US-09-815-242-6301	Sequence 2788, Ap
c 721	10	66.7	723	10	US-09-791-540-5	Sequence 5, Appli	c 794	10	66.7	961	10	US-09-974-300-2788	Sequence 4233, Ap
c 722	10	66.7	724	10	US-09-070-927A-931	Sequence 931, App	c 795	10	66.7	964	10	US-09-974-300-4233	Sequence 1894, Ap
c 723	10	66.7	726	10	US-09-143-127-3	Sequence 3, Appli	c 796	10	66.7	968	10	US-09-974-300-1894	Sequence 1572, Ap
c 724	10	66.7	726	10	US-09-143-127-4	Sequence 4, Appli	c 797	10	66.7	968	10	US-09-864-761-1572	Sequence 2761, Ap
c 725	10	66.7	726	10	US-09-815-242-6075	Sequence 6075, Ap	c 798	10	66.7	969	10	US-09-886-055-254	Sequence 254, App
c 726	10	66.7	747	10	US-09-915-580-806	Sequence 806, App	c 799	10	66.7	978	9	US-09-938-842A-1549	Sequence 1549, Ap
c 727	10	66.7	749	10	US-09-791-578-1	Sequence 1, Appli	c 800	10	66.7	980	10	US-09-752-514-2	Sequence 2, Appli
c 728	10	66.7	753	10	US-09-791-540-1	Sequence 1, Appli	c 801	10	66.7	984	10	US-09-770-445-266	Sequence 266, App
c 729	10	66.7	756	10	US-09-887-576-822	Sequence 822, App	c 802	10	66.7	987	10	US-09-738-396-41	Sequence 41, Appl
c 730	10	66.7	756	10	US-09-915-580-806	Sequence 806, App	c 803	10	66.7	987	10	US-09-974-300-1183	Sequence 1183, Ap
c 731	10	66.7	758	9	US-09-956-086-1	Sequence 1, Appli	c 804	10	66.7	990	10	US-09-919-344-25	Sequence 25, Appl
c 732	10	66.7	758	9	US-09-956-087-1	Sequence 1, Appli	c 805	10	66.7	993	10	US-09-974-300-4796	Sequence 4, Appli
c 733	10	66.7	762	9	US-09-826-025-21	Sequence 21, Appl	c 806	10	66.7	995	12	US-10-021-509-4	Sequence 4, Appli
c 734	10	66.7	763	10	US-09-919-580-862	Sequence 862, App	c 807	10	66.7	995	12	US-10-021-509-12	Sequence 12, Appl
c 735	10	66.7	763	10	US-09-764-877-3667	Sequence 3667, Ap	c 808	10	66.7	1011	10	US-09-742-732-3	Sequence 3, Appli
c 736	10	66.7	772	10	US-09-764-870-95	Sequence 95, Appl	c 809	10	66.7	1017	10	US-09-961-527A-14	Sequence 14, Appl
c 737	10	66.7	772	10	US-09-764-870-95	Sequence 13, Appl	c 810	10	66.7	1030	9	US-09-925-301-334	Sequence 334, App
c 738	10	66.7	782	9	US-09-985-442-1	Sequence 1, Appli	c 811	10	66.7	1035	9	US-09-938-842A-5334	Sequence 5334, Ap
c 739	10	66.7	782	10	US-09-971-578-3	Sequence 3, Appli	c 812	10	66.7	1035	10	US-09-815-242-7269	Sequence 7269, Ap
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c 741	10	66.7	787	10	US-09-983-580-1	Sequence 1, Appli	c 814	10	66.7	1054	9	US-09-966-546-27	Sequence 27, Appl
c 742	10	66.7	787	10	US-09-764-887-60	Sequence 60, Appl	c 815	10	66.7	1054	9	US-09-966-545-27	Sequence 27, Appl
c 743	10	66.7	788	10	US-09-974-300-5996	Sequence 5996, Ap	c 816	10	66.7	1071	9	US-09-815-242-7426	Sequence 7426, Ap
c 744	10	66.7	792	10	US-09-974-300-2830	Sequence 2830, Ap	c 817	10	66.7	1077	10	US-09-938-842A-700	Sequence 700, App
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c 746	10	66.7	799	10	US-09-864-761-19477	Sequence 19477, A	c 819	10	66.7	1077	10	US-09-974-300-3031	Sequence 3031, Ap
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c 748	10	66.7	810	10	US-09-974-300-1331	Sequence 1331, Ap	c 821	10	66.7	1093	10	US-09-969-708-214	Sequence 214, App
c 749	10	66.7	812	10	US-09-759-143-471	Sequence 471, App	c 822	10	66.7	1093	10	US-09-880-107-2302	Sequence 2302, Ap

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c 825	10	66.7	1111	10	US-09-833-381-1175	Sequence 1175, Ap	c 898	10	66.7	1369	10	US-09-815-242-9922	Sequence 9922, Ap
c 826	10	66.7	1122	10	US-09-887-576-802	Sequence 802, App	c 899	10	66.7	1372	10	US-09-822-830A-589	Sequence 589, App
c 827	10	66.7	1128	10	US-09-815-242-5968	Sequence 5968, App	c 900	10	66.7	1372	10	US-09-765-111A-13	Sequence 13, Appl
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c 831	10	66.7	1142	10	US-09-935-390A-11	Sequence 11, Appl	c 904	10	66.7	1383	10	US-09-974-300-916	Sequence 916, App
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c 849	10	66.7	1221	10	US-09-974-300-2319	Sequence 2319, Ap	c 922	10	66.7	1474	10	US-09-840-795-7	Sequence 7, Appli
c 850	10	66.7	1224	10	US-09-974-300-8308	Sequence 8308, Ap	c 923	10	66.7	1476	10	US-09-815-242-7177	Sequence 7177, Ap
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c 855	10	66.7	1246	10	US-09-974-300-38	Sequence 38, Appl	c 928	10	66.7	1485	9	US-09-712-363-76	Sequence 76, Appl
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c 859	10	66.7	1257	9	US-09-971-536-29	Sequence 29, Appl	c 932	10	66.7	1498	10	US-09-919-172-100	Sequence 100, App
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c 867	10	66.7	1278	10	US-09-943-671-18	Sequence 18, Appl	c 940	10	66.7	1575	10	US-09-917-800A-1540	Sequence 1540, Ap
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c 886	10	66.7	1344	10	US-09-790-264-35	Sequence 35, Appl	c 959	10	66.7	1660	10	US-09-866-562-51	Sequence 51, Appl
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c 972 10 66.7 1758 10 US-09-815-242-7656 Sequence 7656, Ap
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c 975 10 66.7 1794 10 US-09-943-671-36 Sequence 36, Appl
c 976 10 66.7 1812 10 US-09-815-242-4147 Sequence 4147, Ap
c 977 10 66.7 1818 10 US-09-758-269-15 Sequence 15, Appl
c 978 10 66.7 1831 10 US-09-853-386-75 Sequence 75, Appl
c 979 10 66.7 1838 10 US-09-764-887-620 Sequence 620, App
c 980 10 66.7 1869 10 US-09-864-761-3765 Sequence 3765, Ap
c 981 10 66.7 1889 10 US-09-779-307-10 Sequence 10, Appl
c 982 10 66.7 1890 10 US-09-791-171-71 Sequence 71, Appl
c 983 10 66.7 1890 10 US-09-880-107-3390 Sequence 3390, Ap
c 984 10 66.7 1891 10 US-09-779-307-9 Sequence 9, Appli
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c 988 10 66.7 1911 10 US-09-815-242-7963 Sequence 7963, Ap
c 989 10 66.7 1917 10 US-09-919-781-1 Sequence 1, Appli
c 990 10 66.7 1918 9 US-09-860-670-77 Sequence 77, Appl
c 991 10 66.7 1926 10 US-09-764-853-238 Sequence 238, App
c 992 10 66.7 1945 10 US-09-925-301-588 Sequence 588, App
c 993 10 66.7 1949 10 US-09-740-027-1 Sequence 1, Appli
c 994 10 66.7 1961 10 US-09-864-761-9239 Sequence 9239, Ap
c 995 10 66.7 1967 10 US-09-880-107-2417 Sequence 2417, Ap
c 996 10 66.7 1969 9 US-09-981-876-107 Sequence 107, App
c 997 10 66.7 1977 10 US-09-954-456-804 Sequence 804, App
c 998 10 66.7 1977 10 US-09-880-107-3407 Sequence 3407, Ap
c 999 10 66.7 1977 10 US-09-967-768A-190 Sequence 190, App
1000 10 66.7 1984 10 US-09-887-576-38 Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-944-807-9 ; Sequence 9, Application US/09944807
; Patent No. US2002011949A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3992
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-944-807-9
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 764 CCTTCTCGCCCTG 776
RESULT 2
US-09-764-878-258/c
; Sequence 258, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 258
; LENGTH: 4558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-258
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTCTCGCCCTGT 14
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RESULT 3
US-09-764-860-937/c
; Sequence 937, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
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; ORGANISM: Homo sapiens
US-09-764-860-937
Query Match 86.7%; Score 13; DB 10; Length 4558;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTCTCGCCCTGT 14
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RESULT 4
US-09-430-029-1/c
; Sequence 1, Application US/09430029
; Patent No. US20020168738A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Canc
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CPO13982US
; CURRENT APPLICATION NUMBER: US/09/430,029
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: JP P1998-310801
; EARLIER FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5828
; TYPE: DNA
; ORGANISM: Burkholderia cepacia

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NAME/KEY: CDS
LOCATION: (234)..(443)
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NAME/KEY: CDS
LOCATION: (3810)..(4871)
OTHER INFORMATION: tomP
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LOCATION: (4876)..(5229)
OTHER INFORMATION: tomQ
US-09-430-029-1

Query Match 86.7%; Score 13; DB 9; Length 5828;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCTG 13
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RESULT 5
US-09-761-534A-17
Sequence 17, Application US/09761534A
Patent No. US20020146426A1
GENERAL INFORMATION:
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Cho, Bryan K.
APPLICANT: Palliser, Deborah
APPLICANT: Chen, Jianzhu
APPLICANT: Eisen, Herman N.
APPLICANT: Young, Richard A.
TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
TITLE OF INVENTION: CD4+T Cell-Independent
FILE REFERENCE: 0399.2006-003
CURRENT APPLICATION NUMBER: US/09/761,534A
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/176,143
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 49
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PCR Primer OQH011
US-09-761-534A-17

Query Match 80.0%; Score 12; DB 10; Length 49;
Best Local Similarity 100.0%; Pred. No. 47;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTCTCGCCT 12
Db 31 CCTTCTCGCCT 42
RESULT 6
US-09-864-761-17150
Sequence 17150, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17150
LENGTH: 152
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF000341.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: NT HIT: AL163303.2, EVALUATE 1.00e-80
; OTHER INFORMATION: SWISSPROT HIT: O60241, EVALUATE 4.00e+00
US-09-864-761-17150

Query Match 80.0%; Score 12; DB 10; Length 152;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13
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Db 56 CTCTCGCCCTG 67

RESULT 7

US-09-974-300-7193/c
; Sequence 7193, Application US/09974300
; Patent No. US20020146721A1

; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7193
; LENGTH: 173
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-7193

Query Match 80.0%; Score 12; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13
|||||
Db 99 CTCTCGCCCTG 88

RESULT 8

US-09-923-876-97/c
; Sequence 97, Application US/09923876
; Patent No. US20020013958A1

; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 97
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700142552H1

US-09-923-876-97

Query Match 80.0%; Score 12; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13
|||||
Db 50 CTCTCGCCCTG 39

RESULT 9

US-09-983-965-5128/c
; Sequence 5128, Application US/09983965
; Patent No. US20020137160A1

; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5128
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 33-LIB34-055-Q1-E1-A2
US-09-983-965-5128

Query Match 80.0%; Score 12; DB 10; Length 356;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13
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Db 216 CTCTCGCCCTG 205

RESULT 10

US-09-867-701-5624
; Sequence 5624, Application US/09867701
; Patent No. US20020132237A1

; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5624
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-5624

Query Match 80.0%; Score 12; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTCGCCCTGTT 15

Db 19 TCTCGCCCTGTT 30
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RESULT 11

US-09-864-761-3392/c
; Sequence 3392, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3392
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109748.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
US-09-864-761-3392

Query Match 80.0%; Score 12; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTG 13
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Db 283 CTTCTCGCCCTG 272

RESULT 12

US-09-954-531-880/c
; Sequence 880, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; FILE REFERENCE: Gene Sets
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0.
; SEQ ID NO 880
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-880

Query Match 80.0%; Score 12; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTG 13
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Db 300 CTTCTCGCCCTG 289

RESULT 13

US-09-864-761-337
; Sequence 337, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
US-09-864-761-337

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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 337
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF000341.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
US-09-864-761-337

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Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTG 13
Db 353 CTTCTCGCCCTG 364
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RESULT 14
US-09-784-423-17
; Sequence 17, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 17
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; LIBRARY: plasmid, pGem3zf(+)
; CLONE: G158
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 5q
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-784-423-17

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Query Match      80.0%; Score 12; DB 10; Length 447;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCT 12
Db 85 CCTTCTCGCCCT 96
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RESULT 15
US-09-954-531-813/c
; Sequence 813, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 813
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)

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; OTHER INFORMATION: n=a,t,g or c
US-09-954-531-813

Query Match 80.0%; Score 12; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCT 12
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Db 342 CCTTCTCGCCCT 331

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:56:23 ; Search time 1655.5 Seconds
(without alignments)
146.743 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 cctctgcgcctgtt 15

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Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Post-processing: Listing first 1000 summaries

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- 7: em_estro:*
- 8: em_htc:*
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- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 82	14	93.3	564	13	BI317565	BI317565 RE58483.5	c 155	13	86.7	296	12	BF665526	BF665526 602119721
c 83	14	93.3	574	9	AI295101	AI295101 LP08633.5	c 156	13	86.7	297	9	AV024534	AV024534
c 84	14	93.3	589	12	BG640795	BG640795 SDI1944.5	c 157	13	86.7	302	17	AF455800	AF455800
c 85	14	93.3	590	13	BI962198	BI962198 ID29f12.y	c 158	13	86.7	316	12	BG013086	BG013086 PMI-GN018
c 86	14	93.3	593	13	BI964495	BI964495 ID38g09.y	c 159	13	86.7	319	10	BB464836	BB464836
c 87	14	93.3	598	12	BF492172	BF492172 AT29061.5	c 160	13	86.7	322	9	AV149524	AV149524
c 88	14	93.3	601	9	AI063162	AI063162 GH02678.5	c 161	13	86.7	329	14	C72317	C72317
c 89	14	93.3	620	10	AV752075	AV752075 AV752075	c 162	13	86.7	339	17	AQ570264	AQ570264 HS_5356_A
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c 92	14	93.3	639	12	BF245279	BF245279 601863755	c 165	13	86.7	351	9	AL589439	AL589439
c 93	14	93.3	641	13	BI612566	BI612566 RH41483.5	c 166	13	86.7	351	13	BM089644	BM089644 503455_MA
c 94	14	93.3	650	17	AQ952273	AQ952273 Sheared.D	c 167	13	86.7	357	17	AZ708915	AZ708915 RPCI-24-1
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c 96	14	93.3	678	12	BG600136	BG600136 ESF505031	c 169	13	86.7	361	9	AA131959	AA131959
c 97	14	93.3	739	12	BG127690	BG127690 ESF473252	c 170	13	86.7	362	14	W32787	W32787
c 98	14	93.3	765	12	BG696837	BG696837 603659892	c 171	13	86.7	364	12	BG072218	BG072218
c 99	14	93.3	765	13	BI655867	BI655867 603284885	c 172	13	86.7	365	10	AW910077	AW910077
c 100	14	93.3	766	12	AQ912735	AQ912735 nbe00380	c 173	13	86.7	366	10	AW751736	AW751736 CM2-C7010
c 101	14	93.3	789	12	BG474591	BG474591 602517381	c 174	13	86.7	367	13	BM639696	BM639696
c 102	14	93.3	792	12	BG862397	BG862397 602796294	c 175	13	86.7	369	9	AA241135	AA241135
c 103	14	93.3	804	13	BI690575	BI690575 603309958	c 176	13	86.7	373	13	BI165328	BI165328
c 104	14	93.3	807	17	AQ916363	AQ916363 nbe00063M	c 177	13	86.7	373	17	AZ100915	AZ100915
c 105	14	93.3	820	9	AA736192	AA736192 HL08145.5	c 178	13	86.7	374	17	AQ772705	AQ772705
c 106	14	93.3	821	17	CNS01ZBM	AL174091 Tetraodon	c 179	13	86.7	378	10	AW711363	AW711363
c 107	14	93.3	831	17	CNS01YK1	AL173098 Tetraodon	c 180	13	86.7	379	10	AW98307	AW98307
c 108	14	93.3	839	12	BG780574	BG780574 SEADM000	c 181	13	86.7	380	14	H00632	H00632
c 109	14	93.3	875	12	BF978039	BF978039 602147938	c 182	13	86.7	381	13	BJ191222	BJ191222
c 110	14	93.3	877	12	BF141948	BF141948 601790438	c 183	13	86.7	383	12	BG085052	BG085052
c 111	14	93.3	879	17	CNS03M2K	AL251417 Tetraodon	c 184	13	86.7	384	10	AW670067	AW670067
c 112	14	93.3	894	12	BF182664	BF182664 601809444	c 185	13	86.7	387	10	AW287074	AW287074
c 113	14	93.3	895	12	BG864418	BG864418 602798623	c 186	13	86.7	387	14	T56696	T56696
c 114	14	93.3	913	12	BG425118	BG425118 602446607	c 187	13	86.7	388	13	BM291738	BM291738
c 115	14	93.3	936	12	BF699731	BF699731 602127158	c 188	13	86.7	392	17	BH284841	BH284841
c 116	14	93.3	936	17	CNS06JQA	AL401352 T7 end of	c 189	13	86.7	392	9	AA636988	AA636988
c 117	14	93.3	976	14	BQ647960	BQ647960 AGENCOURT	c 190	13	86.7	393	10	BM816611	BM816611
c 118	14	93.3	1014	14	BQ895183	BQ895183 AGENCOURT	c 191	13	86.7	396	13	BM343266	BM343266
c 119	14	93.3	1038	17	CNS06FH2	AL398625 T3 end of	c 192	13	86.7	398	10	BB736799	BB736799
c 120	14	93.3	1039	17	CNS03F6G	AL241297 Tetraodon	c 193	13	86.7	399	10	AW479086	AW479086
c 121	14	93.3	1065	14	BM806011	BM806011 AGENCOURT	c 194	13	86.7	400	10	BE036904	BE036904
c 122	14	93.3	1075	12	BG026887	BG026887 602294186	c 195	13	86.7	403	10	AW240878	AW240878
c 123	14	93.3	1300	17	AG064777	AG064777 Pan trogl	c 196	13	86.7	403	13	BI517072	BI517072
c 124	14	93.3	1553	12	BF164622	BF164622 601772403	c 197	13	86.7	404	9	AJ312766	AJ312766
c 125	14	93.3	1686	12	BG256672	BG256672 602370859	c 198	13	86.7	404	13	BI900964	BI900964
c 126	14	93.3	3776	11	BC021653	BC021653 Mus muscu	c 199	13	86.7	404	14	BQ910504	BQ910504
c 127	13	86.7	106	10	AW818491	AW818491 RCL-ST027	c 200	13	86.7	405	9	AA664487	AA664487
c 128	13	86.7	166	12	BF431844	BF431844 nab51b09.	c 201	13	86.7	415	12	BF386784	BF386784
c 129	13	86.7	178	10	BB201173	BB201173 BB201173	c 202	13	86.7	415	9	AI135691	AI135691
c 130	13	86.7	182	9	AV122504	AV122504 AV122504	c 203	13	86.7	416	10	AV646225	AV646225
c 131	13	86.7	192	9	AV287339	AV287339 AV287339	c 204	13	86.7	420	10	AW784309	AW784309
c 132	13	86.7	193	14	BQ041219	BQ041219 9d35c04.y	c 205	13	86.7	420	10	AW784314	AW784314
c 133	13	86.7	196	9	AA254435	AA254435 val6603.r	c 206	13	86.7	422	9	AI018097	AI018097
c 134	13	86.7	199	13	BI187373	BI187373 a2g12fs.r	c 207	13	86.7	423	9	AA290403	AA290403
c 135	13	86.7	201	10	BB425208	BB425208 BB425208	c 208	13	86.7	426	12	BG050015	BG050015
c 136	13	86.7	215	13	BJ194203	BJ194203 BJ194203	c 209	13	86.7	426	12	BM536448	BM536448
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c 139	13	86.7	220	17	BH583033	BH583033 BOHMH1TR	c 212	13	86.7	428	12	BF737928	BF737928
c 140	13	86.7	227	10	BB451401	BB451401 BB451401	c 213	13	86.7	430	17	BH225420	BH225420
c 141	13	86.7	227	10	BB469156	BB469156 BB469156	c 214	13	86.7	431	13	BI215727	BI215727
c 142	13	86.7	228	10	BB394206	BB394206 BB394206	c 215	13	86.7	433	10	BE109473	BE109473
c 143	13	86.7	233	10	BB578929	BB578929 BB578929	c 216	13	86.7	436	13	BI615436	BI615436
c 144	13	86.7	269	10	BB298225	BB298225 BB298225	c 217	13	86.7	437	10	BF046660	BF046660
c 145	13	86.7	270	10	BB373150	BB373150 BB373150	c 218	13	86.7	441	12	BF046660	BF046660
c 146	13	86.7	272	10	BB031537	BB031537 BB031537	c 219	13	86.7	443	10	AW098163	AW098163
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c 148	13	86.7	274	10	BB414286	BB414286 BB414286	c 221	13	86.7	445	14	BM866975	BM866975
c 149	13	86.7	276	10	BB475184	BB475184 BB475184	c 222	13	86.7	445	14	N66187	N66187
c 150	13	86.7	277	10	BB164207	BB164207 BB164207	c 223	13	86.7	445	14	R75714	R75714
c 151	13	86.7	283	10	BB694772	BB694772 BB694772	c 224	13	86.7	447	10	AV940105	AV940105
c 152	13	86.7	287	10	BB159014	BB159014 BB159014	c 225	13	86.7	452	9	AA696511	AA696511

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227	13	86.7	454	13	BI615728	BI615728 RH45462.5	300	13	86.7	519	13	BI610986	BI610986 RH17039.5
c 228	13	86.7	455	9	AI260421	AI260421 LP04279.5	301	13	86.7	520	13	BE630693	BE630693 uu47b07.x
229	13	86.7	455	9	AU081347	AU081347 AU081347	302	13	86.7	520	13	BJ203415	BJ203415 BJ203415
230	13	86.7	455	13	BI482722	BI482722 RE63454.5	303	13	86.7	521	9	AI106861	AI106861 GH06109.5
c 231	13	86.7	456	9	AA710755	AA710755 vt44a10.r	304	13	86.7	521	9	AU030909	AU030909 AU030909
c 232	13	86.7	456	9	AA802868	AA802868 GM06479.5	305	13	86.7	521	9	AA568004	AA568004 HL02118.5
233	13	86.7	457	13	BJ200466	BJ200466 BJ200466	306	13	86.7	521	13	BI365549	BI365549 RE50905.5
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237	13	86.7	464	13	BI619411	BI619411 RH50443.5	310	13	86.7	525	17	AQ466318	AQ466318 HS.5130.A
c 238	13	86.7	468	12	BE855285	BE855285 ux28c10.y	c 311	13	86.7	526	9	AL825622	AL825622 AL825622
239	13	86.7	469	13	BI237894	BI237894 RE34222.5	c 312	13	86.7	526	17	AZ520955	AZ520955 RPT-11-2
c 240	13	86.7	469	14	H05179	H05179 y185c04.r1	c 313	13	86.7	527	13	BI353963	BI353963 GM25730.5
c 241	13	86.7	470	14	H08085	H08085 y186e12.r1	c 314	13	86.7	530	12	EG278092	EG278092 ale02np.f
242	13	86.7	472	13	BI239228	BI239228 RE35859.5	c 315	13	86.7	530	13	BM290997	BM290997 EST577531
243	13	86.7	473	13	BI372794	BI372794 RE59965.5	c 316	13	86.7	531	10	AM670058	AM670058 L13784.MA
244	13	86.7	473	13	BI613472	BI613472 RH42632.5	317	13	86.7	531	13	BJ484881	BJ484881 BJ484881
c 245	13	86.7	475	9	AI239224	AI239224 GM09053.3	318	13	86.7	532	12	BF198983	BF198983 249007.MA
246	13	86.7	477	13	BI608867	BI608867 RH13578.5	319	13	86.7	534	13	BI196323	BI196323 BJ196323
c 247	13	86.7	477	17	AQ811825	AQ811825 HS.5528.B	320	13	86.7	536	13	BI577793	BI577793 RE71538.5
248	13	86.7	478	9	AI106622	AI106622 GH06680.5	321	13	86.7	536	14	BQ798685	BQ798685 EST.854.G
249	13	86.7	480	12	BF623787	BF623787 RH56130.5	322	13	86.7	537	13	BI610256	BI610256 RH15345.5
c 250	13	86.7	480	12	BF651974	BF651974 275400.MA	323	13	86.7	538	9	AI296743	AI296743 LP10808.5
c 251	13	86.7	481	10	AV783662	AV783662 AV783662	324	13	86.7	538	13	BI614737	BI614737 RH44194.5
252	13	86.7	481	12	BF489488	BF489488 AT25444.5	325	13	86.7	539	13	BI241339	BI241339 RE38377.5
253	13	86.7	482	9	AU239566	AU239566 AU239566	326	13	86.7	539	13	BI579102	BI579102 RE73078.5
254	13	86.7	482	13	BM279151	BM279151 ND.ad1.03	327	13	86.7	540	13	BI169418	BI169418 RE10586.5
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258	13	86.7	485	9	AI134755	AI134755 GH12301.5	331	13	86.7	540	13	BI191484	BI191484 BJ191484
c 259	13	86.7	485	10	BE147095	BE147095 PM0-HT022	332	13	86.7	541	13	BI161509	BI161509 RE01015.5
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262	13	86.7	487	13	BI626701	BI626701 RH67720.5	335	13	86.7	541	13	BI609439	BI609439 RH14223.5
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265	13	86.7	488	13	BI201503	BI201503 BJ201503	338	13	86.7	542	13	BI607400	BI607400 RH74463.5
266	13	86.7	489	9	AI518882	AI518882 LD35707.5	339	13	86.7	542	13	BI617234	BI617234 RH47505.5
c 267	13	86.7	490	9	AJ447458	AJ447458 AJ447458	340	13	86.7	543	9	AT002733	AT002733 AT002733
268	13	86.7	490	13	BM309327	BM309327 sak57c11.	341	13	86.7	543	13	BI629035	BI629035 RH57830.5
269	13	86.7	495	13	BI165053	BI165053 RE04858.5	342	13	86.7	543	13	BI634996	BI634996 RH39989.5
c 270	13	86.7	495	13	BI173536	BI173536 RE16472.5	343	13	86.7	544	13	BI231198	BI231198 RE20428.5
271	13	86.7	495	13	BI374597	BI374597 RE52232.5	344	13	86.7	544	13	BI231291	BI231291 RE20739.5
c 272	13	86.7	496	10	AV602894	AV602894 AV602894	345	13	86.7	544	13	BI371124	BI371124 RE57949.5
c 273	13	86.7	497	13	BI128944	BI128944 G083P83Y	346	13	86.7	544	13	BI613562	BI613562 RH42739.5
274	13	86.7	498	13	BI213621	BI213621 RE19058.5	347	13	86.7	546	9	AI517081	AI517081 GH27714.5
275	13	86.7	499	9	AA940917	AA940917 LD23250.5	348	13	86.7	546	10	AV945840	AV945840 AV945840
276	13	86.7	501	9	AI542802	AI542802 SD09267.5	349	13	86.7	546	13	BI581633	BI581633 RH19160.5
277	13	86.7	502	9	AA698182	AA698182 HL03902.5	350	13	86.7	547	13	BI243132	BI243132 RE40689.5
c 278	13	86.7	502	12	BG659553	BG659553 tgeSTzyg4	351	13	86.7	547	13	BI608146	BI608146 RH12321.5
c 279	13	86.7	503	9	AU081722	AU081722 AU081722	352	13	86.7	547	13	BJ206395	BJ206395 BJ206395
280	13	86.7	504	10	AW287123	AW287123 LG1.265.G	353	13	86.7	547	17	AZ015890	AZ015890 RPT-23-3
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c 282	13	86.7	506	12	BF490629	BF490629 AT27162.5	355	13	86.7	548	13	BJ482922	BJ482922 BJ482922
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c 286	13	86.7	511	13	BM115115	BM115115 L0815611-	c 359	13	86.7	549	13	BM328657	BM328657 PICL.24.H
287	13	86.7	512	13	BI235492	BI235492 RE31342.5	c 360	13	86.7	549	13	BI355859	BI355859 GM32619.5
288	13	86.7	513	9	AI534378	AI534378 SD07181.5	361	13	86.7	550	14	BQ041241	BQ041241 qd35e07.y
c 289	13	86.7	513	10	AV601487	AV601487 AV601487	362	13	86.7	551	12	BF491989	BF491989 AT28848.5
290	13	86.7	513	13	BI366667	BI366667 RE52254.5	363	13	86.7	551	13	BI624809	BI624809 RH64508.5
291	13	86.7	513	13	BI618056	BI618056 RH48577.5	c 364	13	86.7	552	10	BE518496	BE518496 EST00072
292	13	86.7	514	9	AI135681	AI135681 GH13519.5	365	13	86.7	552	13	BI366118	BI366118 RE51573.5
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c 295	13	86.7	514	14	BQ038360	BQ038360 p9nic.pk0	368	13	86.7	553	13	BI622940	BI622940 RH34983.5
296	13	86.7	518	9	AI388875	AI388875 GH19918.5	369	13	86.7	554	13	BM495747	BM495747 IPCGB3-2
297	13	86.7	518	13	BI587001	BI587001 RH27249.5	c 370	13	86.7	555	9	AI770230	AI770230 SAL2.C10
298	13	86.7	518	13	BI620636	BI620636 RH51825.5	371	13	86.7	556	13	BI339487	BI339487 364471.MA

372	13	86.7	558	13	BJ174223	BJ174223	BJ174223	BJ174223	C 445	13	86.7	607	13	BM323555	BM323555	PIC1_20_F
373	13	86.7	559	13	BM324075	BM324075	BM324075	BM324075	446	13	86.7	608	13	BF486861	BF486861	BJ486861
374	13	86.7	560	13	BM289761	BM289761	BM289761	BM289761	C 447	13	86.7	609	12	BF686317	BF686317	292073 BA
375	13	86.7	561	14	BQ792032	BQ792032	BQ792032	BQ792032	448	13	86.7	609	14	BQ792070	BQ792070	946118C01
376	13	86.7	562	13	BJ1373689	BJ1373689	BJ1373689	BJ1373689	449	13	86.7	610	9	AI532927	AI532927	SD04578.5
377	13	86.7	562	13	BJ003207	BJ003207	BJ003207	BJ003207	450	13	86.7	611	17	BH001124	BH001124	G154 Gemm
378	13	86.7	563	13	BJ180968	BJ180968	BJ180968	BJ180968	451	13	86.7	612	10	BE499201	BE499201	WHE0970 B
379	13	86.7	563	12	BG468699	BG468699	BG468699	BG468699	452	13	86.7	612	13	BE578936	BE578936	RE2884.5
380	13	86.7	563	13	BI239566	BI239566	BI239566	BI239566	453	13	86.7	613	9	AI108977	AI108977	GHO7462.5
381	13	86.7	563	13	BJ181178	BJ181178	BJ181178	BJ181178	C 454	13	86.7	613	10	BE179105	BE179105	RCO-HT061
382	13	86.7	564	10	AV605290	AV605290	AV605290	AV605290	C 455	13	86.7	613	13	BJ481746	BJ481746	BJ481746
383	13	86.7	564	17	BH319223	BH319223	BH319223	BH319223	C 456	13	86.7	614	13	BI237261	BI237261	RE33453.5
384	13	86.7	565	13	BI243937	BI243937	BI243937	BI243937	457	13	86.7	614	13	BI624688	BI624688	RH64287.5
385	13	86.7	565	13	BJ198307	BJ198307	BJ198307	BJ198307	C 458	13	86.7	615	12	BF041145	BF041145	RP250017A
386	13	86.7	567	12	BF007212	BF007212	BF007212	BF007212	459	13	86.7	616	13	BI215999	BI215999	RE22783.5
387	13	86.7	568	13	BI481677	BI481677	BI481677	BI481677	460	13	86.7	617	12	BF504143	BF504143	AT05443.5
388	13	86.7	568	13	BJ197784	BJ197784	BJ197784	BJ197784	461	13	86.7	617	12	BI216068	BI216068	RE22876.5
389	13	86.7	569	13	BM119201	BM119201	BM119201	BM119201	462	13	86.7	621	13	BI216068	BI216068	HS 5107 B
390	13	86.7	570	13	BI375026	BI375026	BI375026	BI375026	C 463	13	86.7	623	17	AO612634	AO612634	HS 5107 B
391	13	86.7	570	13	BI482562	BI482562	BI482562	BI482562	464	13	86.7	625	13	BI241712	BI241712	RE38848.5
392	13	86.7	570	13	BI618504	BI618504	BI618504	BI618504	465	13	86.7	625	13	BI585483	BI585483	RE38848.5
393	13	86.7	571	17	BH521454	BOHF63TR	BH521454	BOHF63TR	466	13	86.7	626	9	AI134712	AI134712	RE38848.5
394	13	86.7	573	17	AZ494484	IM0329K14	AZ494484	IM0329K14	467	13	86.7	629	9	AI25621	AI25621	RE38848.5
395	13	86.7	574	13	BI213056	RE18369.5	BI213056	RE18369.5	468	13	86.7	629	9	AI25621	AI25621	RE38848.5
396	13	86.7	574	13	BI567467	RE37867.5	BI567467	RE37867.5	469	13	86.7	629	13	BI304029	BI304029	RE14110.5
397	13	86.7	575	9	AI388426	GH19340.5	AI388426	GH19340.5	470	13	86.7	629	13	BJ486860	BJ486860	BJ486860
398	13	86.7	575	10	AM632423	92347 MAR	AM632423	92347 MAR	471	13	86.7	630	9	AI134344	AI134344	GH11780.5
399	13	86.7	575	12	BF642307	NF062A041	BF642307	NF062A041	472	13	86.7	630	9	AI238398	AI238398	GH14436.5
400	13	86.7	575	13	BJ204435	BJ204435	BJ204435	BJ204435	C 473	13	86.7	633	9	AA817125	LD22263.5	
401	13	86.7	575	13	BM130932	PJ11G11.5	BM130932	PJ11G11.5	C 474	13	86.7	634	17	BH183384	023_K_24	
402	13	86.7	577	13	BI636924	SD18770.5	BI636924	SD18770.5	C 475	13	86.7	634	17	CNS07OKD	AL620335 T7 end of	
403	13	86.7	578	14	C79400	C79400 Mous	C79400	C79400 Mous	C 476	13	86.7	635	13	BM490635	BM490635 ppg2n.pk0	
404	13	86.7	579	12	BG753875	602731568	BG753875	602731568	477	13	86.7	637	17	BH737558	BOHF540TF	
405	13	86.7	579	13	BJ202310	BJ202310	BJ202310	BJ202310	C 478	13	86.7	638	9	AI402657	BH21916.5	
406	13	86.7	580	13	BJ195508	BJ195508	BJ195508	BJ195508	479	13	86.7	639	9	AI484708	RE67850.5	
407	13	86.7	580	13	BJ202130	BJ202130	BJ202130	BJ202130	480	13	86.7	640	13	BI361979	RE46426.5	
408	13	86.7	582	12	BF007136	1464287 A	BF007136	1464287 A	481	13	86.7	640	13	BI575115	RE27982.5	
409	13	86.7	582	13	BI168715	RE09561.5	BI168715	RE09561.5	482	13	86.7	640	13	BI575115	RE27982.5	
410	13	86.7	583	13	BI167943	RE08460.5	BI167943	RE08460.5	C 483	13	86.7	642	13	BI238421	RE34880.5	
411	13	86.7	584	13	BJ203828	BJ203828	BJ203828	BJ203828	C 484	13	86.7	642	13	BI238421	RE34880.5	
412	13	86.7	586	13	BI234975	RE30758.5	BI234975	RE30758.5	C 485	13	86.7	643	13	BI873745	BI873745 9631110H08	
413	13	86.7	586	17	AZ038483	RPCI-23-3	AZ038483	RPCI-23-3	486	13	86.7	644	13	BI615762	BI615762 RH45511.5	
414	13	86.7	587	9	AI296685	LP10677.5	AI296685	LP10677.5	C 487	13	86.7	644	13	BI959009	BI959009 RVSMEN001	
415	13	86.7	587	17	BH826096	BACPP23-K	BH826096	BACPP23-K	C 488	13	86.7	645	13	BI392359	RE20802.5	
416	13	86.7	589	9	AI295335	LP08932.5	AI295335	LP08932.5	C 489	13	86.7	646	9	AA184934	AA184934 mu48h06.r	
417	13	86.7	589	10	AV968203	AV968203	AV968203	AV968203	490	13	86.7	646	13	BI358129	BI358129 RE44805.5	
418	13	86.7	589	14	BQ529246	IO91056E1	BQ529246	IO91056E1	491	13	86.7	646	13	BI607080	BI607080 RH74070.5	
419	13	86.7	589	17	DR2169T	AL741054 Danilo rer	DR2169T	AL741054 Danilo rer	492	13	86.7	646	13	BI607080	BI607080 RH74070.5	
420	13	86.7	590	13	BI614732	RH44189.5	BI614732	RH44189.5	C 493	13	86.7	647	13	BI696516	BI696516 603347469	
421	13	86.7	591	9	AI257902	LP06396.5	AI257902	LP06396.5	494	13	86.7	648	9	AI062623	AI062623 GH01902.5	
422	13	86.7	591	9	AI546549	SD06312.5	AI546549	SD06312.5	C 495	13	86.7	648	12	BE777032	BE777032 MX-23-F-0	
423	13	86.7	591	13	BI234616	RE30345.5	BI234616	RE30345.5	496	13	86.7	648	12	BI236745	BI236745 RE32852.5	
424	13	86.7	592	13	BI228913	RE26573.5	BI228913	RE26573.5	497	13	86.7	648	13	BI242077	BI242077 RE39294.5	
425	13	86.7	592	13	BI570782	RH05584.5	BI570782	RH05584.5	C 498	13	86.7	649	9	AI295030	LP08542.5	
426	13	86.7	593	9	AI134740	GH12278.5	AI134740	GH12278.5	C 499	13	86.7	649	10	BB270531	BB270531 B8270531	
427	13	86.7	593	9	AI257158	LP05446.5	AI257158	LP05446.5	C 500	13	86.7	649	14	BQ766134	BQ766134 ER008 SQ	
428	13	86.7	593	13	BI625498	RH65938.5	BI625498	RH65938.5	C 501	13	86.7	650	17	AG024208	AG024208 Oryza sat	
429	13	86.7	594	9	AI260864	LP04854.5	AI260864	LP04854.5	502	13	86.7	651	9	AI064233	AI064233 GH04565.5	
430	13	86.7	594	13	BI139616	BJ139616	BI139616	BJ139616	503	13	86.7	651	9	AI294227	AI294227 LP07548.5	
431	13	86.7	595	13	BM130821	pJ10a07.y	BM130821	pJ10a07.y	504	13	86.7	653	10	BB628399	BB628399 BB628399	
432	13	86.7	597	17	B77391	T3ON8TFC.TA	B77391	T3ON8TFC.TA	505	13	86.7	655	10	BB068345	BB068345 BB068345	
433	13	86.7	598	10	AW553915	LO233D09-	AW553915	LO233D09-	506	13	86.7	655	10	BB068345	BB068345 BB068345	
434	13	86.7	598	13	BI374383	RE61959.5	BI374383	RE61959.5	507	13	86.7	655	13	BI237622	BI237622 RE33874.5	
435	13	86.7	599	9	AI133463	GH11937.5	AI133463	GH11937.5	C 508	13	86.7	655	13	BI237622	BI237622 RE33874.5	
436	13	86.7	599	13	BI356700	RE42902.5	BI356700	RE42902.5	509	13	86.7	657	10	AW918116	AW918116 ESP349420	
437	13	86.7	599	17	A2889669	RPCI-24-2	A2889669	RPCI-24-2	C 510	13	86.7	658	9	AI513788	AI513788 GH26879.5	
438	13	86.7	600	12	BF487776	AT22829.5	BF487776	AT22829.5	511	13	86.7	658	17	AG037086	AG037086 Pan trogl	
439	13	86.7	600	13	BI173485	RE16415.5	BI173485	RE16415.5	512	13	86.7	658	17	AG037086	AG037086 Pan trogl	
440	13	86.7	601	10	AV940666	AV940666	AV940666	AV940666	513	13	86.7	660	14	BI604600	BI604600 RH70023.5	
441	13	86.7	601	17	BH552841	BOHAQ38TR	BH552841	BOHAQ38TR	514	13	86.7	660	14	BQ989196	BQ989196 QGF17A06.6	
442	13	86.7	601	17	DR9K2058	Dani1764 rer	DR9K2058	Dani1764 rer	515	13	86.7	661	13	BI481741	BI481741 RE64342.5	
443	13	86.7	601	17	DR9K2058	Dani1764 rer	DR9K2058	Dani1764 rer	C 516	13	86.7	662	12	BG497121	BG497121 602537608	
444	13	86.7	606	14	BO410548	GA_Ed003	BO410548	GA_Ed003	C 517	13	86.7	662	13	BM101705	BM101705 fv35b06.1	

518	13	86.7	663	9	AA567886	AA567886	HL01944.5	591	13	86.7	806	12	86843178	86843178	1024001G0
519	13	86.7	663	17	AG158219	AG158219	Pan trogl1	592	13	86.7	806	12	BG923173	BG923173	602824014
520	13	86.7	664	13	BI577896	BI577896	RE71660.5	c 593	13	86.7	807	12	BF233687	BF233687	602024723
c 521	13	86.7	664	13	BM328060	BM328060	PTCL20.F	594	13	86.7	809	12	BE889765	BE889765	601512005
c 522	13	86.7	665	13	BI356971	BI356971	RE43289.5	c 595	13	86.7	811	14	BQ443985	BQ443985	UI-M-EWO-
c 523	13	86.7	668	12	BF504646	BF504646	AT06245.5	c 596	13	86.7	811	12	BF382784	BF382784	601816561
524	13	86.7	668	14	BQ412744	BQ412744	GA_E0006	597	13	86.7	817	13	BI683605	BI683605	603306326
525	13	86.7	669	9	AI238336	AI238336	GH14363.5	c 598	13	86.7	824	13	BI161136	BI161136	602865179
526	13	86.7	669	10	BB641769	BB641769	BB641769	c 599	13	86.7	828	12	BF302804	BF302804	602032685
527	13	86.7	669	13	BI369054	BI369054	RE55136.5	c 600	13	86.7	846	17	BH525267	BH525267	BOHOE04TR
528	13	86.7	669	13	BJ523319	BJ523319	BJ523319	c 601	13	86.7	851	10	BE546565	BE546565	601076577
529	13	86.7	670	10	AV646123	AV646123	AV646123	c 602	13	86.7	856	12	BG497157	BG497157	602537658
530	13	86.7	670	13	BI237634	BI237634	RE33888.5	603	13	86.7	859	13	BI248784	BI248784	602992758
c 531	13	86.7	672	12	BF008340	BF008340	I606544.A	c 604	13	86.7	860	17	CNS01ZBN	CNS01ZBN	Tetraodon
c 532	13	86.7	674	13	BI586463	BI586463	RH26415.5	c 605	13	86.7	866	12	BF303388	BF303388	602030114
533	13	86.7	676	12	BF499121	BF499121	AT113616.5	c 606	13	86.7	871	17	AZ127971	AZ127971	OSJNB006
534	13	86.7	676	17	AZ574428	AZ574428	328PVF01	c 607	13	86.7	876	13	BI101360	BI101360	602887114
c 535	13	86.7	677	13	BJ482072	BJ482072	BJ482072	c 608	13	86.7	879	12	BF974098	BF974098	602243701
c 536	13	86.7	677	13	BM645425	BM645425	I70006873	c 609	13	86.7	890	12	BF241496	BF241496	601876555
537	13	86.7	678	9	AI134184	AI134184	GH11565.5	c 610	13	86.7	890	12	CNS04AUK	CNS04AUK	Tetraodon
538	13	86.7	678	17	AZ574323	AZ574323	327PVDO3	c 611	13	86.7	891	12	BF673085	BF673085	602152993
539	13	86.7	680	13	BI214309	BI214309	RE20078.5	c 612	13	86.7	895	12	BG251001	BG251001	602363862
c 540	13	86.7	682	12	BG633804	BG633804	AT29733.5	c 613	13	86.7	905	13	BI460555	BI460555	603201178
541	13	86.7	683	14	BQ990424	BQ990424	OGF20C06.	614	13	86.7	910	12	BF141152	BF141152	601789149
c 542	13	86.7	684	9	AI405800	AI405800	GH25932.5	c 615	13	86.7	911	12	BE959822	BE959822	601654738
c 543	13	86.7	685	13	BI557061	BI557061	603238633	c 616	13	86.7	916	17	AQ743736	AQ743736	HS_5501.A
c 544	13	86.7	686	17	AZ566829	AZ566829	227PVA08	617	13	86.7	919	9	AL548995	AL548995	AL548995
c 545	13	86.7	687	13	BM591656	BM591656	I70006873	c 618	13	86.7	920	13	BI948315	BI948315	HVSME1000
546	13	86.7	690	13	BJ523320	BJ523320	BJ523320	c 619	13	86.7	923	12	BF974200	BF974200	602243830
c 547	13	86.7	692	10	BB388293	BB388293	BB388293	c 620	13	86.7	928	10	AM661684	AM661684	ESTPMC16
c 548	13	86.7	694	12	BE988154	BE988154	601440284	c 621	13	86.7	936	12	BF790002	BF790002	602249973
c 549	13	86.7	695	14	BQ907162	BQ907162	N004C07.O	622	13	86.7	939	12	BF971128	BF971128	602270706
550	13	86.7	698	12	BG074658	BG074658	H3137G04-	623	13	86.7	944	10	BE039851	BE039851	OC09A11.O
551	13	86.7	700	12	BG635476	BG635476	SD12889.5	624	13	86.7	945	17	AG145841	AG145841	Pan trogl1
552	13	86.7	700	14	BU007527	BU007527	QGH3909.Y	c 625	13	86.7	946	10	BE213911	BE213911	HV_CEB000
c 553	13	86.7	701	9	AI405028	AI405028	GH24935.5	c 626	13	86.7	954	17	CNS05LRN	CNS05LRN	Tetraodon
554	13	86.7	701	17	AG080306	AG080306	Pan trogl1	c 627	13	86.7	959	12	BF797734	BF797734	602257679
555	13	86.7	705	9	AU119272	AU119272	AU119272	c 628	13	86.7	970	12	BG105691	BG105691	602312290
556	13	86.7	705	14	BQ241102	BQ241102	TaE05009B	c 629	13	86.7	974	17	CNS02BMG	CNS02BMG	Tetraodon
c 557	13	86.7	708	10	BE455119	BE455119	HVSMEH009	c 630	13	86.7	975	14	BQ890286	BQ890286	AGENCOURT
c 558	13	86.7	708	13	BM627874	BM627874	I70006874	c 631	13	86.7	979	14	BQ679820	BQ679820	AGENCOURT
c 559	13	86.7	710	12	BG844543	BG844543	I024006H0	c 632	13	86.7	985	14	BQ226384	BQ226384	AGENCOURT
c 560	13	86.7	711	12	BF505970	BF505970	AT0R311.5	c 633	13	86.7	991	12	BF164265	BF164265	601773022
c 561	13	86.7	711	14	BQ780720	BQ780720	UI-R-FF0-	c 634	13	86.7	991	12	BM063000	BM063000	603614980
562	13	86.7	712	9	AI517055	AI517055	GH27682.5	c 635	13	86.7	994	12	BF125562	BF125562	601763316
563	13	86.7	712	13	BI231265	BI231265	RE20711.5	c 636	13	86.7	994	17	CNS02KPI	CNS02KPI	Tetraodon
c 564	13	86.7	714	13	BM620991	BM620991	I70006874	c 637	13	86.7	1001	12	BF032661	BF032661	601453191
c 565	13	86.7	716	14	BQ869659	BQ869659	QCD6N05.Y	c 638	13	86.7	1003	12	BF237568	BF237568	601842082
566	13	86.7	721	13	BI544387	BI544387	603241788	c 639	13	86.7	1003	14	BQ884024	BQ884024	AGENCOURT
567	13	86.7	721	14	BU007443	BU007443	QGH2912.Y	c 640	13	86.7	1010	10	BE620575	BE620575	601483079
568	13	86.7	724	9	AI534898	AI534898	SD01167.5	c 641	13	86.7	1012	12	BG614407	BG614407	602642535
c 569	13	86.7	728	17	BH838311	BH838311	LMCR10001	c 642	13	86.7	1016	14	BQ707142	BQ707142	AGENCOURT
c 570	13	86.7	729	12	BF863315	BF863315	963042G03	c 643	13	86.7	1028	14	BM904873	BM904873	AGENCOURT
571	13	86.7	732	13	BM200229	BM200229	OC207E11-	c 644	13	86.7	1034	12	BF531935	BF531935	602072878
c 572	13	86.7	734	10	AQ751483	AQ751483	HS_5576.B	c 645	13	86.7	1042	14	BQ963025	BQ963025	AGENCOURT
573	13	86.7	744	17	AV712791	AV712791	AV712791	c 646	13	86.7	1058	12	BG026430	BG026430	602291812
c 574	13	86.7	745	17	BH386968	BH386968	AG-ND-102	647	13	86.7	1062	17	CNS04NNC	CNS04NNC	Tetraodon
c 575	13	86.7	750	9	AI406247	AI406247	GH26477.5	c 648	13	86.7	1070	12	BF120134	BF120134	601756436
576	13	86.7	756	9	AA697370	AA697370	HL02339.5	c 649	13	86.7	1086	12	BF300932	BF300932	602028939
c 577	13	86.7	758	13	BI080925	BI080925	602878836	c 650	13	86.7	1087	12	BG249508	BG249508	602319571
c 578	13	86.7	769	12	BG854557	BG854557	I024040C0	c 651	13	86.7	1088	13	BM562441	BM562441	AGENCOURT
579	13	86.7	769	12	BF127518	BF127518	601810149	c 652	13	86.7	1090	13	BI655365	BI655365	603285006
c 580	13	86.7	770	9	AJ444359	AJ444359	AJ444359	c 653	13	86.7	1101	17	CNS00EAC	CNS00EAC	Drosophil
581	13	86.7	771	9	AA698039	AA698039	HL03667.5	c 654	13	86.7	1101	17	CNS00E79	CNS00E79	Drosophil
582	13	86.7	772	13	BI217290	BI217290	602933762	c 655	13	86.7	1109	12	BF244595	BF244595	601862612
c 583	13	86.7	778	14	BQ042264	BQ042264	UI-M-EQO-	c 656	13	86.7	1115	17	AG082764	AG082764	Pan trogl1
c 584	13	86.7	783	12	BG810248	BG810248	mgc0003X1	c 657	13	86.7	1122	14	BQ717951	BQ717951	AGENCOURT
c 585	13	86.7	785	17	AQ361717	AQ361717	mgxb0004D	c 658	13	86.7	1128	12	BQ776928	BQ776928	602664121
586	13	86.7	787	17	BI9062	BI9062	T5L21-Sp6.T	c 659	13	86.7	1129	13	BM467209	BM467209	AGENCOURT
c 587	13	86.7	795	13	BI520313	BI520313	603071178	c 660	13	86.7	1132	12	BG257183	BG257183	602370785
c 588	13	86.7	798	12	BF569236	BF569236	602185601	c 661	13	86.7	1134	10	BE572592	BE572592	601329548
589	13	86.7	803	10	BE397525	BE397525	601290163	c 662	13	86.7	1137	12	BG473760	BG473760	602515752
590	13	86.7	805	17	AQ364242	AQ364242	nbxb0060P	c 663	13	86.7	1158	12	BF688714	BF688714	602185366

c 664	13	86.7	1163	12	BG258338	602379785	c 737	12	80.0	172	17	AZ101784	AZ101784 RPCI-23-2
c 665	13	86.7	1167	12	BG536614	602566244	738	12	80.0	173	17	AZ504600	AZ504600 IM0344B05
c 666	13	86.7	1183	13	BI410243	602963694	739	12	80.0	175	9	AA257919	AA257919 EST 376 B
c 667	13	86.7	1210	13	BI256946	602963694	740	12	80.0	179	13	BI239287	BI239287 RE35740.5
c 668	13	86.7	1211	12	BG479463	602525957	741	12	80.0	180	9	A1538252	A1538252 tp55b05.x
c 669	13	86.7	1212	12	BG033864	602301148	742	12	80.0	180	9	AU110801	AU110801 AU110801
c 670	13	86.7	1236	17	AG080176	Pan trogl	743	12	80.0	182	13	BG953195	BG953195 CM4-CT063
c 671	13	86.7	1272	13	BI161234	602865696	744	12	80.0	185	9	AA179003	AA179003 zh22h11.s
c 672	13	86.7	1363	13	BM542097	AGENCOURT	745	12	80.0	188	10	BE003350	BE003350 QV4-BN009
c 673	13	86.7	1367	14	BO886911	AGENCOURT	746	12	80.0	188	13	BJ163151	BJ163151 BJ163151
c 674	13	86.7	1367	14	BO886911	AGENCOURT	747	12	80.0	189	12	BF497730	BF497730 AU11996.5
c 675	13	86.7	1384	12	BF300658	602031833	748	12	80.0	191	9	AA113295	AA113295 zm28d05.s
c 676	13	86.7	1411	12	BE962808	601656518	749	12	80.0	196	9	A1186279	A1186279 qd20c04.x
c 677	13	86.7	1443	12	BG433848	602497372	750	12	80.0	197	9	AA361873	AA361873 ES711197
c 678	13	86.7	1463	12	BG866747	603786566	751	12	80.0	197	10	BE660913	BE660913 6-A7 Gmax
c 679	13	86.7	1493	12	BG298764	603385589	752	12	80.0	198	9	AA112518	AA112518 zm28d05.r
c 680	13	86.7	1507	14	BO886911	AGENCOURT	753	12	80.0	200	14	C74297	C74297 C74297 Rice
c 681	13	86.7	1534	14	BM904434	AGENCOURT	754	12	80.0	200	17	AO629360	AO629360 RPCI-11-4
c 682	13	86.7	1581	12	BG118402	602348017	755	12	80.0	202	17	BF718618	BF718618 KEST89 no
c 683	13	86.7	1612	12	BF690854	602246853	756	12	80.0	202	17	AO091456	AO091456 HS-3016_B
c 684	13	86.7	1642	12	BF570926	602076123	757	12	80.0	203	12	BF718270	BF718270 EST40 mic
c 685	13	86.7	1698	12	BG822684	602725814	758	12	80.0	203	12	BF930644	BF930644 IL5-NT022
c 686	13	86.7	1701	13	BM452308	AGENCOURT	759	12	80.0	206	10	AW139000	AW139000 UT-H-B11-
c 687	13	86.7	1717	12	BG284363	602408469	760	12	80.0	206	10	BF806393	BF806393 RC2-CI008
c 688	13	86.7	3015	11	AK014519	Mus muscu	761	12	80.0	207	10	BM419535	BM419535 BB419535
c 689	13	86.7	5054	11	AK004773	AGENCOURT	762	12	80.0	207	10	BM596021	BM596021 BB596021
c 690	12	80.0	52	12	BG694448	NISC_lv02	763	12	80.0	209	10	BB298438	BB298438 BB298438
c 691	12	80.0	53	17	BH633045	AA708193	764	12	80.0	210	9	AV080134	AV080134 AV080134
c 692	12	80.0	55	9	AA970079	AA708197	765	12	80.0	213	9	AF092807	AF092807 AF092807
c 693	12	80.0	59	9	AA988206	AA708197	766	12	80.0	214	14	T18393	T18393 6c02b09t7 e
c 694	12	80.0	63	13	BI820770	603034371	767	12	80.0	216	9	AI318940	AI318940 a5a09nm.f
c 695	12	80.0	68	17	AZ577398	09409 Sho	768	12	80.0	216	10	BE287391	BE287391 BE287391
c 696	12	80.0	72	13	BI488965	603021690	769	12	80.0	216	12	BE697675	BE697675 RC0-CT047
c 697	12	80.0	83	9	AA708193	AA708193	770	12	80.0	217	9	AI701380	AI701380 wb91f11.x
c 698	12	80.0	85	12	BF024197	603034371	771	12	80.0	217	10	BM414692	BM414692 BB414692
c 699	12	80.0	88	9	AA988206	AA708197	772	12	80.0	217	10	BM422878	BM422878 1006149B0
c 700	12	80.0	91	9	AI018539	AA708197	773	12	80.0	219	14	F02757	F02757 HSCI9E072 n
c 701	12	80.0	93	10	AW722741	603034371	774	12	80.0	221	10	AW327140	AW327140 20733 MAR
c 702	12	80.0	99	17	AZ477457	1M0296019	775	12	80.0	221	10	AW718324	AW718324 14g10nm.f
c 703	12	80.0	109	12	BF900273	PM2-MT020	776	12	80.0	221	14	F02836	F02836 HSCI9G052 n
c 704	12	80.0	110	13	BI756148	603030051	777	12	80.0	223	10	BM589564	BM589564 BB589564
c 705	12	80.0	116	12	BG085551	AGENCOURT	778	12	80.0	226	9	AI669515	AI669515 w88f11.x
c 706	12	80.0	116	12	BF399563	AGENCOURT	779	12	80.0	226	10	BM009372	BM009372 BB009372
c 707	12	80.0	117	12	BF145536	WHE1841-1	780	12	80.0	226	12	BG044841	BG044841 saa33b10.
c 708	12	80.0	120	13	BI818802	603037654	781	12	80.0	226	17	AO527440	AO527440 RPCI-11-3
c 709	12	80.0	121	10	AW303248	RC3-TT000	782	12	80.0	227	12	BF760815	BF760815 RC4-CT062
c 710	12	80.0	123	17	B82206	RC3-TT000	783	12	80.0	229	12	BF811752	BF811752 QV1-CI017
c 711	12	80.0	126	17	AZ100181	RPCI-23-4	784	12	80.0	230	9	AA982299	AA982299 ua53a06.x
c 712	12	80.0	128	17	AZ500419	IM03338H16	785	12	80.0	230	12	BF379273	BF379273 RC6-UT001
c 713	12	80.0	130	17	AZ451984	IM0251A11	786	12	80.0	232	10	AV346323	AV346323 AV346323
c 714	12	80.0	135	10	AW327142	20739 MAR	787	12	80.0	232	10	BE938080	BE938080 MRL-TN004
c 715	12	80.0	137	10	AW832984	RC3-TT000	788	12	80.0	233	17	BH222866	BH222866 1006109F0
c 716	12	80.0	139	17	BH629679	1007075B0	789	12	80.0	234	12	BF918950	BF918950 QV0-NT014
c 717	12	80.0	140	9	AA471103	PMW2037 K	790	12	80.0	234	17	BH403207	BH403207 AG-ND-126
c 718	12	80.0	141	13	BI724512	1031072D0	791	12	80.0	235	14	T16623	T16623 NIB1570 Nor
c 719	12	80.0	142	9	AA441863	zw62d04.r	792	12	80.0	237	9	AI799967	AI799967 wc46e05.x
c 720	12	80.0	143	17	BH230907	1006160A0	793	12	80.0	237	10	AV322152	AV322152 AV322152
c 721	12	80.0	146	14	BO097199	IFHdk0098	794	12	80.0	238	10	BB426394	BB426394 BB426394
c 722	12	80.0	146	17	AO897850	HS_3144-A	795	12	80.0	239	9	AT006295	AT006295 AA006295
c 723	12	80.0	147	13	BM200713	C0215E01-	796	12	80.0	239	12	BF870843	BF870843 CM3-ET009
c 724	12	80.0	148	9	AA774504	zg76c06.s	797	12	80.0	239	13	BI014554	BI014554 CM3-ET009
c 725	12	80.0	148	17	B41513	HS-1053-B2-	798	12	80.0	240	14	CI2313	CI2313 CM3-ET009
c 726	12	80.0	155	9	AV173703	AV173703	799	12	80.0	241	9	AI048764	AI048764 ub32c02.r
c 727	12	80.0	155	12	BG659681	TGEST2ya4	800	12	80.0	241	10	AW482781	AW482781 47074 MAR
c 728	12	80.0	155	14	F03378	HSCI9C072 n	801	12	80.0	242	9	AV223369	AV223369 AV223369
c 729	12	80.0	156	12	BG016125	ST1HW24-8	802	12	80.0	242	13	BI014001	BI014001 PM1-ET020
c 730	12	80.0	158	9	AL363444	AL363444	803	12	80.0	242	17	AZ756867	AZ756867 ew02f10.x
c 731	12	80.0	162	12	BF552165	UT-R-C2p-	804	12	80.0	243	9	BI070571	BI070571 as30h02.x
c 732	12	80.0	163	14	D29185	HUMNK222 Hu	805	12	80.0	243	14	BQ342615	BQ342615 RC4-NN108
c 733	12	80.0	166	10	BB512941	BB512941	806	12	80.0	243	9	BI070571	BI070571 as30h02.x
c 734	12	80.0	166	14	BM857729	1167e09.y	807	12	80.0	243	9	BI070571	BI070571 as30h02.x
c 735	12	80.0	167	17	AO643429	RPCI93-DP	808	12	80.0	243	14	BQ342615	BQ342615 RC4-NN108
c 736	12	80.0	168	10	AV389853	AV389853	809	12	80.0	243	14	BQ342615	BQ342615 RC4-NN108

c 810	12	80.0	244	9	AI524790	AI524790	ti77e01.x	c 883	12	80.0	278	9	AA352372	AA352372	EST60380
c 811	12	80.0	245	12	BE827268	BE827268	QV1-ET000	c 884	12	80.0	278	10	AW355231	AW355231	pnf-b.pk0
c 812	12	80.0	246	10	AW545321	AW545321	C0192C07-	c 885	12	80.0	278	10	BE528288	BE528288	M79011STM
c 813	12	80.0	247	9	AV233291	AV233291	AV233291	c 886	12	80.0	280	10	BB562662	BB562662	BB562662
c 814	12	80.0	247	10	AV374705	AV374705	AV374705	c 887	12	80.0	280	14	F29584	F29584	HSPD19526 H
c 815	12	80.0	247	10	AI327998	AI327998	O6allal.f	c 888	12	80.0	282	9	AI724190	AI724190	RHI21-B_C
c 816	12	80.0	248	14	H26197	H26197	y153a05.r1	c 889	12	80.0	282	10	BB580920	BB580920	BB580920
c 817	12	80.0	249	9	AI213865	AI213865	z6e0a1.f	c 890	12	80.0	282	17	AZ755592	AZ755592	ev01g10.x
c 818	12	80.0	249	9	AV026183	AV026183	AV026183	c 891	12	80.0	282	17	AZ755698	AZ755698	ev05b05.r
c 819	12	80.0	249	10	AW671423	AW671423	LGL1344_F	c 892	12	80.0	282	17	AQ365061	AQ365061	nrbx00620
c 820	12	80.0	249	14	F02756	F02756	HSC19E062 n	c 893	12	80.0	283	9	AI969833	AI969833	wq75e05.x
c 821	12	80.0	250	10	AW074892	AW074892	xa62e06.x	c 894	12	80.0	283	9	AA285163	AA285163	zs48e07.s
c 822	12	80.0	250	14	W40764	W40764	mc38c11.r1	c 895	12	80.0	283	9	AA555778	AA555778	vk50d04.r
c 823	12	80.0	251	9	AI307017	AI307017	qw76b12.x	c 896	12	80.0	283	12	BF837262	BF837262	RC4-HT004
c 824	12	80.0	251	10	AW072899	AW072899	xa60h08.x	c 897	12	80.0	283	14	BM821892	BM821892	K4-EST0091
c 825	12	80.0	252	14	N61346	N61346	TgESTy31c0	c 898	12	80.0	284	9	AI945100	AI945100	bs03a01.y
c 826	12	80.0	253	10	BE662087	BE662087	bs20e09.y	c 899	12	80.0	284	14	C01170	C01170	HUMG5000785
c 827	12	80.0	254	10	AW074765	AW074765	xa70a07.x	c 900	12	80.0	285	9	AA775410	AA775410	ad13c01.s
c 828	12	80.0	254	10	BB599087	BB599087	BB599087	c 901	12	80.0	285	13	BM481391	BM481391	533476 MA
c 829	12	80.0	254	14	BQ372396	BQ372396	QVO-FN018	c 902	12	80.0	286	10	BB585849	BB585849	BB585849
c 830	12	80.0	255	9	AI349796	AI349796	ta96g05.x	c 903	12	80.0	287	9	AI698396	AI698396	tx64e03.x
c 831	12	80.0	255	10	AV525807	AV525807	AV525807	c 904	12	80.0	287	10	AW229783	AW229783	u042h09.y
c 832	12	80.0	255	10	AW718495	AW718495	15f08nm.f	c 905	12	80.0	287	10	BB381078	BB381078	BB381078
c 833	12	80.0	255	10	BE526865	BE526865	M67C05STM	c 906	12	80.0	287	13	BI848981	BI848981	471596 MA
c 834	12	80.0	255	17	AQ275511	AQ275511	RPCI-4-59	c 907	12	80.0	288	9	AI790097	AI790097	ue64e01.r
c 835	12	80.0	256	10	AW18736	AW18736	17b07nm.f	c 908	12	80.0	289	9	AA726913	AA726913	vu37b08.r
c 836	12	80.0	256	10	AW18737	AW18737	17b07nm.f	c 909	12	80.0	289	9	AI453226	AI453226	tj21g03.x
c 837	12	80.0	256	12	BF942278	BF942278	nae90e11.	c 910	12	80.0	289	10	BB500838	BB500838	BB500838
c 838	12	80.0	258	9	AI224664	AI224664	qw97n09.x	c 911	12	80.0	289	13	BJ163858	BJ163858	BJ163858
c 839	12	80.0	258	9	AI345069	AI345069	tb62b03.x	c 912	12	80.0	291	10	BB567423	BB567423	BB567423
c 840	12	80.0	258	9	AI345296	AI345296	tb68c10.x	c 913	12	80.0	292	9	AI370188	AI370188	qu44c09.x
c 841	12	80.0	258	9	AA455998	AA455998	aa02d12.s	c 914	12	80.0	292	9	AL041776	AL041776	DKF2p434A
c 842	12	80.0	258	10	AW722739	AW722739	C6c01nm.f	c 915	12	80.0	292	10	BB721709	BB721709	BB721709
c 843	12	80.0	258	10	BE043381	BE043381	hk37e06.y	c 916	12	80.0	293	10	AV998199	AV998199	AV998199
c 844	12	80.0	258	10	BE151300	BE151300	CM1-HT028	c 917	12	80.0	293	10	AW718686	AW718686	16q09nm.f
c 845	12	80.0	258	14	BQ283590	BQ283590	WHE3094_A	c 918	12	80.0	293	10	BB110385	BB110385	BB110385
c 846	12	80.0	259	9	AA307429	AA307429	o102e11.s	c 919	12	80.0	293	10	BB607761	BB607761	BB607761
c 847	12	80.0	259	10	BB523646	BB523646	BB523646	c 920	12	80.0	294	9	AA077197	AA077197	7B14G04 C
c 848	12	80.0	260	9	AI308902	AI308902	tb50401.x	c 921	12	80.0	295	10	BB599479	BB599479	BB599479
c 849	12	80.0	260	9	AI310785	AI310785	ta42h02.x	c 922	12	80.0	296	9	AI321829	AI321829	efi12nm.f
c 850	12	80.0	260	14	W17791	W17791	mb73d03.r1	c 923	12	80.0	296	10	AW051003	AW051003	wz06b10.x
c 851	12	80.0	261	13	BI035917	BI035917	IL5-NT022	c 924	12	80.0	297	9	AI209755	AI209755	c9b01a1.r
c 852	12	80.0	262	10	AW072708	AW072708	xa59b05.x	c 925	12	80.0	297	9	AI321753	AI321753	e2q08nm.f
c 853	12	80.0	262	17	BH696197	BH696197	BOMCH07TR	c 926	12	80.0	297	10	AW718367	AW718367	i5a07nm.f
c 854	12	80.0	263	17	AZ701528	AZ701528	RPCI-23-2	c 927	12	80.0	297	10	AW859239	AW859239	MRI-CT035
c 855	12	80.0	264	13	BI430968	BI430968	949063E04	c 928	12	80.0	297	13	BI013706	BI013706	RC4-ET013
c 856	12	80.0	264	14	H95220	H95220	yw59e12.s1	c 929	12	80.0	297	14	C27000	C27000	C27000 Rice
c 857	12	80.0	264	14	N89576	N89576	zb08c04.s1	c 930	12	80.0	298	9	AA768025	AA768025	oa60e05.s
c 858	12	80.0	264	17	BH195904	BH195904	TC3-59F15	c 931	12	80.0	298	10	BE001826	BE001826	PM1-BN008
c 859	12	80.0	267	10	BB597613	BB597613	BB597613	c 932	12	80.0	298	13	BM448717	BM448717	DSA027C08
c 860	12	80.0	268	9	AA066316	AA066316	mm08g04.r	c 933	12	80.0	299	9	AA823015	AA823015	vw33f07.r
c 861	12	80.0	268	9	AI556001	AI556001	UI-R-C2p-	c 934	12	80.0	299	10	AV644619	AV644619	AV644619
c 862	12	80.0	269	10	BB598976	BB598976	BB598976	c 935	12	80.0	299	10	BB548971	BB548971	BB548971
c 863	12	80.0	269	17	AA0663198	AA0663198	HS_5463_B	c 936	12	80.0	299	14	H93816	H93816	yv06h10.r1
c 864	12	80.0	271	9	AI111563	AI111563	UI-R-C2-n	c 937	12	80.0	300	9	AJ466877	AJ466877	AJ466877
c 865	12	80.0	271	10	AW427877	AW427877	64454 MAR	c 938	12	80.0	300	10	AV628960	AV628960	AV628960
c 866	12	80.0	271	12	BE760110	BE760110	an_0212 A	c 939	12	80.0	300	10	AW859095	AW859095	MRI-CT035
c 867	12	80.0	271	14	L38101	L38101	BNAP0557E M	c 940	12	80.0	300	12	BF728678	BF728678	1000065F0
c 868	12	80.0	272	9	AA934898	AA934898	op47e07.s	c 941	12	80.0	300	12	BE775574	BE775574	MY-04-A-1
c 869	12	80.0	273	9	AA786415	AA786415	15f07a1.f	c 942	12	80.0	301	9	AA928410	AA928410	on49f10.s
c 870	12	80.0	273	10	BB566740	BB566740	BB566740	c 943	12	80.0	301	9	AI453796	AI453796	tj29a11.x
c 871	12	80.0	274	12	BF764615	BF764615	CM3-CS004	c 944	12	80.0	301	10	BB044485	BB044485	BB044485
c 872	12	80.0	274	14	BQ699391	BQ699391	NXRV127_C	c 945	12	80.0	301	17	AQ115405	AQ115405	RPC111-56
c 873	12	80.0	275	14	BO464819	BO464819	H001K18T	c 946	12	80.0	302	9	AI023671	AI023671	ow67h01.x
c 874	12	80.0	276	9	AI328103	AI328103	t2e10a1.f	c 947	12	80.0	303	9	AA010523	AA010523	z109h05.r
c 875	12	80.0	276	10	AV389613	AV389613	AV389613	c 948	12	80.0	304	9	AA414328	AA414328	vc60f07.s
c 876	12	80.0	276	12	BF478123	BF478123	7q21e07.x	c 949	12	80.0	304	13	BM425320	BM425320	IPSPn0158
c 877	12	80.0	276	12	BF357264	BF357264	PM2-HT093	c 950	12	80.0	304	14	D25082	D25082	RICR3125A R
c 878	12	80.0	276	13	BI023427	BI023427	CM4-WT024	c 951	12	80.0	305	9	AA834380	AA834380	of67e08.s
c 879	12	80.0	276	14	BM770032	BM770032	K-EST0053	c 952	12	80.0	305	10	BB517965	BB517965	BB517965
c 880	12	80.0	276	17	TA65C12P	TA65C12P	T. brucei	c 953	12	80.0	305	10	BB601268	BB601268	BB601268
c 881	12	80.0	277	10	BB468508	BB468508	BB468508	c 954	12	80.0	306	10	AW974222	AW974222	EST386325
c 882	12	80.0	278	9	AA341775	AA341775	EST47205	c 955	12	80.0	306	12	BE864600	BE864600	UI-M-BH1-

```

c 956 12 80.0 306 13 BI530279 1024104H0
c 957 12 80.0 307 13 BI189550 f2e01fs.f
c 958 12 80.0 307 13 BI192229 m2b08fs.f
c 959 12 80.0 307 13 BI189194 TgESTzyb4
c 960 12 80.0 307 17 AQ050614 RPCL-11-2
c 961 12 80.0 308 9 AT471782 t166905.x
c 962 12 80.0 308 10 BB026857 BB026857
c 963 12 80.0 308 10 BB005888 BB400588
c 964 12 80.0 309 9 AA911900 AA911900 oh0912.s
c 965 12 80.0 309 9 AV024356 AV024356
c 966 12 80.0 309 9 AA261738 AA261738 va51f05.r
c 967 12 80.0 310 10 AW115025 rs62b04.y
c 968 12 80.0 310 10 BB394344 BB394344
c 969 12 80.0 310 13 BM258707 BM258707 523575 MA
c 970 12 80.0 311 9 AI925095 AI925095 wn44d03.x
c 971 12 80.0 311 9 AU254098 AU254098
c 972 12 80.0 311 9 AV168223 AV168223
c 973 12 80.0 311 12 BF810106 BF810106 RCL-C1016
c 974 12 80.0 311 13 BI187702 BI187702 blh01fs.f
c 975 12 80.0 311 13 BI307470 BI307470 PTSS0879
c 976 12 80.0 312 9 AV045008 AV045008
c 977 12 80.0 312 9 AV102654 AV102654
c 978 12 80.0 312 14 BQ316818 BQ316818 CMI-CR006
c 979 12 80.0 312 14 H24720 H24720 y141d10.r1
c 980 12 80.0 313 9 AI806655 AI806655 wf35b05.x
c 981 12 80.0 313 9 AV128341 AV128341
c 982 12 80.0 313 12 BF197531 BF197531 7084b12.x
c 983 12 80.0 315 12 BG465745 BG465745 RHTZ2.48
c 984 12 80.0 316 17 AZ065724 AZ065724 RPCL-23-4
c 985 12 80.0 317 9 AA712562 AA712562 31695 Lam
c 986 12 80.0 317 9 AI733337 AI733337 op95b11.x
c 987 12 80.0 317 9 AJ284776 AJ284776 4A3B-AAAC-
c 988 12 80.0 317 10 BB144518 BB144518
c 989 12 80.0 317 10 BB461943 BB461943
c 990 12 80.0 318 9 AA971709 AA971709 op95b11.s
c 991 12 80.0 318 10 BB600156 BB600156
c 992 12 80.0 318 14 D47132 D47132 RICS12273A
c 993 12 80.0 318 14 F02835 F02835 HSCICG042 n
c 994 12 80.0 320 10 BB143612 BB143612
c 995 12 80.0 321 9 AI652650 AI652650 wb30b12.x
c 996 12 80.0 321 14 C97210 C97210 C97210 Rice
c 997 12 80.0 322 14 H45960 H45960 y081e09.r1
c 998 12 80.0 323 14 D49193 D49193 RICS16301A
c 999 12 80.0 324 9 AI932842 AI932842 w038c10.x
c 1000 12 80.0 324 10 BE119265 BE119265 UI-R-CA0-

```

ALIGNMENTS

```

RESULT 1 309 bp mRNA linear EST 06-FEB-1995
T48892/c yb07a09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone
LOCUS IMAGE:70456 5' similar to SP:S28778 S28778 COLLAGEN
DEFINITION ALPHA 1(XV) CHAIN - HUMAN, mRNA sequence.

```

```

ACCESSION T48892
VERSION T48892.1 GI:650752
KEYWORDS EST.
SOURCE human.

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ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

1 (bases 1 to 309)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
, M., Mullis, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

```

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 239

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: M13RPI

High quality sequence stop: 239.

FEATURES

source

```

1..309
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GB:491353"
/db_xref="taxon:9606"
/clone="IMAGE:70456"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"
BASE COUNT 82 a 70 c 101 g 51 t
ORIGIN

```

```

Query Match 100.0%; Score 15; DB 14; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 CCTTCTCGCCCTGTT 15
| | | | | | | | | | | | | | | | | |
DB 107 CCTTCTCGCCCTGTT 93

```

RESULT 2

BH019102

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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1..313
Location/Qualifiers
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="L2358k"
/clone_lib="Leishmania major Friedlin Cosmid Genomic
Library"
/lab_host="E. coli ED8767"

```

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BH019102 313 bp DNA linear GSS 25-MAY-2001
L2358k.d.HygrT3.1 Leishmania major Friedlin Cosmid Genomic Library
Leishmania major genomic clone L2358k, DNA sequence.
BH019102
BH019102.1 GI:14197808
GSS
KEYWORDS
SOURCE Leishmania major.
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.

```

```

1 (bases 1 to 313)
AUTHORS Myler, P.J., Vogt, C., Cawthra, J., Klackner, M., Marty, A., Mack, J.,
Munden, H., Nguyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal
, G., Nelson, S., Seyler, A., Worthey, E., and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
Unpublished (2000)
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: HygrT3
Class: Cosmid ends.

```

FEATURES

source

```

1..313
Location/Qualifiers
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="L2358k"
/clone_lib="Leishmania major Friedlin Cosmid Genomic
Library"
/lab_host="E. coli ED8767"

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/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI, size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The cLHYG vector (Acc. No. CVU59231) is described in Ryan et al., Gene, 131:145-150 (1993)"

BASE COUNT 90 a 86 c 68 g 67 t 2 others
 ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
 |||||

Db 57 CCTTCTCGCCCTGTT 71
 |||||

RESULT 3
 BM273267/c

LOCUS BM273267 505 bp mRNA linear EST 12-MAR-2002
 DEFINITION if28e01.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5677896 5' similar to SW:CALE_HUMAN P39059 COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1]; mRNA sequence.

ACCESSION BM273267
 VERSION BM273267.1 GI:17966560
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 505)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Other_ESTs: if28e01.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brownj@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 432.
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5677896"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 133 a 138 c 148 g 86 t
 ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 505;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
 |||||

Db 50 CCTTCTCGCCCTGTT 36
 |||||

RESULT 4
 BH019101

LOCUS BH019101 513 bp DNA linear GSS 25-MAY-2001
 DEFINITION L2357K.d.Hygt3.1 Leishmania major Friedlin Cosmid Genomic Library Leishmania major genomic clone L2357K, DNA sequence.

ACCESSION BH019101
 VERSION BH019101.1 GI:14197807
 KEYWORDS GSS.
 SOURCE Leishmania major.
 ORGANISM Leishmania major
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

REFERENCE 1 (bases 1 to 513)
 Myler,P.J., Vogt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J., Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.
 Leishmania major Friedlin Cosmid End Sequences
 Unpublished (2000)
 Contact: Myler PJ
 Seattle Biomedical Research Institute
 4 Nickerson Street, Seattle, WA 98109-1651, USA
 Tel: 206 284-8846
 Fax: 206 284-0313
 Email: mylerpj@sbri.org
 Seq primer: Hygt3
 Class: cosmid ends.
 Location/Qualifiers
 1..513
 /organism="Leishmania major"
 /strain="Friedlin"
 /db_xref="taxon:5664"
 /clone="L2357K"
 /clone_lib="Leishmania major Friedlin Cosmid Genomic Library"
 /lab_host="E. coli ED8767"
 /note="vector: cHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI, size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The cLHYG vector (Acc. No. CVU59231) is described in Ryan et al., Gene, 131:145-150 (1993)"

BASE COUNT 141 a 154 c 100 g 118 t
 ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
 |||||

Db 52 CCTTCTCGCCCTGTT 66

RESULT 5
AV434035

LOCUS AV434035 543 bp mRNA linear EST 23-AUG-2000
DEFINITION AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone
PM037d06_r 5', mRNA sequence.

ACCESSION AV434035
VERSION AV434035.1 GI:8589260

KEYWORDS EST.
SOURCE Porphyra yezoensis.

ORGANISM

REFERENCE Porphyra yezoensis.
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
Porphyra.

AUTHORS 1 (bases 1 to 543)
Nikaido, I., Asamizu, E., Nakajima, M., Nakamura, Y., Saga, N. and
Tabata, S.

TITLE Generation of 10,154 expressed sequence tags from a leafy
gametophyte of a marine red alga, Porphyra yezoensis
JOURNAL DNA Res. 7, 223-227 (2000)
MEDLINE 20363100

COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source

1..543
/organism="Porphyra yezoensis"
/strain="TU-1"
/db_xref="taxon:2788"
/clone="PM037d06_r"
/clone_lib="Porphyra yezoensis TU-1"
/note="vector: phluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 55 a 163 c 190 g 135 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 543;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

|||||
Db 423 CCTTCTCGCCCTGTT 437

RESULT 6
BM142008/c

LOCUS BM142008 551 bp mRNA linear EST 12-MAR-2002
DEFINITION if25d08.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5677479 5' similar to SW:CALE_HUMAN P39059
COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1]; mRNA sequence.

ACCESSION BM142008
VERSION BM142008.1 GI:17152075

KEYWORDS EST.
SOURCE human.

ORGANISM

REFERENCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 551)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,
Jackson, Y. and Bowers, Y.

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: if25d08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 414.

FEATURES

source

Location/Qualifiers

1..551
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5677479"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

BASE COUNT 145 a 148 c 159 g 99 t

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 551;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

|||||
Db 50 CCTTCTCGCCCTGTT 36

RESULT 7

BF971415/c

LOCUS BF971415 617 bp mRNA linear EST 22-JAN-2001
DEFINITION 602272934F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361024 5',
mRNA sequence.

ACCESSION BF971415

VERSION BF971415.1 GI:12338630

KEYWORDS EST.

SOURCE human.

ORGANISM

REFERENCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 617)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM10003 row: c column: 09
 High quality sequence stop: 614.

FEATURES

Location/Qualifiers
 1. .617

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4361024"
 /clone_lib="NIH_MGC_84"
 /tissue_type="adrenal cortex carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
 NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt
 primed. Average insert size 1.229 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 157 a 158 c 195 g 107 t
 ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 617;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTCTGCGCCCTGTT 15
 |||||
 Db 375 CCTTCTGCGCCCTGTT 361

RESULT 8

AA102111 626 bp mRNA linear EST 11-MAY-1997
 LOCUS zk87h09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
 DEFINITION IMAGE:489857 3' similar to SW:CALE_HUMAN P39059 COLLAGEN ALPHA 1(XV
) CHAIN PRECURSOR. ; mRNA sequence.

ACCESSION AA102111.1 GI:1646031

VERSION EST.
 KEYWORDS human.

SOURCE
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
 , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL MEDLINE

COMMENT Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 867 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 453.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/db_xref="GDB:380444"

/db_xref="taxon:9606"

/clone="IMAGE:489857"

/clone_lib="Soares_pregnant_uterus_NbHPU"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 AACTGGAAGATTCGCGCCCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."

BASE COUNT 116 a 179 c 161 g 166 t 4 others
 ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 626;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCCTGTT 15

|||||

Db 527 CCTTCTGCGCCCTGTT 541

RESULT 9

AA099915 628 bp mRNA linear EST 11-MAY-1997
 LOCUS zk87h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
 DEFINITION IMAGE:489857 5' similar to SW:CALE_HUMAN P39059 COLLAGEN ALPHA 1(XV
) CHAIN PRECURSOR. ; mRNA sequence.

ACCESSION AA099915

VERSION AA099915.1 GI:1646057

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 628)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
 , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

97044478

CONTACT: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 867 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 492.

Location/Qualifiers

1. .628

/organism="Homo sapiens"

/db_xref="GDB:380444"

/db_xref="taxon:9606"

/clone="IMAGE:489857"

/clone_lib="Soares_pregnant_uterus_NbHPU"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5',

AACTGGAAGATTCGCGCCCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

```

BASE COUNT      154 a      158 c      189 g      122 t      5 others
ORIGIN

Query Match      100.0%; Score 15; DB 9; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 252 CCTTCTCGCCCTGTT 238

RESULT 10
BI997613/c
LOCUS
DEFINITION
1031050H04.y2 C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION
BI997613
VERSION
BI997613.1 GI:16432387
KEYWORDS
EST.
SOURCE
Chlamydomonas reinhardtii.
ORGANISM
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE
1 (bases 1 to 653)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre
,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
1..653
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Mellis et al.,(2000) plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
Polya mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda Zap clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
BASE COUNT      141 a      174 c      252 g      86 t
ORIGIN

Query Match      100.0%; Score 15; DB 13; Length 653;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 644 CCTTCTCGCCCTGTT 630

RESULT 11
BE313934
LOCUS
DEFINITION
601147310F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162555 5',
mRNA sequence.
ACCESSION
BE313934
VERSION
BE313934.1 GI:9134434
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 659)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-femail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. consortium/LLNL at: image.llnl.gov
Plate: LLC122 row: c column: 04
High quality sequence stop: 618.
FEATURES
source
1..659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3162555"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."
BASE COUNT      125 a      203 c      166 g      165 t
ORIGIN

Query Match      100.0%; Score 15; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 42 CCTTCTCGCCCTGTT 56

RESULT 12
BE776197/c
LOCUS
DEFINITION
MY-12-B-02 PinfeustansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION
BE776197
VERSION
BE776197.1 GI:10229852
KEYWORDS
EST.
SOURCE
potato late blight agent.
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
1 (bases 1 to 676)
Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
20056376
Contact: Govers F
Laboratory of Phytopathology

```

Wageningen University
 Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
 Tel: 31 317 483 138
 Fax: 31 317 483 412
 Email: Francine.Govers@medew.fyto.wau.nl.

FEATURES

Location/Qualifiers
 1. .676
 /organism="Phytophthora infestans"
 /strain="DDR7602, Al mating type"
 /db_xref="taxon:4787"
 /clone_lib="PinfestansMY"
 /dev_stage="4-week old vegetative, non-sporulating mycelium in synthetic medium"
 /lab_host="E. coli, strain DH5-alpha"
 /note="Vector: pSPORT1; Site.1: Sali; Site.2: NotI; Total RNA was isolated from mycelium of P. infestans DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelial) and the successive number of the microtiter plate (e.g. MY-06-A-04)."
 144 a 180 c 198 g 151 t 3 others

BASE COUNT

Query Match 100.0%; Score 15; DB 12; Length 676;

Best Local Similarity: 100.0%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15

|||||

Db 110 CCTCTCGCCCTGTT 96

RESULT 13

BF315344/c

LOCUS 601902627F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135278 5',
 mRNA sequence.

ACCESSION BF315344.1 GI:11263579

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 713)
 NIH-MGC http://mgc.nhl.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: LLC1039 row: e column: 07
 High quality sequence stop: 644.

FEATURES

source

Location/Qualifiers
 1. .713
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4135278"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 189 a 169 c 203 g 152 t

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 713;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15

|||||

Db 274 CCTCTCGCCCTGTT 260

RESULT 14

BG444893/c

LOCUS BG444893 830 bp mRNA linear EST 15-MAR-2001
 DEFINITION GA_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_Ea0025P19f, mRNA sequence.

ACCESSION BG444893

VERSION BG444893.1 GI:13354545

KEYWORDS EST.

SOURCE

Gossypium arboreum.

ORGANISM

Gossypium arboreum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE

AUTHORS

1 (bases 1 to 830)
 Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 High quality sequence stop: 182.

FEATURES

source

Location/Qualifiers
 1. .830
 /organism="Gossypium arboreum"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone="GA_Ea0025P19f"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
 /lab_host="E. coli"
 /note="Vector: pBK-CMV; Site.1: EcoRI; Site.2: XhoI"
 218 a 111 c 385 g 116 t

BASE COUNT

218 a 111 c 385 g 116 t

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 830;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15

|||||

Db 752 CCTCTCGCCCTGTT 738

RESULT 15

BQ609181

LOCUS BQ609181 839 bp mRNA linear EST 25-JUN-2002
 DEFINITION BRY_5105 wheat EST endosperm library Triticum aestivum cDNA 5',
 mRNA sequence.

ACCESSION BQ609181

VERSION BQ609181.1 GI:21558520

KEYWORDS EST.

```

SOURCE      bread wheat.
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 839)
AUTHORS     Clarke,B., Lambrecht,M. and Rhee,S.
TITLE       Assessing the utility of Arabidopsis genomic information for
            interpreting wheat EST sequences
JOURNAL      Unpublished (2002)
COMMENT     Contact: Lambrecht M
            The Arabidopsis Information Resource
            Carnegie Institution of Washington, Dept. of Plant Biology
            260 Panama Street, Stanford, CA 94305, USA
            Tel: 1 650 325 1521 x 251
            Fax: 1 650 325 3748
            Email: rhee@acoma.stanford.edu.

FEATURES             Location/Qualifiers
     source            1..839
                        /organism="Triticum aestivum"
                        /cultivar="Wyuna"
                        /db_xref="taxon:4565"
                        /clone_lib="wheat EST endosperm library"
                        /tissue_type="endosperm"
                        /dev_stage="developing endosperm tissue 8, 10 and 12 DPA
                        (days post anthesis)"
                        /note="Vector: Bluescript II SK(-)"

BASE COUNT      36 a    409 c    68 g    326 t

ORIGIN
Query Match      100.0%; Score 15; DB 14; Length 839;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTCTCGCCCTGTT 15
        |||||
DB      399 CCTCTCGCCCTGTT 413

Search completed: December 11, 2002, 19:00:29
Job time : 1722.5 secs

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GenCore version 5.1.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:26:07 ; Search time 1657 Seconds
(without alignments)
263.453 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 cctctgcgcctgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
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- 17: em.hum.*
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- 21: em.or.*
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- 32: em.htg.other.*
- 33: em.htg.mus.*
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- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15	100.0	920	6	AX194629 Sequence
2	15	100.0	920	6	AX194634 Sequence
3	15	100.0	980	9	HSNETEX9
4	15	100.0	1411	9	BC000563
5	15	100.0	1983	9	HUMNORTR
c 6	15	100.0	2127	9	HUMCOLA1XV
c 7	15	100.0	5161	9	HUMCOLXVAL
8	15	100.0	14621	2	AC020425
9	15	100.0	61956	2	AC101376
10	15	100.0	65851	2	AC124280
11	15	100.0	80669	2	AC130797
c 12	15	100.0	90280	2	AC009031
13	15	100.0	110000	2	LMFLCHR12_1
14	15	100.0	150765	2	AC094766
15	15	100.0	160755	6	AX195074
16	15	100.0	167094	9	AC007602
17	15	100.0	169763	2	AC120748
c 18	15	100.0	178965	2	AC096167
19	15	100.0	181066	2	AC099635
c 20	15	100.0	181650	2	AC097825
21	15	100.0	183105	3	AC104606
c 22	15	100.0	187359	8	OSJN00259
c 23	15	100.0	188913	9	AC026802
24	15	100.0	224592	2	AC074209
c 25	15	100.0	285272	3	AE003441
c 26	14	93.3	7708	6	AX120618
27	14	93.3	1773	9	AB057774
28	14	93.3	1987	10	AF158025
29	14	93.3	1989	10	MUSCAT2A
30	14	93.3	1989	10	MUSCAAT2X
c 31	14	93.3	2072	3	AF145606
c 32	14	93.3	2306	9	AK054811
c 33	14	93.3	2324	8	SCYGR002C
c 34	14	93.3	2393	8	AF435646
c 35	14	93.3	2397	6	AR054116
36	14	93.3	2397	6	IL13751
37	14	93.3	2723	10	MUSTEAB
c 38	14	93.3	3507	10	AF301152
39	14	93.3	3698	10	MUSMEMPROT
c 40	14	93.3	4420	1	CGL300822
c 41	14	93.3	5245	1	AF130462
c 42	14	93.3	12563	1	AE000769
c 43	14	93.3	13782	1	AE009777
44	14	93.3	16387	5	AF002935
45	14	93.3	18518	1	AE001068

ALIGNMENTS

RESULT 1	AX194629	920 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	Sequence 99 from Patent WO0151659.				
DEFINITION	AX194629				
ACCESSION	AX194629.1	GI:15385276			
VERSION					
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 920)				
AUTHORS	Chu,T., Blumenfeld,M. and Cohen,D.				
TITLE	Blallelic markers derived from genomic regions carrying genes involved in central nervous system disorders				

JOURNAL Patent: WO 0151659-A 99 19-JUL-2001;
GENSET (FR)

FEATURES
source Location/Qualifiers
1. .920
/organism="Homo sapiens"
/db_xref="taxon:9606"
20. .39
primer_bind /note="upstream amplification primer"
misc_feature 76. .94
misc_feature /note="16-2-76.misl"
83. .107
variation /note="16-2-76 potential probe"
95
misc_feature /note="16-2-76 : polymorphic base A or G"
96. .114
primer_bind /note="16-2-76.mis2, complement"
240. .260
/note="downstream amplification primer, complement"
204 a 260 c 225 g 227 t 4 others

BASE COUNT 204 a 260 c 225 g 227 t 4 others

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 920;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 170 CCTTCTCGCCCTGTT 184

RESULT 2
AX194634
LOCUS AX194634 920 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 104 from Patent WO0151659.
ACCESSION AX194634
VERSION AX194634.1 GI:15385281
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS Chu,T., Blumenfeld,M. and Cohen,D.
TITLE Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders
JOURNAL Patent: WO 0151659-A 104 19-JUL-2001;
GENSET (FR)

FEATURES
source Location/Qualifiers
1. .920
/organism="Homo sapiens"
/db_xref="taxon:9606"
20. .39
primer_bind /note="upstream amplification primer"
misc_feature 183. .205
misc_feature /note="16-2-187.misl"
194. .218
variation /note="16-2-187 potential probe"
206
misc_feature /note="16-2-187 : polymorphic base A or G"
207. .225
primer_bind /note="16-2-187.mis2, complement"
240. .260
/note="downstream amplification primer, complement"
204 a 260 c 225 g 227 t 4 others

BASE COUNT 204 a 260 c 225 g 227 t 4 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 170 CCTTCTCGCCCTGTT 184

RESULT 3
HSNETEX9
LOCUS HSNETEX9 980 bp DNA linear PRI 06-JUL-2001
DEFINITION Homo sapiens partial SLC6A2 gene for norepinephrine transporter, exons 9-10.
X91127
ACCESSION X91127.1 GI:1143488
VERSION X91127
KEYWORDS norepinephrine transporter; SLC6A2 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 980)
AUTHORS Porzgen,P., Bonisch,H. and Bruss,M.
TITLE Molecular cloning and organization of the coding region of the human norepinephrine transporter gene
JOURNAL Biochem. Biophys. Res. Commun. 215 (3), 1145-1150 (1995)
MEDLINE 96028030
PUBMED 748042
REFERENCE 2 (bases 1 to 980)
AUTHORS Porzgen,P., Bonisch,H., Hammermann,R. and Bruss,M.
TITLE The human noradrenaline transporter gene contains multiple polyadenylation sites and two alternatively spliced C-terminal exons
JOURNAL Biochim. Biophys. Acta 1398 (3), 365-370 (1998)
MEDLINE 98322125
PUBMED 9655936
REFERENCE 3 (bases 1 to 980)
AUTHORS Bonisch,H.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1995) H. Bonisch, Institut fuer Pharmacologie und Toxikologie, Universitaet Bonn, Reuterstr 2b, 53113 Bonn, FRG
COMMENT Related sequences: M65105 and X57700.
FEATURES
1. .980
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16q12.2"
/cell_line="W138"
/cell_type="fibroblast"
/tissue_type="lung"
/clone_lib="lambda FIX (Stratagene)"
129. .800
/gene="SLC6A2"
129. .257
/gene="SLC6A2"
/number=9
/usedin=X91117:SLC6A2_CDSA
/usedin=X91117:SLC6A2_mRNAa
/usedin=X91117:SLC6A2_mRNAB
701. .800
/gene="SLC6A2"
/number=10
/usedin=X91117:SLC6A2_CDSA
/usedin=X91117:SLC6A2_mRNAa
/usedin=X91117:SLC6A2_mRNAB
218 a 275 c 246 g 238 t 3 others

BASE COUNT 218 a 275 c 246 g 238 t 3 others

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 980;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 230 CCTTCTCGCCCTGTT 244

RESULT 4
BC000563

LOCUS BC000563 1411 bp mRNA linear PRI 12-JUL-2001
 DEFINITION Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.
 ACCESSION BC000563
 VERSION BC000563.1 GI:12653576
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1411)
 Strausberg,R.
 Direct Submission
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Guan,J., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
 Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
 McDowell,J., Pearson,R., Snyder,B., Stantirpop,S., Thomas,P.J.,
 Tionson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
 Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 5 Row: 1 Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3162672"
 /tissue_type="Brain, neuroblastoma"
 /clone_lib="NIH_MGC_19"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"
 <1..988
 /codon_start=2
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 /protein_id="AAH00563.1"
 /db_xref="GI:12653577"
 /translation="ARGLYFLSKGVKTSKGVWIDATATIFFSLGAGFGLVIAFASYN
 KFDNCRDALLTSSINCLTSFVSGFAIFSLCYMAHEHKNVEDVATEGGLVFLY
 PRAITSLSGSTFWAVFFVLLALGLDSSMGMEAVITGLADDFQVLRKRKLFTFGV
 TPTSLALFCITKGGIYVLLDITFAAGTSILFAVLEAIGVSWFVGVDRFSNDIOQ
 MGFRLGLWRCLWKFVSPAFLLFVVVSIINFKPLTYDDYIFPPANWYGVGIALSS
 MVLPIYIVYKFLSTQGSLEWRLAYGTTPEHHLVAQRDIRQFQLQHLAI"
 BASE COUNT 304 a 378 c 356 g 373 t
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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 Db 496 CCTTCTCGCCCTGTT 510

RESULT 5
 HUMNORTH 1983 bp mRNA linear PRI 07-JAN-1995
 LOCUS Human noradrenaline transporter mRNA, complete cds.
 DEFINITION M65105
 ACCESSION M65105.1 GI:189257
 VERSION noradrenaline transporter.
 KEYWORDS Human, CDNA to mRNA.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1983)
 Pacholczyk,T., Blakely,R.D. and Amara,S.G.
 Expression cloning of a cocaine- and antidepressant-sensitive human
 noradrenaline transporter
 JOURNAL Nature 350 (6316), 350-354 (1991)
 MEDLINE 91179515
 PUBMED 2008212
 FEATURES
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 1..1983
 /organism="Homo sapiens"
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 GI..1914
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 LHLHSSGIDHIDLPQWLLCLMVVIVLYFLSKGVKTSKGVWITATLPVFLFV
 LLVHGVTPLGASNGINAYLHIDFYLRKEATVVIDATQIFSLGAGFGLVIAFASYNK
 FDNNGYRDALLTSSINCLTSFVSGFAIFSLCYMAHEHKNVEDVATEGGLVFLY
 EAITSLSGSTFWAVFFVLLALGLDSSMGMEAVITGLADDFQVLRKRKLFTFGV
 FSTFLALFCITKGGIYVLLDITFAAGTSILFAVLEAIGVSWFVGVDRFSNDIOQ
 MGFRLGLWRCLWKFVSPAFLLFVVVSIINFKPLTYDDYIFPPANWYGVGIALSSM
 VLVPIYIVYKFLSTQGSLEWRLAYGTTPEHHLVAQRDIRQFQLQHLAI"
 BASE COUNT 383 a 602 c 530 g 468 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 9; Length 1983;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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 Db 1422 CCTTCTCGCCCTGTT 1436

RESULT 6
 HUMCOLA1XV/c 2127 bp mRNA linear PRI 27-APR-1993
 LOCUS Homo sapiens alpha-1 type XV collagen mRNA sequence.
 DEFINITION L01697
 ACCESSION L01697
 VERSION L01697.1 GI:180858
 KEYWORDS alpha-1 type XV collagen.
 SOURCE Homo sapiens (library: gtl1 from Clonotech Laboratories) placenta
 CDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2127)
 Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
 Pihlajaniemi,T.
 Identification of a previously unknown human collagen chain, alpha
 1(XV), characterized by extensive interruptions in the

```

triple-helical region
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)
MEDLINE 93066196
PUBMED 1279671
FEATURES
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        /db_xref="taxon:9606"
        /tissue_type="placenta"
        /tissue_lib="gt11 from Clontech Laboratories"
BASE COUNT      508 a 593 c 644 g 392 t
ORIGIN
Query Match      100.0%; Score 15; DB 9; Length 2127;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 955 CCTTCTCGCCCTGTT 941

RESULT 7
HUMCOLXVA1/c
LOCUS HUMCOLXVA1 5161 bp mRNA linear PRI 31-DEC-1994
DEFINITION Homo sapiens alpha-1 type XV collagen mRNA, complete cds.
ACCESSION L25286
VERSION L25286.1 GI:461396
KEYWORDS alpha-1 type XV collagen.
SOURCE Homo sapiens (tissue library: Clontech bases 955-5167) umbilical cord (bases 1-954) cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5161)
AUTHORS Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
Pihlajaniemi,T.
TITLE Identification of a previously unknown human collagen chain, alpha
1(XV), characterized by extensive interruptions in the
triple-helical region
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)
MEDLINE 93066196
PUBMED 1279671
REFERENCE 2 (bases 1 to 5161)
AUTHORS Kivirikko,S., Heinamaki,P., Rehn,M., Honkanen,N., Myers,J.C. and
Pihlajaniemi,T.
TITLE Primary structure of the alpha 1 chain of human type XV collagen
and exon-intron organization in the 3' region of the corresponding
gene
JOURNAL J. Biol. Chem. 269 (7), 4773-4779 (1994)
MEDLINE 94148920
PUBMED 8106446
FEATURES
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        /tissue_lib="Clontech bases 955-5167"
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        /label=5'UTR
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gene
5'UTR
CDS

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/db_xref="GI:461397"
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WNRFAMIVQGEVEVTLVNCBEHSRIPQRSSOALAFESSAGIFMGNAGATGLERTGS
LQOLTVPDPTPEELCDPESSASGETSGLOEADGVAILEAVTYTOASKEAKVEP
INTPTTSPFPDELMSEPEVTEGTLTETNNMSIIHQSPKQSGEILNDTLEGVHSVD
GPIITDSGAGAFLDIAEKNLAATAAGLAEPVISTAGAEASVPTGGPTLSMSTE
NPEGVTPGPDNERLRATAAGEALASMPGEVEASGAPGELDLSMSAQSLSIEAT
VGPSSDSLTTAAATVSLSTFEDEASGVPTDGLAPLTATMAPERAVTSGPDEED
LAAATTEPLITAGGEESGSPDPDPLPTVTAERHITPAQREHVGMKQAGPKGE
KDAGEELPDPPEFSGVPTAGAEAGSLGSDVSGSDLVGSEQLLRGPDPGP
PGPLPGIPKPGTDVFMGPPGSPGDPGAGPEPGPGEGQVGDGATLPGMKGEKG
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DTGSGSTQLLNBPKLSRPTAAI GLKGEKGRGPKGERMDGASIVGPPGPRGPGHI
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GLNGLGTKGDGVI MGPGPLPGPPGPGAVINIKGAIPIPVPRHCKMPVDTA
HPCSPELITFHGVKGEKSGWGLPGKGEKGDQAGPPGLDLAYLRHFLNNLKGN
GDKGFKGEKGEKGDINGSLMGSPGLPGNPGPAGQKGTVVGPGPPGAPGLPGPQ
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PNPISSANKEKPAHLAALNMPESGDIRADFCQKQARAAGLLSTYRAFLSSHQLDLS
TIVYKAEVSLPIVNLKGQVLFNNWDSIFSGHGGQFNHIIPIYSFDGDMTDFSWPQ
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        /gene="COL15A1"
BASE COUNT      1254 a 1420 c 1363 g 1124 t
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Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CCTTCTCGCCCTGTT 15
LOCUS   2673 CCTTCTCGCCCTGTT 2659
DEFINITION
Drosophila melanogaster, 14621 bp DNA linear HTG 03-JAN-2000
pieces.
ACCESSION
AC020425
VERSION AC020425.1 GI:6664472
KEYWORDS HTG; HTGS_PHASE2.
SOURCE   Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
REFERENCE
AUTHORS Adams,M. and Venter,J.C.
TITLE    Direct Submission
JOURNAL  Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT  This sequence was identified as CDM:10213135 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
Source
1. .14621
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/db_xref="taxon:7227"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTTCTCGCCCTGTT 15
LOCUS   4882 CCTTCTCGCCCTGTT 4896
DEFINITION
Mus musculus clone RP23-117I21, LOW-PASS SEQUENCE SAMPLING.
ACCESSION
AC101376
VERSION AC101376.1 GI:17060151
KEYWORDS HTG; HTGS_PHASE0.
SOURCE   Mus musculus.
ORGANISM Mus musculus.
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE    Unpublished
JOURNAL  Unpublished
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campolano,A., Chang,J., Chazaro,B.,
Choepe,Y., Collangelo,M., Collins,S., Collumore,A., Cook,B.,
Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Hearford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L16579
Center clone name: L17_I_21
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* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 630: contig of 630 bp in length
631 730: gap of 100 bp
731 1391: contig of 661 bp in length
1392 1491: gap of 100 bp
1492 2138: contig of 647 bp in length
2139 2238: gap of 100 bp
2239 3005: contig of 767 bp in length
3006 3105: gap of 100 bp
3106 3860: contig of 755 bp in length
3861 3960: gap of 100 bp
3961 4639: contig of 679 bp in length
4640 4739: gap of 100 bp
4740 5414: contig of 675 bp in length
5415 5514: gap of 100 bp
5515 6290: contig of 776 bp in length
6291 6390: gap of 100 bp
6391 7071: contig of 681 bp in length
7072 7171: gap of 100 bp
7172 7853: contig of 682 bp in length
7854 7953: gap of 100 bp
7954 8627: contig of 674 bp in length
8628 8727: gap of 100 bp
8728 9409: contig of 682 bp in length
9410 9509: gap of 100 bp
9510 10180: contig of 671 bp in length
10181 10280: gap of 100 bp
10281 10969: contig of 689 bp in length
10970 11069: gap of 100 bp
11070 11740: contig of 671 bp in length
11741 11840: gap of 100 bp
11841 12509: contig of 669 bp in length
12510 12609: gap of 100 bp
12610 13254: contig of 645 bp in length
13255 13354: gap of 100 bp
13355 14028: contig of 674 bp in length
14029 14128: gap of 100 bp

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* 14129 14795: contig of 667 bp in length
* 14796 14895: gap of 100 bp
* 14896 15570: contig of 675 bp in length
* 15571 15670: gap of 100 bp
* 15671 16330: contig of 660 bp in length
* 16331 16430: gap of 100 bp
* 16431 17099: contig of 669 bp in length
* 17100 17199: gap of 100 bp
* 17200 17903: contig of 704 bp in length
* 17904 18003: gap of 100 bp
* 18004 18692: contig of 689 bp in length
* 18693 18792: gap of 100 bp
* 18793 19467: contig of 675 bp in length
* 19468 19567: gap of 100 bp
* 19568 20238: contig of 671 bp in length
* 20239 20338: gap of 100 bp
* 20339 21007: contig of 669 bp in length
* 21008 21107: gap of 100 bp
* 21108 21852: contig of 745 bp in length
* 21853 21952: gap of 100 bp
* 21953 22635: contig of 683 bp in length
* 22636 22735: gap of 100 bp
* 22736 23384: contig of 649 bp in length
* 23385 23484: gap of 100 bp
* 23485 24154: contig of 670 bp in length
* 24155 24254: gap of 100 bp
* 24255 24914: contig of 660 bp in length
* 24915 25014: gap of 100 bp
* 25015 25697: contig of 683 bp in length
* 25698 25797: gap of 100 bp
* 25798 26470: contig of 673 bp in length
* 26471 26570: gap of 100 bp
* 26571 27328: contig of 758 bp in length
* 27329 27428: gap of 100 bp
* 27429 28117: contig of 689 bp in length
* 28118 28217: gap of 100 bp
* 28218 28864: contig of 647 bp in length
* 28865 28964: gap of 100 bp
* 28965 29633: contig of 669 bp in length
* 29634 29733: gap of 100 bp
* 29734 30482: contig of 749 bp in length
* 30483 30582: gap of 100 bp
* 30583 31343: contig of 761 bp in length
* 31344 31443: gap of 100 bp
* 31444 32204: contig of 761 bp in length
* 32205 32304: gap of 100 bp
* 32305 32972: contig of 668 bp in length
* 32973 33072: gap of 100 bp
* 33073 33838: contig of 766 bp in length
* 33839 33938: gap of 100 bp
* 33939 34620: contig of 682 bp in length
* 34621 34720: gap of 100 bp
* 34721 35467: contig of 747 bp in length
* 35468 35567: gap of 100 bp
* 35568 36222: contig of 655 bp in length
* 36223 36322: gap of 100 bp
* 36323 36998: contig of 676 bp in length
* 36999 37098: gap of 100 bp
* 37099 37770: contig of 672 bp in length
* 37771 37870: gap of 100 bp
* 37871 38547: contig of 677 bp in length
* 38548 38647: gap of 100 bp
* 38648 39387: contig of 740 bp in length
* 39388 39487: gap of 100 bp
* 39488 40243: contig of 756 bp in length
* 40244 40343: gap of 100 bp
* 40344 41003: contig of 660 bp in length
* 41004 41103: gap of 100 bp
* 41104 41784: contig of 681 bp in length
* 41785 41884: gap of 100 bp
* 41885 42572: contig of 688 bp in length
* 42573 42672: gap of 100 bp
* 42673 43330: contig of 658 bp in length
```

```
* 43331 43430: gap of 100 bp
* 43431 44096: contig of 666 bp in length
* 44097 44196: gap of 100 bp
* 44197 44852: contig of 656 bp in length
* 44853 44952: gap of 100 bp
* 44953 45627: contig of 675 bp in length
* 45628 45727: gap of 100 bp
* 45728 46410: contig of 683 bp in length
* 46411 46510: gap of 100 bp
* 46511 47187: contig of 677 bp in length
* 47188 47287: gap of 100 bp
* 47288 48012: contig of 725 bp in length
* 48013 48112: gap of 100 bp
* 48113 48784: contig of 672 bp in length
* 48785 48884: gap of 100 bp
* 48885 49549: contig of 665 bp in length
* 49550 49649: gap of 100 bp
* 49650 50338: contig of 689 bp in length
* 50339 50438: gap of 100 bp
* 50439 51107: contig of 669 bp in length
* 51108 51207: gap of 100 bp
* 51208 51871: contig of 664 bp in length
* 51872 51971: gap of 100 bp
* 51972 52651: contig of 680 bp in length
* 52652 52751: gap of 100 bp
* 52752 53427: contig of 676 bp in length
* 53428 53527: gap of 100 bp
* 53528 54200: contig of 673 bp in length
* 54201 54300: gap of 100 bp
```

Query Match 100.0%; Score 15; DB 2; Length 61956;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCTGTT 15

Db 57817 CCTTCTCGCCTGTT 57831

RESULT 10
AC124280

LOCUS

DEFINITION

AC124280

VERSION

AC124280.3 GI:22004380

KEYWORDS

HTG; HTGS_PHASE0.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AC124280
Homo sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS
SEQUENCE SAMPLING.

AC124280

AC124280.3 GI:22004380

HTG; HTGS_PHASE0.

human.

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 65851)

2 (bases 1 to 65851)

Anderson, S., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Bouckhalter, B., Brown, A., Camarata, J., Campotiano, A., Chang, J.,

Chazaro, B., Choepel, I., Colangelo, M., Collins, S., Collamore, A.,

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Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,

Meneus, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C.,

Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,

Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,

Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 65851)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 30, 2002 this sequence version replaced gi:21699374.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L27356

Center clone name: 519_O19

* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 707: contig of 707 bp in length
* 708 807: gap of 100 bp
* 808 1542: contig of 735 bp in length
* 1543 1642: gap of 100 bp
* 1643 2336: contig of 694 bp in length
* 2337 2436: gap of 100 bp
* 2437 3166: contig of 730 bp in length
* 3167 3266: gap of 100 bp
* 3267 3987: contig of 721 bp in length
* 3988 4087: gap of 100 bp
* 4088 4813: contig of 726 bp in length
* 4814 4913: gap of 100 bp
* 4914 5651: contig of 738 bp in length
* 5652 5751: gap of 100 bp
* 5752 6473: contig of 722 bp in length
* 6474 6573: gap of 100 bp
* 6574 7300: contig of 727 bp in length
* 7301 7400: gap of 100 bp
* 7401 8134: contig of 734 bp in length

* 8135 8234: gap of 100 bp
* 8235 8966: contig of 732 bp in length
* 8967 9066: gap of 100 bp
* 9067 9714: contig of 648 bp in length
* 9715 9814: gap of 100 bp
* 9815 10534: contig of 720 bp in length
* 10535 10634: gap of 100 bp
* 10635 11348: contig of 714 bp in length
* 11349 11448: gap of 100 bp
* 11449 12160: contig of 712 bp in length
* 12161 12260: gap of 100 bp
* 12261 12986: contig of 726 bp in length
* 12987 13086: gap of 100 bp
* 13087 13816: contig of 730 bp in length
* 13817 13916: gap of 100 bp
* 13917 14633: contig of 717 bp in length
* 14634 14733: gap of 100 bp
* 14734 15446: contig of 713 bp in length
* 15447 15546: gap of 100 bp
* 15547 16272: contig of 726 bp in length
* 16273 16372: gap of 100 bp
* 16373 17115: contig of 743 bp in length
* 17116 17215: gap of 100 bp
* 17216 17930: contig of 715 bp in length
* 17931 18030: gap of 100 bp
* 18031 18748: contig of 718 bp in length
* 18749 18848: gap of 100 bp
* 18849 19574: contig of 726 bp in length
* 19575 19674: gap of 100 bp
* 19675 20393: contig of 719 bp in length
* 20394 20493: gap of 100 bp
* 20494 21206: contig of 713 bp in length
* 21207 21306: gap of 100 bp
* 21307 22020: contig of 714 bp in length
* 22021 22120: gap of 100 bp
* 22121 22852: contig of 732 bp in length
* 22853 22952: gap of 100 bp
* 22953 23692: contig of 740 bp in length
* 23693 23792: gap of 100 bp
* 23793 24520: contig of 728 bp in length
* 24521 24620: gap of 100 bp
* 24621 25368: contig of 748 bp in length
* 25369 25468: gap of 100 bp
* 25469 26186: contig of 718 bp in length
* 26187 26286: gap of 100 bp
* 26287 27015: contig of 729 bp in length
* 27016 27115: gap of 100 bp
* 27116 27837: contig of 722 bp in length
* 27838 27937: gap of 100 bp
* 27938 28649: contig of 712 bp in length
* 28650 28749: gap of 100 bp
* 28750 29479: contig of 730 bp in length
* 29480 29579: gap of 100 bp
* 29580 30264: contig of 685 bp in length
* 30265 30364: gap of 100 bp
* 30365 31103: contig of 739 bp in length
* 31104 31203: gap of 100 bp
* 31204 31943: contig of 740 bp in length
* 31944 32043: gap of 100 bp
* 32044 32786: contig of 743 bp in length
* 32787 32886: gap of 100 bp
* 32887 33595: contig of 709 bp in length
* 33596 33695: gap of 100 bp
* 33696 34433: contig of 738 bp in length
* 34434 34533: gap of 100 bp
* 34534 35276: contig of 743 bp in length
* 35277 35376: gap of 100 bp
* 35377 36124: contig of 748 bp in length
* 36125 36224: gap of 100 bp
* 36225 36946: contig of 722 bp in length
* 36947 37046: gap of 100 bp
* 37047 37776: contig of 730 bp in length
* 37777 37876: gap of 100 bp

[illegible]

* 6274 6962: contig of 689 bp in length
* gap of unknown length
* 6963 7734: contig of 772 bp in length
* gap of unknown length
* 7735 8478: contig of 744 bp in length
* gap of unknown length
* 8479 9239: contig of 761 bp in length
* gap of unknown length
* 9240 9982: contig of 743 bp in length
* gap of unknown length
* 9983 10641: contig of 659 bp in length
* gap of unknown length
* 10642 11388: contig of 747 bp in length
* gap of unknown length
* 11389 12220: contig of 832 bp in length
* gap of unknown length
* 12221 12989: contig of 769 bp in length
* gap of unknown length
* 12990 13644: contig of 655 bp in length
* gap of unknown length
* 13645 14446: contig of 802 bp in length
* gap of unknown length
* 14447 15320: contig of 874 bp in length
* gap of unknown length
* 15321 15914: contig of 594 bp in length
* gap of unknown length
* 15915 16670: contig of 756 bp in length
* gap of unknown length
* 16671 17491: contig of 821 bp in length
* gap of unknown length
* 17492 18135: contig of 644 bp in length
* gap of unknown length
* 18136 18738: contig of 603 bp in length
* gap of unknown length
* 18739 19363: contig of 625 bp in length
* gap of unknown length
* 19364 20076: contig of 713 bp in length
* gap of unknown length
* 20077 20849: contig of 773 bp in length
* gap of unknown length
* 20850 22064: contig of 1215 bp in length
* gap of unknown length
* 22065 23060: contig of 996 bp in length
* gap of unknown length
* 23061 23683: contig of 623 bp in length
* gap of unknown length
* 23684 24344: contig of 661 bp in length
* gap of unknown length
* 24345 24969: contig of 625 bp in length
* gap of unknown length
* 24970 25267: contig of 298 bp in length
* gap of unknown length
* 25268 25891: contig of 624 bp in length
* gap of unknown length
* 25892 26674: contig of 783 bp in length
* gap of unknown length
* 26675 27382: contig of 708 bp in length
* gap of unknown length
* 27383 27459: contig of 77 bp in length
* gap of unknown length
* 27460 28325: contig of 866 bp in length
* gap of unknown length
* 28326 29243: contig of 918 bp in length
* gap of unknown length
* 29244 30009: contig of 766 bp in length
* gap of unknown length
* 30010 30770: contig of 761 bp in length
* gap of unknown length
* 30771 31472: contig of 702 bp in length
* gap of unknown length
* 31473 32518: contig of 1046 bp in length
* gap of unknown length
* 32519 33729: contig of 1211 bp in length

* 33730 gap of unknown length
* 33804: contig of 75 bp in length
* gap of unknown length
* 34775: contig of 971 bp in length
* gap of unknown length
* 35568: contig of 793 bp in length
* gap of unknown length
* 36526: contig of 958 bp in length
* gap of unknown length
* 37178: contig of 652 bp in length
* gap of unknown length
* 38597: contig of 1419 bp in length
* gap of unknown length
* 39399: contig of 802 bp in length
* gap of unknown length
* 40532: contig of 1133 bp in length
* gap of unknown length
* 41611: contig of 1079 bp in length
* gap of unknown length
* 42657: contig of 1046 bp in length
* gap of unknown length
* 43644: contig of 987 bp in length
* gap of unknown length
* 44808: contig of 1164 bp in length
* gap of unknown length
* 46147: contig of 1339 bp in length
* gap of unknown length
* 47217: contig of 1070 bp in length
* gap of unknown length
* 48521: contig of 1304 bp in length
* gap of unknown length
* 49309: contig of 788 bp in length
* gap of unknown length
* 50843: contig of 1534 bp in length
* gap of unknown length
* 52193: contig of 1350 bp in length
* gap of unknown length
* 53317: contig of 1124 bp in length
* gap of unknown length
* 54463: contig of 1146 bp in length
* gap of unknown length
* 55711: contig of 1248 bp in length
* gap of unknown length
* 56683: contig of 972 bp in length
* gap of unknown length
* 58209: contig of 1526 bp in length
* gap of unknown length
* 59763: contig of 1554 bp in length
* gap of unknown length
* 61209: contig of 1446 bp in length
* gap of unknown length
* 62915: contig of 1706 bp in length
* gap of unknown length
* 64134: contig of 1219 bp in length
* gap of unknown length
* 65998: contig of 1864 bp in length
* gap of unknown length
* 67325: contig of 1327 bp in length
* gap of unknown length
* 68610: contig of 1285 bp in length
* gap of unknown length
* 70086: contig of 1476 bp in length
* gap of unknown length
* 71288: contig of 1202 bp in length
* gap of unknown length
* 73310: contig of 2022 bp in length
* gap of unknown length
* 74258: contig of 948 bp in length
* gap of unknown length
* 75836: contig of 1578 bp in length
* gap of unknown length

Query Match

100.0%; Score 15; DB 2; Length 90280;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 63309 CCTTCTCGCCCTGTT 63295

RESULT 13

LMFLCHR12_1

WPCOMMENT

Sequence split into 8 fragments LOCUS LMFLCHR12 Accession AL390114

Fragment Name	Begin	End
LMFLCHR12_0	1	110000
LMFLCHR12_1	100001	210000
LMFLCHR12_2	200001	310000
LMFLCHR12_3	300001	410000
LMFLCHR12_4	400001	510000
LMFLCHR12_5	500001	610000
LMFLCHR12_6	600001	710000
LMFLCHR12_7	700001	757191

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Continuation (2 of 8) of LMFLCHR12 from base 100001 (AL390114 Leishmania major chromosome)

Query Match

Best Local Similarity 100.0%; Score 15; DB 2; Length 110000;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 46567 CCTTCTCGCCCTGTT 46581

RESULT 14

AC094766

LOCUS

DEFINITION

AC094766 Rattus norvegicus clone CH230-5L5, *** SEQUENCING IN PROGRESS ***
65 unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 150765)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Blimie,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burke,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Duggan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
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Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulsegh,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,

Oruh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Roife,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonaie,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 150765)

Worley,K.C.

Direct Submission

Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624602.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GBID

Center clone name: CH230-5L5

----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to

findPhrapList

Consensus quality: 115371 bases at least Q40

Consensus quality: 123148 bases at least Q30

Consensus quality: 129020 bases at least Q20

Estimated insert size: 114258; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
consists of 65 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

* be preserved.

1 7731: contig of 7731 bp in length

7732 7831: gap of unknown length

7832 12932: contig of 5101 bp in length

12933 13032: gap of unknown length

13033 13264: contig of 6232 bp in length

13265 19364: gap of unknown length

19365 24766: contig of 5402 bp in length

24767 24866: gap of unknown length

24867 29281: contig of 4415 bp in length

29282 35253: contig of 5872 bp in length

35254 35353: gap of unknown length

35354 38906: contig of 3553 bp in length

38907 39006: gap of unknown length

39007 43062: contig of 4056 bp in length

43063 43162: gap of unknown length

43163 46845: contig of 3683 bp in length

46846 50669: gap of unknown length

50670 50769: gap of unknown length

50770 52753: contig of 1984 bp in length

52754 52853: gap of unknown length

52854 56708: contig of 3855 bp in length

56709 56808: gap of unknown length

* 56809 60130: contig of 3322 bp in length
* 60131 60230: gap of unknown length
* 60231 62896: contig of 2666 bp in length
* 62897 62996: gap of unknown length
* 62997 65284: contig of 2288 bp in length
* 65285 65384: gap of unknown length
* 65385 68543: contig of 3159 bp in length
* 68544 68643: gap of unknown length
* 68644 71605: contig of 2962 bp in length
* 71606 73043: contig of 1338 bp in length
* 73044 73143: gap of unknown length
* 73144 75325: contig of 2182 bp in length
* 75326 75426: gap of unknown length
* 75427 77827: contig of 2402 bp in length
* 77828 77927: gap of unknown length
* 77928 79747: contig of 1820 bp in length
* 79748 79847: gap of unknown length
* 79848 82048: contig of 2201 bp in length
* 82049 82148: gap of unknown length
* 82149 84544: contig of 2396 bp in length
* 84545 84644: gap of unknown length
* 84645 86064: contig of 1420 bp in length
* 86065 86164: gap of unknown length
* 86165 88210: contig of 2046 bp in length
* 88211 88310: gap of unknown length
* 88311 89982: contig of 1672 bp in length
* 89983 90082: gap of unknown length
* 90083 91934: contig of 1852 bp in length
* 91935 92034: gap of unknown length
* 92035 94820: contig of 2786 bp in length
* 94821 94920: gap of unknown length
* 94921 96405: contig of 1485 bp in length
* 96406 96505: gap of unknown length
* 96506 98196: contig of 1691 bp in length
* 98197 98296: gap of unknown length
* 98297 100079: contig of 1783 bp in length
* 100080 100179: gap of unknown length
* 100180 101420: contig of 1241 bp in length
* 101421 101520: gap of unknown length
* 101521 103845: contig of 2325 bp in length
* 103846 103945: gap of unknown length
* 103946 105477: contig of 1532 bp in length
* 105478 105577: gap of unknown length
* 105578 106976: contig of 1398 bp in length
* 106976 107075: gap of unknown length
* 107076 108224: contig of 1149 bp in length
* 108225 108324: gap of unknown length
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* 109717 109816: gap of unknown length
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* 111021 111120: gap of unknown length
* 111121 113035: contig of 1915 bp in length
* 113036 113135: gap of unknown length
* 113136 114902: contig of 1767 bp in length
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* 115003 116304: contig of 1302 bp in length
* 116305 116404: gap of unknown length
* 116405 117754: contig of 1350 bp in length
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* 117855 119553: contig of 1699 bp in length
* 119554 119653: gap of unknown length
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* 120689 120788: gap of unknown length
* 120789 121913: contig of 1125 bp in length
* 121914 122013: gap of unknown length
* 122014 123345: contig of 1332 bp in length
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* 127138 128572: contig of 1435 bp in length

* 128573 128672: gap of unknown length
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* 130025 131222: contig of 1198 bp in length
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* 134382 135794: contig of 1413 bp in length
* 135795 135894: gap of unknown length
* 135895 137173: contig of 1279 bp in length
* 137174 137273: gap of unknown length
* 137274 138283: contig of 1010 bp in length
* 138284 138383: gap of unknown length

Query Match 100.0%; Score 15; DB 2; Length 150765;
Best Local Similarity 100.0%; Pred. No. 6.5e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTGCGCCGTT 15
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Db 76250 CCTTCTGCGCCGTT 76264

RESULT 15
AX195074
LOCUS AX195074 160755 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 544 from Patent WO0151659.
ACCESSION AX195074
VERSION AX195074.1 GI:15385721
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 160755)
AUTHORS Chu,T., Blumenfeld,M. and Cohen,D.
TITLE Biallelic markers derived from genomic regions carrying genes
involved in central nervous system disorders
JOURNAL Patent: WO 0151659-A 544 19-JUL-2001;
GENSET (FR)

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="5' regulatory region"
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/note="exon 1A"
exon 21864..22188
/note="exon 1"
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/note="99-32148.rp"
primer_bind 31528..31546
/note="99-32148-315.mis"
misc_feature 31535..31559
/note="99-32148-315.probe"
variation 31547
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primer_bind 31548..31566
/note="99-32148-315.mis complement"
primer_bind 31844..31862
/note="99-32148.pu complement"
exon 34799..34930
/note="exon 2"
exon 37172..37409
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exon 50385..50523
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primer_bind 50539..50557

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exon /note="19-51.rp complement"
57261..57395
exon /note="exon 5"
59355..59458
exon /note="exon 6"
60623..60747
exon /note="exon 7"
61570..61682
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63131..63150
exon /note="19-56.pu"
63244..63372
primer_bind /note="exon 9"
63251..63269
misc_feature /note="19-56-140.mis"
63258..63282
variation /note="19-56-140.probe"
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64775..64793
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64902..65002
primer_bind /note="exon 11"
65006..65024
misc_feature /note="19-44-251.mis"
65013..65037
variation /note="19-44-251.probe"
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primer_bind /note="19-44-251 : polymorphic base C or T"
65026..65044
primer_bind /note="19-44-251.mis complement"
65176..65194
exon /note="19-44.rp complement"
65487..65654
primer_bind /note="exon 12"
67027..67045
exon /note="19-46.pu"
67211..67282
primer_bind /note="exon 13"
67329..67347
misc_feature /note="19-46-322.mis"
67336..67360
variation /note="19-46-322.probe"
67348
primer_bind /note="19-46-322 : polymorphic base C or T"
67349..67367
primer_bind /note="19-46-322.mis complement"
67435..67452
primer_bind /note="19-46.rp complement"
67649..67667
exon /note="19-47.pu"
67671..67928
misc_feature /note="exon 14"
67929..68055
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67951..67975
/note="19-47-315.probe"
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67964..67982
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/note="19-47.rp complement"
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Query Match 100.0%; Score 15; DB 6; Length 160755;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 63345 CCTTCTCGCCCTGTT 63359
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Search completed: December 11, 2002, 14:35:19
Job time : 1782 secs

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:23:57 : Search time 212.5 Seconds
(without alignments)
158.965 Million cell updates/sec

Title: US-09-750-609-9

Perfect score: 15

Sequence: 1 cctctcgcctgtt 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
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- 20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
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- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AAH28084	Probe for human no
2	15	100.0	920	AAH88259	CNS disorder-relat
3	15	100.0	920	AAH88264	CNS disorder-relat
4	15	100.0	980	AAH28088	Nucleotide sequenc
5	15	100.0	1044	AAH80746	DNA encoding novel
6	15	100.0	1854	AAH28082	Nucleotide sequenc
7	15	100.0	1854	AAH28086	Nucleotide sequenc
8	15	100.0	1983	AAQ28118	Human norepinepher
9	15	100.0	5161	ABK83862	Human cDNA differe

10	15	100.0	160755	23	AAH88704	Human DNA sequence
11	14	93.3	336	24	ABN18096	Human ORFX polynuc
12	14	93.3	655	24	ABQ56203	Human ovarian anti
13	14	93.3	708	22	AAH65499	C glutamicum codin
14	14	93.3	2036	23	ABL11823	Drosophila melanog
15	14	93.3	2397	12	AAQ14533	Tea gene (cDNA 20.
16	14	93.3	2397	15	AAQ63614	T-cell transembra
17	14	93.3	2397	20	AAV59846	Human T-cell early
18	14	93.3	5031	23	ABL11822	Drosophila melanog
19	14	93.3	349980	22	AAH68525	C glutamicum codin
20	13.4	89.3	15	22	AAH28085	Probe for human no
21	13.4	89.3	114	22	ABA40720	Probe #19186 for g
22	13.4	89.3	114	22	AAK24835	Human brain expres
23	13.4	89.3	114	22	AAI56840	Probe #25526 used
24	13.4	89.3	114	22	ABS24326	Human genome-deriv
25	13.4	89.3	324	19	AAV27204	Homo sapiens TSH r
26	13.4	89.3	328	22	ABA15500	Human nervous syst
27	13.4	89.3	331	24	ABN17269	Human ORFX polynuc
28	13.4	89.3	334	24	ABN24354	Human ORFX polynuc
29	13.4	89.3	352	21	AAC09241	Human secreted pro
30	13.4	89.3	374	22	AAK69418	Human immune/haema
31	13.4	89.3	374	22	AAK69419	Human immune/haema
32	13.4	89.3	375	22	ABA11654	Human nervous syst
33	13.4	89.3	389	22	ABA11693	Human nervous syst
34	13.4	89.3	400	22	AAK57066	Human immune/haema
35	13.4	89.3	411	12	AAQ11640	Human TSH-receptor
36	13.4	89.3	417	22	AAI81399	Human polynucleoti
37	13.4	89.3	445	23	ABV50337	Human prostate exp
38	13.4	89.3	450	22	AAI22903	Human breast cance
39	13.4	89.3	458	24	ABS23895	Human genome-deriv
40	13.4	89.3	509	23	AAH81898	DNA encoding novel
41	13.4	89.3	517	24	ABN73664	Bovine embryonic g
42	13.4	89.3	543	24	ABS11537	Human genome-deriv
43	13.4	89.3	549	23	AAH66052	DNA encoding novel
44	13.4	89.3	573	17	AAI16644	Hepatitis C virus
45	13.4	89.3	580	22	ABA31138	Probe #9604 for ge

ALIGNMENTS

RESULT 1

AAH28084

ID AAH28084 standard; DNA; 15 BP.

AC AAH28084;

XX

XX 05-SEP-2001 (first entry)

DT

XX Probe for human norepinephrine transporter gene wild type allele.

DE

XX Norepinephrine transporter; orthostatic intolerance; gene therapy;

KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;

KW amphetamine abuse; probe; ss.

XX

OS Homo sapiens.

XX

PN WO200148246-A1.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-US35491.

XX

PR 29-DEC-1999; 99US-0173682.

PR 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

PI Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

XX

PT Screening for susceptibility to sub-optimal norepinephrine transport,

PT particularly orthostatic intolerance in a subject by detecting a
 PT polymorphism of norepinephrine transporter gene -
 PS Claim 15; Page 69; 133pp; English.
 XX
 CC The present sequence represents a probe for the wild type allele of
 CC a human norepinephrine transporter gene. The specification a method
 CC for screening for susceptibility to sub-optimal norepinephrine transport
 CC in a subject. The method comprises obtaining a biological sample from
 CC the subject and detecting a polymorphism of a norepinephrine transporter
 CC gene in the sample from the subject, the presence of the polymorphism
 CC indicating the susceptibility of the subject to sub-optimal
 CC norepinephrine transport. The method is useful for screening for
 CC susceptibility of a subject to orthostatic intolerance. Norepinephrine
 CC transporter genes are useful for gene therapy for modulating
 CC norepinephrine transport in a target cell and treating susceptibility
 CC to impaired norepinephrine transporter function, orthostatic intolerance
 CC or other relevant diseases in humans and animals such as mental illness,
 CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
 CC amphetamine abuse.
 XX
 SQ Sequence 15 BP; 0 A; 7 C; 2 G; 6 T; 0 other;
 Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTCTCGCCCTGTT 15
 Db 1 CCTTCTCGCCCTGTT 15
 RESULT 2
 AAH88259
 ID AAH88259 standard; DNA; 920 BP.
 XX
 AC AAH88259;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE CNS disorder-related biallelic marker #10 from NET gene.
 XX
 KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;
 KW central nervous system disorder; CNS; NET; norepinephrine transporter.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 95
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200151659-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 11-JAN-2001; 2001WO-IB00116.
 XX
 PR 13-JAN-2000; 2000US-0175854.
 XX
 PA (GEST) GENSET.
 XX
 PI Chu T, Blumenfeld M, Cohen D;
 XX WPI; 2001-483085/52.
 XX
 DR Isolated polynucleotides, useful for genotyping nucleic acids for
 PT biallelic markers for the diagnosis of depression, comprises central
 PT nervous system disorder related biallelic marker -
 XX
 PS Claim 1; Page 248; 519pp; English.
 XX
 CC The present invention relates to biallelic markers derived from human

CC genes involved in central nervous system (CNS) disorders. The present
 CC sequence is one such biallelic marker derived from human norepinephrine
 CC transporter (NET) gene. This marker has a single nucleotide polymorphism
 CC (SNP) and is useful in determining the genetic predisposition of
 CC individuals to CNS disorders, by identifying the nucleotides at a set of
 CC genetic markers in a biological sample, where the markers comprise at
 CC least one CNS disorder related marker.
 XX
 SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
 Query Match 100.0%; Score 15; DB 23; Length 920;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTCTCGCCCTGTT 15
 Db 170 CCTTCTCGCCCTGTT 184
 RESULT 3
 AAH88264
 ID AAH88264 standard; DNA; 920 BP.
 XX
 AC AAH88264;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE CNS disorder-related biallelic marker #15 from NET gene.
 XX
 KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;
 KW central nervous system disorder; CNS; NET; norepinephrine transporter.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 206
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200151659-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 11-JAN-2001; 2001WO-IB00116.
 XX
 PR 13-JAN-2000; 2000US-0175854.
 XX
 PA (GEST) GENSET.
 XX
 PI Chu T, Blumenfeld M, Cohen D;
 XX WPI; 2001-483085/52.
 XX
 DR Isolated polynucleotides, useful for genotyping nucleic acids for
 PT biallelic markers for the diagnosis of depression, comprises central
 PT nervous system disorder related biallelic marker -
 XX
 PS Claim 1; Pages 251-252; 519pp; English.
 XX
 CC The present invention relates to biallelic markers derived from human
 CC genes involved in central nervous system (CNS) disorders. The present
 CC sequence is one such biallelic marker derived from human norepinephrine
 CC transporter (NET) gene. This marker has a single nucleotide polymorphism
 CC (SNP) and is useful in determining the genetic predisposition of
 CC individuals to CNS disorders, by identifying the nucleotides at a set of
 CC genetic markers in a biological sample, where the markers comprise at
 CC least one CNS disorder related marker.
 XX
 SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
 Query Match 100.0%; Score 15; DB 23; Length 920;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15
|||||
Db 170 CCTTCTGCGCCTGTT 184

RESULT 4
AAH28088
ID AAH28088 standard; DNA; 980 BP.
XX
AC AAH28088;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a exon 9 of norepinephrine transporter gene.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 129..257
FT /*tag= a
FT intron 257..700
FT /*tag= b
FT exon 701..802
FT /*tag= c
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45. ~
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
PS Disclosure; Page 125; 133pp; English.
XX
CC The present sequence represents exon 9 of the human norepinephrine
CC transporter gene. The specification a method for screening for
CC susceptibility to sub-optimal norepinephrine (NE) transport in a
CC subject. The method comprises obtaining a biological sample from the
CC subject and detecting a polymorphism of a norepinephrine transporter
CC gene in the sample from the subject, the presence of the polymorphism
CC indicating the susceptibility of the subject to sub-optimal
CC norepinephrine transport. The method is useful for screening for
CC susceptibility of a subject to orthostatic intolerance. Norepinephrine
CC transporter genes are useful for gene therapy for modulating
CC norepinephrine transport in a target cell and treating susceptibility
CC to impaired norepinephrine transporter function, orthostatic intolerance
CC or other relevant diseases in humans and animals such as mental illness,
CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
CC amphetamine abuse.
XX
SQ Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 3 other;

Query Match 100.0%; Score 15; DB 22; Length 980;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15
|||||
Db 230 CCTTCTGCGCCTGTT 244

RESULT 5
AAS80746/c
ID AAS80746 standard; cDNA; 1044 BP.
XX
AC AAS80746;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #16550.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
P-PSDB; ABG16559.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 16550; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 1044;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15
|||||

XX DT 15-MAR-1993 (first entry)
 XX DE Human norepinephrine transporter protein cDNA clone.
 XX KW NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;
 KW ss.
 XX KW Homo sapiens.
 XX OS
 XX FH Key Location/Qualifiers
 XX FT CDS 61..1914
 XX FT /*tag= a
 XX PN WO9217568-A.
 XX PD 15-OCT-1992.
 XX PF 20-FEB-1992; 92WO-US01376.
 XX PR 28-MAR-1991; 91US-0676980.
 XX PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX PI Amara SG, Blakely RD, Pacholczyk T;
 XX DR WPI: 1992-366242/44.
 XX DR P-PSDB; AAR26416.
 XX CC Complementary DNA clone encoding human norepinephrine transporter
 PT protein - isolated from human neuroblastoma cells and useful for
 PT determining action of e.g. antidepressant drugs
 XX PS Claim 3: Fig 1: 37pp; English.
 XX CC Pools of clones from a human SK-N-SH cell (a human neuroblastoma
 CC cell line) cDNA library were transfected into COS-1 cells. The
 CC transfected clones were in the form of expression vectors (pXM)
 CC having an SV-40 replication origin to enable amplification.
 CC Transfectants of these cells expressing the norepinephrine
 CC transporter were identified by employing an assay exploiting the
 CC fact that the norepinephrine analogue m-iodobenzylguanidine (m-IBG)
 CC is accumulated intracellularly by SK-N-SH cells expressing the
 CC intact NT. The accumulated radiolabelled m-IBG allows direct
 CC autoradiographic visualisation of transporter expressing
 CC transfectants. DNA was rescued from positive colonies and the
 CC resulting plasmid pools rescreened and subdivided until a single
 CC clone was obtd. Transfected cells become capable of norepinephrine
 CC uptake, which may be inhibited by various drugs, e.g. cocaine, to
 CC a degree similar to the effect of such drugs on noradrenergic
 CC neurons. The cloned cDNA makes possible well-controlled studies
 CC of neurotransmitter transporter function in non-neuronal cells
 CC without the abfuscating influence of other transporters in the
 CC same cell. Such studies include the relative effects of various
 CC (psychotropic) drugs such as antidepressants.
 XX SQ Sequence 1983 BP; 384 A; 602 C; 529 G; 468 T; 0 other;
 Query Match 100.0%; Score 15; DB 13; Length 1983;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTCGCGCCGTGT 15
 |||||||
 Db 1422 CCTTCGCGCCGTGT 1436
 RESULT 9
 ABK83862/c
 ID ABK83862 standard; cDNA; 5161 BP.
 XX AC
 XX ABK83862;

DT 14-AUG-2002 (first entry)
 XX Human cDNA differentially expressed in granulocytic cells #433.
 XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX OS Homo sapiens.
 XX PN WO200228999-A2.
 XX PD 11-APR-2002.
 XX PF 03-OCT-2001; 2001WO-US30821.
 XX PR 03-OCT-2000; 2000US-237189P.
 XX PA (GENE-) GENE LOGIC INC.
 XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX DR WPI: 2002-435328/46.
 XX CC Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity
 XX PS Claim 1: SEQ ID No 433; 114pp; English.
 XX CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 5161;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCCCTGTT 15

Db 2673 CCTTCTGCCCTGTT 2659

RESULT 10

AAH88704
ID AAH88704 standard; DNA; 160755 BP.

XX AC AAH88704;

XX DT 26-FEB-2002 (first entry)

XX DE Human DNA sequence SEQ ID 544.

XX KW Single nucleotide polymorphism; SNP; biallelic marker; human;
XX KW central nervous system disorder; CNS; ds.
XX OS Homo sapiens.
XX PN WO200151659-A2.
XX PD 19-JUL-2001.

XX PF 11-JAN-2001; 2001WO-IB00116.

XX PR 13-JAN-2000; 2000US-0175854.

XX PA (GEST) GENSET.

XX PI Chu T, Blumenfeld M, Cohen D;

XX DR WPI; 2001-483085/52.

XX PT Isolated polynucleotides, useful for genotyping nucleic acids for
PT biallelic markers for the diagnosis of depression, comprises central
PT nervous system disorder related biallelic marker -
XX PS Disclosure; Page 476-519; 519pp; English.
XX CC The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders (see
CC AH88161-AAH88702). The markers have a single nucleotide polymorphism
CC (SNP) and are useful in determining the genetic predisposition of
CC individuals to CNS disorders, by identifying the nucleotides at a set of
CC genetic markers in a biological sample, where the markers comprise at
CC least one CNS disorder related marker. The present sequence was used
CC to illustrate the invention.

SQ Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;

Query Match 100.0%; Score 15; DB 23; Length 160755;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCCCTGTT 15

Db 63345 CCTTCTGCCCTGTT 63359

RESULT 11

ABN18096
ID ABN18096 standard; cDNA; 336 BP.

XX AC ABN18096;

XX DT 24-JUN-2002 (first entry)

XX

DE

XX

KW

KW

KW

KW

KW

KW

KW

KW

OS

XX

PN

XX

XX

PD

XX

PF

XX

PR

PR

XX

PA

XX

PI

XX

DR

DR

XX

PT

PT

XX

PS

XX

CC

CC

CC

CC

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CC

CC

CC

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CC

CC

CC

CC

CC

CC

CC

CC

CC

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CC

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CC

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CC

CC

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CC

CC

Human ORFX polynucleotide sequence SEQ ID NO:4669.

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
degenerative disorder; osteoarthritis; neurodegenerative disorder;
cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
hypertension; hypothyroidism; cholesterol ester storage disease;
immune deficiency; immune disorder; infectious disease;
autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
myasthenia gravis; gene; ss.

Homo sapiens.

WO200192523-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US10836.

30-MAY-2000; 2000US-206132p.

29-AUG-2000; 2000US-228716p.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach MD;

WPI; 2002-106308/14.

P-PSDB; ABP02344.

Novel human polypeptides and polynucleotides useful for diagnosing,
preventing and treating cardiovascular disease, neurodegenerative,
hyperproliferative disorders and autoimmune disorders -

Disclosure; SEQ ID 4669; 1037pp; English.

The present invention describes substantially purified human proteins
(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
in the specification). ABN15762 to ABN27252 encode the human ORFX
proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
treating or preventing a pathology associated with an ORFX-associated
disorder in humans, and in the manufacture of a medicament for treating a
syndrome associated with ORFX-associated disorder. ORFX polynucleotide
sequences can be used in gene therapy. ORFX sequences can be used in the
treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
osteoarthritis, neurodegenerative disorders, disorders related to organ
transplantation, cardiovascular diseases, diabetes mellitus, systemic
lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
storage disease, various immune deficiencies and disorders, infectious
diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
disease and autoimmune inflammatory eye disease. ORFX proteins are also
useful for treating burns, incisions, ulcers, for treating osteoporosis,
bone degenerative disorders, or periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues and conditions resulting from
systemic cytokine damage.
N.B. The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;

Query Match 93.3%; Score 14; DB 24; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTGCCCTGTT 15

Db 82 CTTCTGCCCTGTT 95

RESULT 12
ABQ56203/c
ID ABQ56203 standard; cDNA; 655 BP.
XX
AC ABQ56203;
XX
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HVVAW26 cDNA, SEQ ID NO:2083.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR P-PSDB; ABP43126.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
XX Claim 1; SEQ ID NO 2083; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention.
XX Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 655 BP; 182 A; 168 C; 177 G; 116 T; 12 other;
Query Match 93.3%; Score 14; DB 24; Length 655;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTCTCGCCCTGTT 15
DB 556 CTTCTCGCCCTGTT 543
RESULT 13
AAH65499/c
ID AAH65499 standard; DNA; 708 BP.
AC AAH65499;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 534.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG90280.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
PS Claim 8; SEQ ID NO: 534; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 708 BP; 152 A; 212 C; 196 G; 148 T; 0 other;
Query Match 93.3%; Score 14; DB 22; Length 708;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CC	TCTCGCCCTGT	14
Db	250	CC	TCTCGCCCTGT	237

RESULT 14
ABL11823/c
ID ABL11823 standard; cDNA; 2036 BP.

RESULT 15
AAQ14533
ID AAQ14533 standard; DNA; 2397 BP.
XX
XX AAQ14533;
XX AC
DT 29-JAN-1992 (first entry)

Search completed: December 11, 2002, 13:38:15
Job time : 241.5 secs

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:29:32 ; Search time 47 seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 ccttcgcgcctgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	93.3	2397	1 US-07-686-322A-5	Sequence 5, Appli
2	14	93.3	2397	1 US-08-002-999-5	Sequence 5, Appli
3	14	93.3	2397	2 US-08-132-990A-5	Sequence 5, Appli
4	14	93.3	2397	5 PCR-US92-09382-5	Sequence 5, Appli
5	13.4	89.3	573	2 US-08-290-665A-137	Sequence 137, App
6	13.4	89.3	573	5 PCR-US95-10398-137	Sequence 137, App
7	13.4	89.3	630	3 US-08-612-973-29	Sequence 29, Appl
8	13.4	89.3	630	4 US-08-927-597-29	Sequence 29, Appl
9	13.4	89.3	738	4 US-09-605-785-747	Sequence 747, App
10	13.4	89.3	1458	4 US-09-105-537-9	Sequence 9, Appli
11	13.4	89.3	1475	4 US-08-961-527-320	Sequence 320, App
12	13.4	89.3	1565	3 US-09-320-878-24	Sequence 24, Appl
13	13.4	89.3	1678	3 US-08-650-766-2	Sequence 2, Appli
14	13.4	89.3	1954	3 US-08-922-635-2	Sequence 2, Appli
15	13.4	89.3	2169	1 US-08-379-496-1	Sequence 1, Appli
16	13.4	89.3	3318	3 US-08-650-766-3	Sequence 3, Appli
17	13.4	89.3	3318	3 US-08-922-635-3	Sequence 3, Appli
18	13.4	89.3	3385	3 US-08-650-766-1	Sequence 1, Appli
19	13.4	89.3	3385	3 US-08-922-635-1	Sequence 1, Appli
20	13.4	89.3	3405	4 US-09-281-481A-18	Sequence 18, Appl
21	13.4	89.3	9785	1 US-08-319-387-1	Sequence 1, Appli
22	13.4	89.3	10322	4 US-09-330-330-3	Sequence 3, Appli
23	13.4	89.3	13613	4 US-09-105-537-3	Sequence 3, Appli
24	13.4	89.3	13202	3 US-08-922-635-21	Sequence 21, Appl
25	13.4	89.3	4403765	4 US-09-103-840A-2	Sequence 2, Appli
26	13.4	89.3	4411529	4 US-09-103-840A-1	Sequence 1, Appli
27	13	86.7	485	4 US-09-400-208B-22	Sequence 22, Appl

c 28	13	86.7	491	4	US-09-400-208B-23	Sequence 23, Appl
c 29	13	86.7	497	4	US-09-400-208B-24	Sequence 24, Appl
c 30	13	86.7	2001	4	US-09-400-208B-4	Sequence 4, Appli
c 31	13	86.7	2023	4	US-09-491-522-6	Sequence 6, Appli
c 32	13	86.7	2450	4	US-09-491-522-2	Sequence 2, Appli
c 33	13	86.7	3240	4	US-09-171-337A-4	Sequence 4, Appli
c 34	13	86.7	3748	1	US-08-261-206A-76	Sequence 76, Appl
c 35	13	86.7	4657	3	US-09-254-325-1	Sequence 1, Appli
c 36	13	86.7	6692	4	US-09-491-522-1	Sequence 1, Appli
c 37	13	86.7	35100	1	US-08-306-691B-19	Sequence 19, Appl
c 38	13	86.7	35100	5	PCR-US93-06251-19	Sequence 19, Appl
c 39	12.4	82.7	23	4	US-09-177-650-37	Sequence 37, Appl
c 40	12.4	82.7	318	4	US-09-177-650-108	Sequence 108, App
c 41	12.4	82.7	358	1	US-07-925-920-1	Sequence 1, Appli
c 42	12.4	82.7	361	1	US-08-094-079-12	Sequence 12, Appl
c 43	12.4	82.7	361	1	US-08-094-079-18	Sequence 18, Appl
c 44	12.4	82.7	361	1	US-08-094-079-20	Sequence 20, Appl
c 45	12.4	82.7	361	1	US-08-094-079-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-07-686-322A-5
; Sequence 5, Application US/07686322A
; Patent No. 5312733
; GENERAL INFORMATION:
; APPLICANT: Macleod Dr., Carol L.
; TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department, Fulbright & Jaworski
; STREET: 1301 McKinney, Suit 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/686,322A
; FILING DATE: 19910411
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/509684
; FILING DATE: 13-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Launer, Charlene A.
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: D-52332-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 651-3634
; TELEFAX: (713) 651-5246
; TELEX: Western Union 762829
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: AKR1 Jackson
; INDIVIDUAL ISOLATE: SL12 cell line
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4
; IMMEDIATE SOURCE:

CLONE: 20.5
US-07-686-322A-5

Query Match 93.3%; Score 14; DB 1; Length 2397;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 2
US-08-002-999-5
; Sequence 5, Application us/08002999
; Patent No. 5440017
; GENERAL INFORMATION:
; APPLICANT: MacLeod Dr., Carol L.
; TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department, Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,999
; FILING DATE: 19930111
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/686,322
; FILING DATE: 11-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D-5232-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 651-5587
; TELEFAX: (713) 651-5246
; TELEX: Western Union 762829
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: AKR1 Jackson
; INDIVIDUAL ISOLATE: SL12 cell line
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4
; IMMEDIATE SOURCE:
; CLONE: 20.5
US-08-002-999-5

Query Match 93.3%; Score 14; DB 1; Length 2397;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 3
US-08-132-990A-5
; Sequence 5, Application US/08132990A
; Patent No. 5834589
; GENERAL INFORMATION:
; APPLICANT: MERUELO, DANIEL
; APPLICANT: YOSHIMOTO, TAKAYUKI
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/132,990A
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/084,729
; FILING DATE: 29-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05569
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/899,075
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/806,178
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: 07/627,950
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8105-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 410..1768
US-08-132-990A-5

Query Match 93.3%; Score 14; DB 2; Length 2397;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 4
PCT-US92-09382-5
; Sequence 5, Application PC/TUS9209382
; GENERAL INFORMATION:

APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09382
FILING DATE: 19921213
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: MERUELO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 410..1768
PCT-US92-09382-5

Query Match 93.3%; Score 14; DB 5; Length 2397;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTGTT 15
|||||

Db 1379 CTCTCGCCCTGTT 1392

RESULT 5
US-08-290-665A-137
Sequence 137, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R. H. AND
APPLICANT: PURCELL, R. H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S2
US-08-290-665A-137

Query Match 89.3%; Score 13.4; DB 2; Length 573;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCCTGTT 15

|||||

Db 531 CCTTCTGCGCCCTGTT 545

RESULT 6
PCT-US95-10398-137
Sequence 137, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R. H. AND
APPLICANT: PURCELL, R. H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849

TELEX: 421792
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ORGANISM: hominids
INDIVIDUAL ISOLATE: S2
PCT-US95-10398-137

Query Match 89.3%; Score 13.4; DB 5; Length 573;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

DB 531 CCTTCTCGCCCTGTT 545

RESULT 7

US-08-612-973-29
Sequence 29, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..627
NAME/KEY: mat_peptide
LOCATION: 1..624
US-08-612-973-29

Query Match 89.3%; Score 13.4; DB 3; Length 630;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
|||||

DB 177 CCTTCTCGCTCTGTT 191

RESULT 8

US-08-927-597-29
Sequence 29, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..627
NAME/KEY: mat_peptide
LOCATION: 1..624
US-08-927-597-29

Query Match 89.3%; Score 13.4; DB 4; Length 630;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

DB 177 CCTTCTCGCTCTGTT 191

RESULT 9

US-09-605-785-747/c
; Sequence 747, Application US/09605785
; Patent No. 6321716

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT FILING DATE: 1998-06-26
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 747
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-605-785-747

Query Match 89.3%; Score 13.4; DB 4; Length 738;

Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 469 CCTTCTCTCCCTGTT 455

RESULT 10

US-09-105-537-9
; Sequence 9, Application US/09105537A
; Patent No. 6265202

GENERAL INFORMATION:

; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438U51
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-9

Query Match

Best Local Similarity 89.3%; Score 13.4; DB 4; Length 1458;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 246 CCTTCTCGCCCTGTT 260

RESULT 11

US-08-961-527-320/c
; Sequence 320, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 320:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1475 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-08-961-527-320

Query Match 89.3%; Score 13.4; DB 4; Length 1475;

Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 641 CCTTCTCGCCCTGTT 627

RESULT 12

US-09-320-878-24
; Sequence 24, Application US/09320878A
; Patent No. 6117659

GENERAL INFORMATION:

; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538

; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 24
; LENGTH: 1565
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-24

Query Match 89.3%; Score 13.4; DB 3; Length 1565;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||| ||||| |||||

Db 295 CCTCTCGCCCTGTT 309

RESULT 13

US-08-650-766-2/c

; Sequence 2, Application US/08650766D
; Patent No. 6015690
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
; TITLE OF INVENTION: METHOD FOR CLONING THE SAME
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6015690
; CURRENT APPLICATION NUMBER: US/08/650,766D
; CURRENT FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: US 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-650-766-2

Query Match 89.3%; Score 13.4; DB 3; Length 1678;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||| ||||| |||||

Db 679 CCTCTCGCCCTGTT 665

RESULT 14

US-08-922-635-2/c

; Sequence 2, Application US/08922635A
; Patent No. 6033871
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
; TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6033871
; CURRENT APPLICATION NUMBER: US/08/922,635A
; CURRENT FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 08/650,766
; EARLIER FILING DATE: 1996-05-20

; EARLIER APPLICATION NUMBER: 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1954
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-922-635-2

Query Match 89.3%; Score 13.4; DB 3; Length 1954;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||| ||||| |||||

Db 679 CCTCTCGCCCTGTT 665

RESULT 15

US-08-379-496-1/c
; Sequence 1, Application US/08379496
; Patent No. 5593833
; GENERAL INFORMATION:
; APPLICANT: MORRISON, Nigel A
; APPLICANT: EISMAN, John A
; APPLICANT: KELLY, Paul J
; TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic
; TITLE OF INVENTION: Variation
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 13th Street.N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,496
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 783-6040
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-379-496-1

Query Match 89.3%; Score 13.4; DB 1; Length 2169;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||||| |||||

Db 164 CCTTCTCTCCCTGTT 150

Search completed: December 11, 2002, 15:30:43
Job time : 52 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:35:52 ; Search time 52.5 Seconds
(without alignments)
111.409 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 ccttctgcctgttt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.4	89.3	114	10	US-09-864-761-26040
C 2	13.4	89.3	458	10	US-09-864-761-32413
C 3	13.4	89.3	543	10	US-09-864-761-15909
C 4	13.4	89.3	580	10	US-09-864-761-9604
C 5	13.4	89.3	592	10	US-09-864-761-12426
C 6	13.4	89.3	738	10	US-09-759-143-747
C 7	13.4	89.3	738	10	US-09-780-669-747
C 8	13.4	89.3	738	10	US-09-822-827-747
C 9	13.4	89.3	1458	9	US-09-860-846-9
C 10	13.4	89.3	1458	10	US-09-861-289-9
C 11	13.4	89.3	2109	10	US-09-815-242-6020
C 12	13.4	89.3	5828	9	US-09-430-029-1
C 13	13.4	89.3	5881	10	US-09-764-869-2353
C 14	13.4	89.3	9377	10	US-09-801-874-3
C 15	13.4	89.3	13613	9	US-09-860-846-3
C 16	13.4	89.3	13613	10	US-09-861-289-3
C 17	13.4	89.3	15016	10	US-09-880-107-3783
C 18	13.4	89.3	15857	10	US-09-764-864-1704
C 19	13.4	89.3	42450	10	US-09-815-048-3

ALIGNMENTS

RESULT 1

US-09-864-761-26040/C
; Sequence 26040, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

Sequence 9, Appli
Sequence 258, App
Sequence 937, App
Sequence 6989, Ap
Sequence 14438, A
Sequence 7193, Ap
Sequence 6987, Ap
Sequence 3974, Ap
Sequence 15063, A
Sequence 906, App
Sequence 5128, Ap
Sequence 881, App
Sequence 1626, Ap
Sequence 553, App
Sequence 1577, Ap
Sequence 3234, Ap
Sequence 14333, A
Sequence 968, App
Sequence 928, App
Sequence 17, Appl
Sequence 723, App
Sequence 528, App
Sequence 813, App
Sequence 10365, A
Sequence 1452, Ap
Sequence 28, Appl

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26040
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006427.13
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EST_HUMAN HIT: BF345368.1, EVALUE 5.00e-31
; OTHER INFORMATION: NT HIT: gill1430273, EVALUE 4.00e-31
US-09-864-761-26040

Query Match 89.3%; Score 13.4; DB 10; Length 114;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15
|||||

Db 91 CCTCTCGCGCTGTT 77

RESULT 2

US-09-864-761-32413
; Sequence 32413, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32413
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121787.22
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: NT HIT: gi6671607, EVALUE 2.00e-91
; OTHER INFORMATION: SWISSPROT HIT: P97303, EVALUE 1.00e-37
; OTHER INFORMATION: EST_HUMAN HIT: BE890758.1, EVALUE 4.30e-01
US-09-864-761-32413

Query Match 89.3%; Score 13.4; DB 10; Length 458;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15
|||||

Db 259 CCTCTCGCCCTGTT 273

RESULT 3

US-09-864-761-15909
; Sequence 15909, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15909
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121787.22
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
US-09-864-761-15909

Query Match 89.3%; Score 13.4; DB 10; Length 543;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCGCCCTGTT 15
||| ||||| |||||
Db 295 CCTCTCGCCCTGTT 309

RESULT 4

US-09-864-761-9604/c
; Sequence 9604, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9604
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006427.13
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
US-09-864-761-9604

Query Match 89.3%; Score 13.4; DB 10; Length 580;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCGCCCTGTT 15
||| ||||| |||||
Db 391 CCTCTCGCCCTGTT 377

RESULT 5

US-09-864-761-12426
; Sequence 12426, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12426
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL138956.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
US-09-864-761-12426

Query Match 89.3%; Score 13.4; DB 10; Length 592;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||||| |||||||
Db 578 CCTTCTCGCCCTGTT 592

RESULT 6
US-09-759-143-747/c
; Sequence 747, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Jennifer L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09759,143
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 747
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-759-143-747
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 747
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||||| |||||||
Db 469 CCTTCTCTCCCTGTT 455

RESULT 7
US-09-780-669-747/c
; Sequence 747, Application US/097800669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 747
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
||||| |||||||
Db 469 CCTTCTCTCCCTGTT 455

RESULT 8
US-09-822-827-747/c
; Sequence 747, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 747
; LENGTH: 738

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-822-827-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
||||| |||||
Db 469 CCTTCTCGCCCTGTT 455

RESULT 9

US-09-860-846-9
; Sequence 9, Application US/09860846
; Patent No. US20020164742A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860,846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-860-846-9

Query Match 89.3%; Score 13.4; DB 9; Length 1458;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
||||| |||||
Db 246 CCTCTCGCCCTGTT 260

RESULT 10

US-09-861-289-9
; Sequence 9, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/861,289
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-9

Query Match 89.3%; Score 13.4; DB 10; Length 1458;

Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
||||| |||||
Db 246 CCTCTCGCCCTGTT 260

RESULT 11

US-09-815-242-6020/C
; Sequence 6020, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6020
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2109)
US-09-815-242-6020

Query Match 89.3%; Score 13.4; DB 10; Length 2109;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
||||| |||||
Db 1492 CCTTCTCGCCCTGTT 1478

RESULT 12

US-09-430-029-1/C
; Sequence 1, Application US/09430029
; Patent No. US20020168738A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Can
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CF013982U\$
; CURRENT APPLICATION NUMBER: US/09/430,029

; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: JP P1998-310801
; EARLIER FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5828
; TYPE: DNA
; ORGANISM: Burkholderia cepacia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (234)..(443)
; OTHER INFORMATION: comL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (463)..(1455)
; OTHER INFORMATION: comL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1495)..(1761)
; OTHER INFORMATION: comL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1803)..(3350)
; OTHER INFORMATION: comN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3428)..(3781)
; OTHER INFORMATION: comO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3810)..(4871)
; OTHER INFORMATION: comP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4876)..(5229)
; OTHER INFORMATION: comQ
US-09-430-029-1

Query Match 89.3%; Score 13.4; DB 9; Length 5828;
Best Local Similarity 93.3%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 2013 CCTTCTCGCCCTGTT 1999

RESULT 13
US-09-764-869-2353
; Sequence 2353, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2353
; LENGTH: 5881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2353

Query Match 89.3%; Score 13.4; DB 10; Length 5881;
Best Local Similarity 93.3%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 4343 CCTTCTCTCCCTGTT 4357
RESULT 14
US-09-801-874-3/c
; Sequence 3, Application US/09801874
; Patent No. US20020048801A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN AMINOTRANSFERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: AMINOTRANSFERASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00615
; CURRENT APPLICATION NUMBER: US/09/801,874
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9377
; TYPE: DNA
; ORGANISM: Human
US-09-801-874-3

Query Match 89.3%; Score 13.4; DB 10; Length 9377;
Best Local Similarity 93.3%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 3421 CCTTCTCACCTGTT 3407

RESULT 15
US-09-860-846-3/c
; Sequence 3, Application US/09860846
; Patent No. US2002016472A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860,846
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-860-846-3

Query Match 89.3%; Score 13.4; DB 9; Length 13613;
Best Local Similarity 93.3%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 11394 CCTTCTCGCCCTGTT 11380

Search completed: December 11, 2002, 17:01:24
Job time : 55.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:27:12 ; Search time 1661 Seconds
(without alignments)
146.257 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 ccttcgcgcctgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	15	100.0	309	14	T48892
c 2	15	100.0	313	17	BH019102
c 3	15	100.0	505	13	BM273267
c 4	15	100.0	513	17	BH019101
c 5	15	100.0	543	10	AV434035
c 6	15	100.0	551	13	BM142008

c 7	15	100.0	617	12	BF971415
c 8	15	100.0	626	9	AA102111
c 9	15	100.0	628	9	AA099915
c 10	15	100.0	653	13	BI997613
c 11	15	100.0	659	10	BE313934
c 12	15	100.0	676	12	BE776197
c 13	15	100.0	713	12	BF315344
c 14	15	100.0	830	12	EG444893
c 15	15	100.0	839	14	BQ609181
c 16	15	100.0	859	17	AG100084
c 17	15	100.0	939	12	BF180250
c 18	15	100.0	972	12	EG169177
c 19	15	100.0	1005	17	AG085931
c 20	15	100.0	1146	12	EG323915
c 21	14	93.3	226	10	BB068653
c 22	14	93.3	236	10	BB037017
c 23	14	93.3	257	10	BB054187
c 24	14	93.3	274	10	BB460985
c 25	14	93.3	279	10	BB464879
c 26	14	93.3	280	10	BB038101
c 27	14	93.3	282	9	AA140425
c 28	14	93.3	284	10	BB402819
c 29	14	93.3	288	10	BB163513
c 30	14	93.3	292	10	BB408502
c 31	14	93.3	297	10	AA436133
c 32	14	93.3	302	12	BF895478
c 33	14	93.3	308	17	CNS06WIC
c 34	14	93.3	313	10	BB045638
c 35	14	93.3	317	10	BB403227
c 36	14	93.3	318	14	BQ693297
c 37	14	93.3	319	10	BB464805
c 38	14	93.3	343	9	AA493073
c 39	14	93.3	360	14	BQ739202
c 40	14	93.3	362	14	W41213
c 41	14	93.3	370	10	BB872281
c 42	14	93.3	372	9	AI450145
c 43	14	93.3	400	14	BQ103252
c 44	14	93.3	403	12	BF743003
c 45	14	93.3	421	9	AI546215

ALIGNMENTS

RESULT 1
T48892/c
LOCUS
DEFINITION
yB07a09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70456 5' similar to similar to SP:S28778 S28778 COLLAGEN ALPHA 1(XV) CHAIN - HUMAN, mRNA sequence.
T48892
GI:650752
ACCESSION
VERSION
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiuidae; Homo.
REFERENCE
AUTHORS
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favell,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
TITLE
JOURNAL
MEDLINE
COMMENT
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 239
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: M13RP1

High quality sequence stop: 239.

Location/Qualifiers

1. .309
 /organism="Homo sapiens"
 /db_xref="GDB:491353"
 /db_xref="taxon:9606"
 /clone="IMAGE:70456"
 /clone_lib="Stratagene placenta (#937225)"
 /sex="male"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: placenta; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
 XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3',
 adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'."

BASE COUNT 82 a 70 c 101 g 51 t 5 others

Query Match 100.0%; Score 15; DB 14; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

|||||

Db 107 CCTTCTCGCCCTGTT 93

RESULT 2

LOCUS

BM273267 313 bp DNA linear GSS 25-MAY-2001
 L2358k.d.Hygr3.1 Leishmania major Friedlin Cosmid Genomic Library
 Leishmania major genomic clone L2358k, DNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Leishmania major.
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Leishmania.

1 (bases 1 to 313)

Myler,P.J., Vogt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J.,
 Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal
 ,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.
 Leishmania major Friedlin Cosmid End Sequences
 Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Myler PJ
 Seattle Biomedical Research Institute
 4 Nickerson Street, Seattle, WA 98109-1651, USA
 Tel: 206 284-8846
 Fax: 206 284-0313
 Email: mylerpj@brii.org
 Seq primer: Hygr3
 Class: cosmid ends.

FEATURES

source

1. .313
 /organism="Leishmania major"
 /strain="Friedlin"
 /db_xref="taxon:5664"
 /clone="L2358k"
 /clone_lib="Leishmania major Friedlin Cosmid Genomic
 Library"
 /lab_host="E. coli ED8767"
 /note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from
 Leishmania major Friedlin was partially digested with
 Sau3AI, size selected, and ligated with BamHI-digested
 cLHYG cosmid vector DNA. 9216 clones were picked and
 arrayed. Library construction is described in Ivens et
 al., Genomics Research, 8:135-145 (1998). The cLHYG

vector (Acc. NO. CVU59231) is described in Ryan et al,
 Gene, 131:145-150 (1993)"
 90 a 86 c 68 g 67 t 2 others

BASE COUNT

ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 313;

Best Local Similarity 100.0%; Pred. No. 6.2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

|||||

Db 57 CCTTCTCGCCCTGTT 71

RESULT 3

BM273267/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OTHER_FEATURES

CONTACT

DEPT

MA

TEL

FAX

EMAIL

LIBRARY

Obtaining a clone please contact:

consortium, for clone orders contact:

Seq primer:

High quality sequence stop:

Location/Qualifiers

1. .505

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5677896"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of

20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 133 a 138 c 148 g 86 t

Query Match 100.0%; Score 15; DB 13; Length 505;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||

Db 50 CCTTCTCGCCCTGTT 36

RESULT 4

BH019101

LOCUS

DEFINITION L2357k.d.HyGT3.1 Leishmania major Friedlin Cosmid Genomic Library

Leishmania major genomic clone L2357k, DNA sequence.

ACCESSION

BH019101

VERSION

BH019101.1

KEYWORDS

GSS.

SOURCE

Leishmania major.

ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Leishmania.

REFERENCE

AUTHORS

1 (bases 1 to 513)

Myler,P.J., Voigt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J.,

Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal

,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.

Leishmania major Friedlin Cosmid End Sequences

Unpublished (2000)

Contact: Myler PJ

Seattle Biomedical Research Institute

4 Nickerson Street, Seattle, WA 98109-1651, USA

Tel: 206 284-8846

Fax: 206 284-0313

Email: mylerpj@sbri.org

Seq primer: Hygt3

Class: cosmid ends.

FEATURES

Location/Qualifiers.

1..513

/organism="Leishmania major"

/strain="Friedlin"

/db_xref="taxon:5664"

/clone_lib="L2357k"

/clone_lib="Leishmania major Friedlin Cosmid Genomic

Library"

/lab_host="E. coli ED8767"

/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from

Leishmania major Friedlin was partially digested with

Sau3AI, size selected, and ligated with BamHI-digested

cLHYG cosmid vector DNA. 9216 clones were picked and

arrayed. Library construction is described in Ivens et

al., Genomics research, 8:135-145 (1998). The cLHYG

vector (Acc.No. CV059231) is described in Ryan et al.,

Gene, 131:145-150 (1993)."

BASE COUNT 141 a 154 c 100 g 118 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 15; DB 17; Length 513;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 52 CCTTCTCGCCCTGTT 66

RESULT 5

AV434035

LOCUS

DEFINITION

AV434035

ACCESSION

AV434035

VERSION

AV434035.1

KEYWORDS

EST.

SOURCE

Porphyra yezoensis.

ORGANISM

Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;

Porphyra.

REFERENCE

AUTHORS

1 (bases 1 to 543)

Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and

Tabata,S.

Generation of 10,154 expressed sequence tags from a leafy

gametophyte of a marine red alga, Porphyra yezoensis

DNA Res. 7, 223-227 (2000)

JOURNAL

MEDLINE

20363100

COMMENT

Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

FEATURES

Location/Qualifiers

1..543

/organism="Porphyra yezoensis"

/strain="TU-1"

/db_xref="taxon:2788"

/clone_lib="PM037d06_r"

/clone_lib="porphyra yezoensis TU-1"

/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT 55 a 163 c 190 g 135 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 15; DB 10; Length 543;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 423 CCTTCTCGCCCTGTT 437

RESULT 6

BM142008/c

LOCUS

DEFINITION

If25d08.y1 Melton Normalized Human Islet 4 M4-HIS 1 Homo sapiens

cDNA clone IMAGE:5677479 5' similar to SW:CALE_HUMAN P39059

COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1] ; mRNA sequence.

ACCESSION

BM142008

VERSION

BM142008.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 551)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas

,M., Gibbons M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.

, Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other_ESTs: If25d08.x1

Contact: Douglas Melton

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brownjefas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -48RP from Gibco
High quality sequence stop: 414.
Location/Qualifiers

FEATURES

source

```
1. .551
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5677479"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
```

```
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
```

BASE COUNT 145 a 148 c 159 g 99 t

ORIGIN

```
Query Match 100.0%; Score 15; DB 13; Length 551;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CCTTCTCGCCCTGTT 15

Db 50 CCTTCTCGCCCTGTT 36

RESULT 7

BF971415/c

LOCUS 617 bp mRNA linear EST 22-JAN-2001
DEFINITION 602272934F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361024 5',
mRNA sequence.

ACCESSION BF971415

VERSION BF971415.1 GI:12338630

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 617)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10003 Row: c column: 09

High quality sequence stop: 614.

Location/Qualifiers

1. .617

/organism="Homo sapiens"

FEATURES

source

```
/db_xref="taxon:9606"
/clone_lib="IMAGE:4361024"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
```

BASE COUNT 157 a 158 c 195 g 107 t

ORIGIN

```
Query Match 100.0%; Score 15; DB 12; Length 617;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CCTTCTCGCCCTGTT 15

Db 375 CCTTCTCGCCCTGTT 361

RESULT 8

AA102111

LOCUS AA102111

DEFINITION 626 bp mRNA linear EST 11-MAY-1997

IMAGE:489857 3' similar to SW:CAIE_HUMAN P39059 COLLAGEN ALPHA 1(XV

) CHAIN PRECURSOR. ; mRNA sequence.

ACCESSION AA102111

VERSION AA102111.1 GI:1646031

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 626)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBucq,T., Favello,A., Gish,W., Hawkins

,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore

,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,

Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

CONTACT: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert length: 867 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 453.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/db_xref="GDB:380444"

/db_xref="taxon:9606"

/clone="IMAGE:489857"

/clone_lib="Soares_pregnant_uterus_NbHPU"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not 1;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'

AACTGGAAGAAATTCGCCGCCCTTTTTTTTTTTTTTTT 3']

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

BASE COUNT 116 a 179 c 161 g 166 t 4 others
 ORIGIN went through one round of normalization. Library constructed by M. Fatima Bonaldo."

Query Match 100.0%; Score 15; DB 9; Length 626;
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15
 |||||

Db 527 CCTCTCGCCCTGTT 541

RESULT 9
 AA099915/c
 LOCUS 628 bp mRNA linear EST 11-MAY-1997
 DEFINITION zk87h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
 IMAGE:489857 5' similar to SW:CALE.HUMAN P39059 COLLAGEN ALPHA 1(XV
) CHAIN PRECURSOR. ; mRNA sequence.

ACCESSION AA099915
 VERSION AA099915.1 GI:1646057
 KEYWORDS EST.

SOURCE human.

ORGANISM

REFERENCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DuBuque,T., Favell,A., Gish,W., Hawkins
 ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Marldis,E., Moore
 ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
 Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.E.,
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE 97044478

JOURNAL

MEDLINE

COMMENT

Contact: Wilton RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 867 Std Error: 0.00
 Seq primer: -28ML3 rev2 from Amersham
 High quality sequence stop: 492.

FEATURES

source

1. .628
 /organism="Homo sapiens"
 /db_xref="GDB:380444"
 /db_xref="taxon:9606"
 /clone="IMAGE:489857"
 /clone_lib="Soares_pregnant_uterus_NbHPU"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5'
 AACTGGAAGAAATCGCGCGCTTTTTTTTTTTTTTTT 3'].
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."

BASE COUNT 154 a 158 c 189 g 122 t 5 others
 ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 628;
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15
 |||||

Db 252 CCTCTCGCCCTGTT 238

RESULT 10

BI997613/c

LOCUS 653 bp mRNA linear EST 25-OCT-2001

DEFINITION 1031050H04.y2 C. reinhardtii CC-1690, Stress II (normalized),

Lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION BI997613

VERSION BI997613

KEYWORDS EST.

SOURCE Chlamydomonas reinhardtii.

ORGANISM Chlamydomonas reinhardtii.

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 653)

AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre

,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.

Analyses of the Chlamydomonas reinhardtii Genome: A Model,

Unicellular System for Analyzing Gene Function and Regulation in

Vascular Plants. Project: 1031

JOURNAL Unpublished (2001)

COMMENT Contact: Charles Hauser

DCMB Box 91000

Duke University

Durham, NC 27708-1000

Tel: 919 613 8159

Fax: 919 613 8177

Email: chauser@duke.edu.

FEATURES

source

1. .653
 /organism="Chlamydomonas reinhardtii"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda zap II"
 /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
 XhoI; Stress condition II library, constructed by John
 Davies and Jeffrey McDermott, combines cDNAs from CC-1690
 cells grown to mid-log phase in TAP (NH4+ - containing)
 and shifted to TAP - NO3- (24hrs); H2 production
 conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
 Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
 sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
 PolyA mRNA was purified from each sample, pooled and cDNA
 synthesized. The cDNA was directionally cloned into lambda
 Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
 sites. pBluescript II SK- plasmids were excised from the
 lambda Zap clones by superinfection with EXAssist
 (Stratagene) phage. The library was normalized using
 method 4 described in Bonaldo et al., (1996) Genome
 Research 6: 791-806."

BASE COUNT 141 a 174 c 252 g 86 t
 ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 653;
 Best Local Similarity 100.0%; Pred. No. 7.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15
 |||||

Db 644 CCTCTCGCCCTGTT 630

RESULT 11

BE313934

LOCUS 659 bp mRNA linear EST 26-OCT-2000

DEFINITION 601147310F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162555 5',

mRNA sequence.

ACCESSION BE313934

```

VERSION BE313934.1 GI:9134434
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 659)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM122 row: c column: 04
High quality sequence stop: 618.
FEATURES
source
1. .659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3162555"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 125 a 203 c 166 g 165 t
ORIGIN
Query Match 100.0%; Score 15; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 42 CCTTCTCGCCCTGTT 56
RESULT 12
BE776197/c
LOCUS BE776197 676 bp mRNA linear EST 20-SEP-2000
DEFINITION MV-12-B-02 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION BE776197
VERSION BE776197.1 GI:10229852
KEYWORDS EST.
SOURCE potato late blight agent.
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 676)
Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
20056376
Contact: Govers F
Laboratory of Phytopathology
Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
Location/Qualifiers
FEATURES
source
1. .676
/organism="Phytophthora infestans"
/strain="DDR7602, A1 mating type"
/db_xref="taxon:4787"
/clone_lib="PinfestansMY"
/dev_stage="4-week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
BASE COUNT 144 a 180 c 198 g 151 t
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 110 CCTTCTCGCCCTGTT 96
RESULT 13
BF315344/c
LOCUS BF315344 713 bp mRNA linear EST 21-NOV-2000
DEFINITION 601902627F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135278 5',
mRNA sequence.
ACCESSION BF315344
VERSION BF315344.1 GI:11263579
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1039 row: e column: 07
High quality sequence stop: 644.
FEATURES
source
1. .713
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4135278"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 189 a 169 c 203 g 152 t
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
 |||
 Db 274 CCTTCTCGCCCTGTT 260

RESULT 14
 BG444893/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BG444893 830 bp mRNA linear EST 15-MAR-2001
 GA_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_Ea0025P19f, mRNA sequence.
 BG444893
 EST.
 BG444893.1 GI:13354545
 Gossypium arboreum.
 Gossypium arboreum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 1 (bases 1 to 830)
 WING, R.A., FRISCH, D., YU, Y., MAIN, D., RAMBO, T., SIMMONS, J., HENRY
 D., WOOD, T.C., LESLIE, A. and WILKINS, T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 Unpublished (2000)
 CONTACT: WING RA
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 TEL: 864 656 7288
 FAX: 864 656 4293
 EMAIL: rwing@clemson.edu

Seq primer: TAATACGACTACTATAGG
 High quality sequence stop: 182.
 Location/Qualifiers
 1..830
 /organism="Gossypium arboreum"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone="GA_Ea0025P19f"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /tissue_type="Fibers isolated from bolls harvested 7-10
 dpa"
 /lab_host="E. coli"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE.COUNT 218 a 111 c 385 g 116 t
 ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 830;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
 |||
 Db 752 CCTTCTCGCCCTGTT 738

RESULT 15
 BQ609181
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ609181 839 bp mRNA linear EST 25-JUN-2002
 BRY_5105 wheat EST endosperm library Triticum aestivum cDNA 5',
 mRNA sequence.
 BQ609181
 BQ609181.1 GI:21558520
 EST.
 bread wheat.
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticaceae; Triticum.
 1 (bases 1 to 839)

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Clarke,B., Lambrecht,M. and Rhee,S.
 Assessing the utility of Arabidopsis genomic information for
 interpreting wheat EST sequences
 Unpublished (2002)
 Contact: Lambrecht M
 The Arabidopsis Information Resource
 Carnegie Institution of Washington, Dept. of Plant Biology
 260 Panama Street, Stanford, CA 94305, USA
 Tel: 1 650 325 1521 x 251
 Fax: 1 650 325 3748
 Email: rhee@coma.stanford.edu.

FEATURES
 source
 1..839
 Location/Qualifiers
 /organism="Triticum aestivum"
 /cultivar="Wyuna"
 /db_xref="taxon:4565"
 /clone_lib="wheat EST endosperm library"
 /tissue_type="endosperm"
 /dev_stage="developing endosperm tissue 8, 10 and 12 DPA
 (days post anthesis)"
 /note="Vector: Bluescript II SK(-)"

BASE COUNT 36 a 409 c 68 g 326 t
 ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 839;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
 |||
 Db 399 CCTTCTCGCCCTGTT 413

Search completed: December 11, 2002, 15:28:53
 Job time : 1664 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:30:57 ; Search time 2560.5 Seconds
(without alignments)
147.290 Million cell updates/sec

Title: US-09-750-609-9

Perfect score: 15
Sequence: 1 cttctcgccctgtt 15.

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*

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13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*

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21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*

22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*

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25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*

26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*

27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*

28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*

29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*

30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*

31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*

32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*

33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*

34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*

35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*

36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*

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68: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*

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80: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

81: /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*

82: /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15	100.0	15	1	PCT-US000-35491-9	Sequence 9, Appli
2	15	100.0	15	29	US-09-750-609-9	Sequence 9, Appli
3	15	100.0	15	61	US-60-173-682-9	Sequence 470, App
4	15	100.0	257	18	US-09-440-302A-470	Sequence 470, App
5	15	100.0	257	18	US-09-440-302B-470	Sequence 470, App
6	15	100.0	258	18	US-09-440-302-470	Sequence 309, App
7	15	100.0	258	18	US-09-442-366A-309	Sequence 309, App
8	15	100.0	472	27	US-09-698-012-481	Sequence 481, App
9	15	100.0	510	20	US-09-534-856-18784	Sequence 18784, A
10	15	100.0	592	67	US-60-230-445-2923	Sequence 2923, Ap
11	15	100.0	601	35	US-09-948-933-4005	Sequence 4005, Ap
12	15	100.0	601	35	US-09-948-933-4006	Sequence 4006, Ap
13	15	100.0	601	35	US-09-948-933-4007	Sequence 4007, Ap
14	15	100.0	601	35	US-09-948-933-4008	Sequence 4008, Ap
15	15	100.0	817	24	US-09-634-306B-7016	Sequence 7016, Ap
16	15	100.0	817	24	US-09-634-306B-7017	Sequence 7017, Ap
17	15	100.0	817	38	US-10-027-632-7016	Sequence 7016, Ap
18	15	100.0	817	38	US-10-027-632-7017	Sequence 7017, Ap
19	15	100.0	920	61	US-60-175-854-99	Sequence 99, Appli
20	15	100.0	920	61	US-60-175-854-104	Sequence 104, App
21	15	100.0	980	1	PCT-US000-35491-15	Sequence 15, Appli

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22 15 100.0 980 1 PCT-US02-25060-1
23 15 100.0 980 29 US-09-750-609-15
24 15 100.0 980 42 US-10-213-948-1
25 15 100.0 980 61 US-60-173-682-15
26 15 100.0 1044 1 PCT-US01-08631-16550
27 15 100.0 1093 29 US-09-758-468-90
28 15 100.0 1093 42 US-10-211-625-90
29 15 100.0 1209 39 US-10-098-754-16300
30 15 100.0 1462 16 US-09-270-849B-35413
31 15 100.0 1573 65 US-60-213-177-929
32 15 100.0 1591 65 US-60-213-177-926
33 15 100.0 1597 65 US-60-213-177-928
34 15 100.0 1606 65 US-60-213-177-927
35 15 100.0 1831 65 US-60-213-177-1027
36 15 100.0 1854 1 PCT-US00-35491-1
37 15 100.0 1854 1 PCT-US00-35491-11
38 15 100.0 1854 29 US-09-750-609-1
39 15 100.0 1854 29 US-09-750-609-11
40 15 100.0 1854 61 US-60-173-682-1
41 15 100.0 1854 61 US-60-173-682-11
42 15 100.0 1983 3 US-07-676-980B-1
43 15 100.0 1983 18 US-09-440-302A-1067
44 15 100.0 1983 18 US-09-440-302B-1067
45 15 100.0 2049 61 US-60-172-373-18619

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ALIGNMENTS

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RESULT 1
PCT-US00-35491-9
; Sequence 9, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-35491-9

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
| | | | | | | | | | | | | | |
DB 1 CCTTCTCGCCCTGTT 15

RESULT 2
US-09-750-609-9
; Sequence 9, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 1242-27-2
; CURRENT APPLICATION NUMBER: US/09750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456

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; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-9

Query Match 100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
| | | | | | | | | | | | | | |
DB 1 CCTTCTCGCCCTGTT 15

RESULT 3
US-60-173-682-9
; Sequence 9, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 1242-27
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-9

Query Match 100.0%; Score 15; DB 61; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
| | | | | | | | | | | | | | |
DB 1 CCTTCTCGCCCTGTT 15

RESULT 4
US-09-440-302A-470
; Sequence 470, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Inkashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302A-470

Query Match 100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCTTCTCGCCCTGTT 15
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Db 45 CCTTCTCGCCCTGTT 59

RESULT 5

US-09-440-302B-470
; Sequence 470, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-470

Query Match 100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 45 CCTTCTCGCCCTGTT 59

RESULT 6

US-09-440-302-470
; Sequence 470, Application US/09440302
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302-470

Query Match 100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 45 CCTTCTCGCCCTGTT 59

RESULT 7

US-09-442-366A-309
; Sequence 309, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex

; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-309

Query Match 100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 45 CCTTCTCGCCCTGTT 59

RESULT 8

US-09-698-012-481/c
; Sequence 481, Application US/09698012
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2002-001
; CURRENT APPLICATION NUMBER: US/09/698,012
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,166
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 9719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-698-012-481

Query Match 100.0%; Score 15; DB 27; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 76 CCTTCTCGCCCTGTT 62

RESULT 9

US-09-534-856-18784/c
; Sequence 18784, Application US/09534856
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED,
; FILE REFERENCE: PD-1015 CIP
; CURRENT APPLICATION NUMBER: US/09/534,856
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 26334

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; SOFTWARE: PERL Program
; SEQ ID NO 18784
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01124269
; NAME/KEY: unsure
; LOCATION: 488
; OTHER INFORMATION: a, t, c, g, or other
US-09-534-856-18784

Query Match      100.0%; Score 15; DB 20; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 185 CCTTCTCGCCCTGTT 171

RESULT 10
US-60-230-445-2923
; Sequence 2923, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2923
; LENGTH: 592
; TYPE: DNA
; ORGANISM: HUMAN
US-60-230-445-2923

Query Match      100.0%; Score 15; DB 67; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 44 CCTTCTCGCCCTGTT 58

RESULT 11
US-09-948-933-4005/c
; Sequence 4005, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4005
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4005

Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 226 CCTTCTCGCCCTGTT 212

RESULT 12
US-09-948-933-4006/c
; Sequence 4006, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4006
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4006

Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 126 CCTTCTCGCCCTGTT 112

RESULT 13
US-09-948-933-4007/c
; Sequence 4007, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4007
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4007

Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 226 CCTTCTCGCCCTGTT 212

RESULT 14
US-09-948-933-4008/c
; Sequence 4008, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL000787

; CURRENT APPLICATION NUMBER: US/09/948,933

; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,399

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 6404

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4008

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-948-933-4008

Query Match 100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 337 CCTTCTCGCCCTGTT 323

RESULT 15

US-09-634-306B-7016/c

; Sequence 7016, Application US/09634306B

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/09/634,306B

; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7016

; LENGTH: 817

; TYPE: DNA

; ORGANISM: Human

US-09-634-306B-7016

Query Match 100.0%; Score 15; DB 24; Length 817;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 138 CCTTCTCGCCCTGTT 124

Search completed: December 11, 2002, 16:56:14
Job time : 2562.5 secs

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GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:38:27 ; Search time 88 Seconds
(without alignments)
122.513 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1 ccttctgcgcctgtt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 407964 seqs, 359371392 residues

Total number of hits satisfying chosen parameters: 815928

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	15	100.0	4338	5	US-09-724-676A-24273 Sequence 24273, A
5	15	100.0	4848	5	US-09-724-676-24268 Sequence 24268, A
6	15	100.0	4848	5	US-09-724-676A-24268 Sequence 24268, A
7	15	100.0	5222	6	US-10-133-937-67 Sequence 67, Appl
8	15	100.0	5589	5	US-09-724-676-24272 Sequence 24272, A
9	15	100.0	5589	5	US-09-724-676A-24272 Sequence 24272, A
10	15	100.0	5642	5	US-09-724-676-24271 Sequence 24271, A
11	15	100.0	5642	5	US-09-724-676A-24271 Sequence 24271, A
12	15	100.0	6099	5	US-09-724-676-24267 Sequence 24267, A
13	15	100.0	6099	5	US-09-724-676A-24267 Sequence 24267, A
14	15	100.0	6152	5	US-09-724-676-24266 Sequence 24266, A
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17	13.4	89.3	352	6	US-09-513-999C-13316 Sequence 13316, A
18	13.4	89.3	1458	6	US-10-271-889-52 Sequence 52, Appl
19	13.4	89.3	1565	6	US-10-201-365-22 Sequence 22, Appl
20	13.4	89.3	1565	6	US-10-160-539A-24 Sequence 24, Appl
21	13.4	89.3	2177	6	US-10-161-493-75 Sequence 75, Appl
22	13.4	89.3	2520	6	US-10-264-237-1036 Sequence 1036, Ap
23	13.4	89.3	5128	6	US-10-284-499-2 Sequence 2, Appl
24	13.4	89.3	5132	6	US-10-293-017-5 Sequence 5, Appl
25	13.4	89.3	7430	1	PCT-US02-32727-4 Sequence 4, Appl
26	13.4	89.3	7430	6	US-10-057-498-4 Sequence 4, Appl

C	27	13.4	89.3	9377	6	US-10-274-994-3	Sequence 3, Appli
	28	13.4	89.3	11547	1	PCT-US02-32727-86	Sequence 86, Appl
	29	13.4	89.3	11547	6	US-10-057-498-86	Sequence 86, Appl
C	30	13.4	89.3	13613	6	US-10-271-889-46	Sequence 46, Appl
C	31	13.4	89.3	45000	1	PCT-US02-36692-12	Sequence 12, Appl
C	32	13	86.7	1936	5	US-09-724-676-32136	Sequence 32136, A
C	33	13	86.7	1936	5	US-09-724-676A-32136	Sequence 32136, A
C	34	13	86.7	3590	5	US-09-724-676-24360	Sequence 24360, A
C	35	13	86.7	3590	5	US-09-724-676A-24360	Sequence 24360, A
C	36	13	86.7	276820	1	PCT-US02-32700-9	Sequence 9, Appli
C	37	13	86.7	276820	6	US-10-271-416-9	Sequence 9, Appli
C	38	12.4	82.7	237	5	US-09-513-999C-35434	Sequence 35434, A
C	39	12.4	82.7	248	5	US-09-620-607B-1245	Sequence 1245, Ap
C	40	12.4	82.7	261	5	US-09-513-999C-35759	Sequence 35759, A
C	41	12.4	82.7	319	5	US-09-513-999C-29349	Sequence 29349, A
C	42	12.4	82.7	353	5	US-09-513-999C-22349	Sequence 22349, A
	43	12.4	82.7	354	5	US-09-513-999C-3109	Sequence 3109, Ap
	44	12.4	82.7	476	6	US-10-203-138A-1480	Sequence 1480, Ap
C	45	12.4	82.7	480	5	US-09-724-676-45475	Sequence 45475, A

ALIGNMENTS

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; Sequence 47407, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47407
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-47407

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Db 1422 CCTTCTCGCCCTGTT 1436

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; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47407
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-47407

Query Match 100.0%; Score 15; DB 5; Length 2876;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 1422 CCTTCTCGCCCTGTT 1436

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; Sequence 24273, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24273
; LENGTH: 4338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24273

Query Match 100.0%; Score 15; DB 5; Length 4338;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 4
US-09-724-676A-24273/c
; Sequence 24273, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24273
; LENGTH: 4338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24273

Query Match 100.0%; Score 15; DB 5; Length 4338;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 5
US-09-724-676-24268/c
; Sequence 24268, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24268
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24268

Query Match 100.0%; Score 15; DB 5; Length 4848;

Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 6
US-09-724-676A-24268/c
; Sequence 24268, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24268
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24268

Query Match 100.0%; Score 15; DB 5; Length 4848;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 7
US-10-133-937-67/c
; Sequence 67, Application US/10133937
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 5222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-67

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2749 CCTTCTCGCCCTGTT 2735

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US-09-724-676-24272/c
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; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24272
; LENGTH: 5589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24272

Query Match 100.0%; Score 15; DB 5; Length 5589;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 9

US-09-724-676A-24272/c
; Sequence 24272, Application US/09724676A
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24272
; LENGTH: 5589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24272

Query Match 100.0%; Score 15; DB 5; Length 5589;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 10

US-09-724-676-24271/c
; Sequence 24271, Application US/09724676
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24271
; LENGTH: 5642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24271

Query Match 100.0%; Score 15; DB 5; Length 5642;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 11

US-09-724-676A-24271/c
; Sequence 24271, Application US/09724676A

; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24271
; LENGTH: 5642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24271

Query Match 100.0%; Score 15; DB 5; Length 5642;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 12

US-09-724-676-24267/c
; Sequence 24267, Application US/09724676
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24267
; LENGTH: 6099
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 13

US-09-724-676A-24267/c
; Sequence 24267, Application US/09724676A
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24267
; LENGTH: 6099
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

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; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24266
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24266

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Best Local Similarity 100.0%; Pred. No. 53;
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Db 3331 CCTTCTCGCCCTGTT 3317

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; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24266
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24266

Query Match      100.0%; Score 15; DB 5; Length 6152;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.3
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Title: US-09-750-609-9

Perfect score: 15

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- 58: /cgn2_6/ptodata/2/pna/US6014_COMB.seq.*
- 59: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
- 60: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
- 61: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
- 62: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
- 63: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
- 64: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
- 65: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
- 71: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
- 72: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
- 76: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
- 77: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
- 78: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 79: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 80: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*
- 81: /cgn2_6/ptodata/2/pna/US6037_COMB.seq.*
- 82: /cgn2_6/ptodata/2/pna/US6038_COMB.seq.*
- 83: /cgn2_6/ptodata/2/pna/US6039_COMB.seq.*
- 84: /cgn2_6/ptodata/2/pna/US6040_COMB.seq.*
- 85: /cgn2_6/ptodata/2/pna/US6041_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15	100.0	15	1	PCT-US00-35491-9
2	15	100.0	15	29	US-09-750-609-9
3	15	100.0	15	61	US-60-173-682-9
4	15	100.0	257	18	US-09-440-302A-470
5	15	100.0	257	18	US-09-440-302B-470
6	15	100.0	258	18	US-09-440-302-470
7	15	100.0	258	18	US-09-442-366A-309
8	15	100.0	472	27	US-09-698-012-481
9	15	100.0	510	20	US-09-534-856-18784
10	15	100.0	592	67	US-60-230-445-2923
11	15	100.0	601	35	US-09-948-933-4005
12	15	100.0	601	35	US-09-948-933-4006
13	15	100.0	601	35	US-09-948-933-4007
14	15	100.0	601	35	US-09-948-933-4008
15	15	100.0	817	24	US-09-634-306B-7016
16	15	100.0	817	24	US-09-634-306B-7017
17	15	100.0	817	38	US-10-027-632-7015
18	15	100.0	817	38	US-10-027-632-7017
19	15	100.0	920	61	US-60-175-854-99
20	15	100.0	920	61	US-60-175-854-104
21	15	100.0	980	1	PCT-US00-35491-15

22	15	100.0	980	1	PCT-US02-25060-1	Sequence 1, Appli	95	14	93.3	271	16	US-09-250-002B-711	Sequence 711, App
23	15	100.0	980	29	US-09-750-609-15	Sequence 15, Appl	96	14	93.3	271	20	US-09-534-846B-24502	Sequence 24502, A
24	15	100.0	980	42	US-10-213-948-1	Sequence 1, Appli	97	14	93.3	272	16	US-09-250-002B-1380	Sequence 1380, Ap
25	15	100.0	980	61	US-60-173-682-15	Sequence 15, Appl	98	14	93.3	272	20	US-09-534-846B-24519	Sequence 24519, A
c 26	15	100.0	1044	1	PCT-US01-08631-16550	Sequence 16550, A	99	14	93.3	272	19	US-09-500-900-1749	Sequence 1749, Ap
c 27	15	100.0	1093	29	US-09-758-468-90	Sequence 90, Appl	100	14	93.3	274	20	US-09-534-846B-24528	Sequence 24528, A
c 28	15	100.0	1093	42	US-10-211-625-90	Sequence 90, Appl	101	14	93.3	274	56	US-60-120-015-1749	Sequence 1749, Ap
c 29	15	100.0	1209	39	US-10-098-754-16300	Sequence 16300, A	102	14	93.3	275	20	US-09-534-846B-24498	Sequence 24498, A
c 30	15	100.0	1462	16	US-09-270-849B-35413	Sequence 35413, A	103	14	93.3	281	15	US-09-148-483-204	Sequence 204, App
c 31	15	100.0	1573	65	US-60-213-177-929	Sequence 929, App	104	14	93.3	281	15	US-09-534-846B-24514	Sequence 24514, A
c 32	15	100.0	1591	65	US-60-213-177-926	Sequence 926, App	105	14	93.3	281	49	US-60-058-920-204	Sequence 204, App
c 33	15	100.0	1597	65	US-60-213-177-928	Sequence 928, App	106	14	93.3	289	18	US-09-420-691-1257	Sequence 1257, Ap
c 34	15	100.0	1606	65	US-60-213-177-928	Sequence 927, App	107	14	93.3	289	20	US-09-534-846B-24518	Sequence 24518, A
c 35	15	100.0	1831	65	US-60-213-177-1027	Sequence 1027, Ap	108	14	93.3	291	20	US-09-534-846B-24503	Sequence 24503, A
c 36	15	100.0	1854	1	PCT-US00-35491-1	Sequence 1, Appli	109	14	93.3	291	58	US-60-141-584-356	Sequence 356, App
c 37	15	100.0	1854	1	PCT-US00-35491-11	Sequence 11, Appl	110	14	93.3	293	20	US-09-534-846B-940	Sequence 940, App
c 38	15	100.0	1854	29	US-09-750-609-11	Sequence 11, Appli	111	14	93.3	293	20	US-09-534-846B-24517	Sequence 24517, A
c 39	15	100.0	1854	29	US-09-750-609-11	Sequence 11, Appli	112	14	93.3	298	20	US-09-420-691-1364	Sequence 1364, Ap
c 40	15	100.0	1854	61	US-60-173-682-11	Sequence 11, Appli	113	14	93.3	302	18	US-09-534-846B-24499	Sequence 24499, A
c 41	15	100.0	1854	61	US-60-173-682-11	Sequence 11, Appli	114	14	93.3	302	15	US-09-128-809-600	Sequence 600, App
c 42	15	100.0	1983	3	US-07-676-980B-1	Sequence 1, Appli	115	14	93.3	309	20	US-09-534-846B-24512	Sequence 24512, A
c 43	15	100.0	1983	18	US-09-440-302A-1067	Sequence 1067, Ap	116	14	93.3	309	24	US-09-625-102-1056	Sequence 1056, Ap
c 44	15	100.0	1983	18	US-09-440-302B-1067	Sequence 1067, Ap	117	14	93.3	345	28	US-09-704-424-861	Sequence 861, App
c 45	15	100.0	2049	61	US-60-172-373-18619	Sequence 18619, A	118	14	93.3	359	28	US-09-534-846B-24517	Sequence 24517, A
c 46	15	100.0	2128	67	US-60-230-445-2244	Sequence 2244, Ap	119	14	93.3	372	13	US-08-971-197-5159	Sequence 5159, Ap
c 47	15	100.0	2136	35	US-09-948-933-117	Sequence 117, App	120	14	93.3	426	57	US-08-971-197-5159	Sequence 5159, Ap
c 48	15	100.0	5161	18	US-09-442-589B-881	Sequence 881, App	121	14	93.3	435	5	US-60-138-830-146	Sequence 146, App
c 49	15	100.0	5204	36	US-09-971-392-159	Sequence 159, App	122	14	93.3	435	5	US-08-187-634-8	Sequence 8, Appli
c 50	15	100.0	5204	36	US-60-237-652-159	Sequence 159, App	123	14	93.3	435	57	US-60-132-861-1244	Sequence 1244, Ap
c 51	15	100.0	5204	71	US-60-278-258-10692	Sequence 10692, A	124	14	93.3	435	57	US-60-125-817-5173	Sequence 5173, Ap
c 52	15	100.0	5205	76	US-60-324-185-14003	Sequence 14003, A	125	14	93.3	446	22	US-09-570-582B-108	Sequence 108, App
c 53	15	100.0	5497	25	US-09-644-867-7621	Sequence 7621, Ap	126	14	93.3	486	22	US-09-570-582B-108	Sequence 108, App
c 54	15	100.0	5497	26	US-09-663-693-1074	Sequence 1074, Ap	127	14	93.3	487	25	US-09-654-617-174767	Sequence 174767, A
c 55	15	100.0	5497	27	US-09-698-012-8717	Sequence 8717, Ap	128	14	93.3	487	25	US-09-684-016-174767	Sequence 174767, A
c 56	15	100.0	5497	27	US-09-698-012-8717	Sequence 8717, Ap	129	14	93.3	500	18	US-09-404-520-22058	Sequence 22058, A
c 57	15	100.0	5497	28	US-09-699-997-11832	Sequence 11832, A	130	14	93.3	514	27	US-09-698-012-4153	Sequence 4153, Ap
c 58	15	100.0	5497	28	US-09-710-285-2191	Sequence 2191, Ap	131	14	93.3	526	52	US-60-082-300-12476	Sequence 12476, A
c 59	15	100.0	5497	28	US-09-716-473-2179	Sequence 2179, Ap	132	14	93.3	537	25	US-09-654-617-33652	Sequence 33652, A
c 60	15	100.0	5497	28	US-09-726-475-3362	Sequence 3362, Ap	133	14	93.3	537	27	US-09-684-016-33652	Sequence 33652, A
c 61	15	100.0	5497	29	US-09-726-475-3362	Sequence 3362, Ap	134	14	93.3	552	20	US-09-534-847-23771	Sequence 23771, A
c 62	15	100.0	5547	61	US-60-172-373-9131	Sequence 9131, Ap	135	14	93.3	556	20	US-09-534-847-23674	Sequence 23674, A
c 63	15	100.0	12331	24	US-09-620-392-37557	Sequence 37557, A	136	14	93.3	562	57	US-09-534-847-23613	Sequence 23613, A
c 64	15	100.0	29748	19	US-09-528-237A-279	Sequence 279, App	137	14	93.3	592	20	US-60-132-861-2848	Sequence 2848, Ap
c 65	15	100.0	50050	35	US-09-948-933-535	Sequence 535, App	138	14	93.3	595	20	US-09-534-847-23636	Sequence 23636, A
c 66	15	100.0	63038	24	US-09-620-392-37557	Sequence 37557, A	139	14	93.3	655	43	PCT-US01-18569-2083	Sequence 2083, Ap
c 67	15	100.0	108634	31	US-09-815-264-6252	Sequence 6252, A	140	14	93.3	656	56	US-60-126-265-706	Sequence 706, App
c 68	15	100.0	108634	31	US-09-815-264-6252	Sequence 6252, A	141	14	93.3	659	24	US-09-634-306B-199074	Sequence 199074, A
c 69	14	93.3	215	20	US-09-534-846B-35357	Sequence 35357, A	142	14	93.3	659	24	US-09-634-306B-199075	Sequence 199075, A
c 70	14	93.3	215	53	US-60-096-664-879	Sequence 879, App	143	14	93.3	659	24	US-10-027-632-199076	Sequence 199076, A
c 71	14	93.3	228	15	US-09-113-753-13	Sequence 13, Appl	144	14	93.3	659	38	US-10-027-632-199074	Sequence 199074, A
c 72	14	93.3	228	15	US-09-534-846B-24527	Sequence 24527, A	145	14	93.3	659	38	US-10-027-632-199075	Sequence 199075, A
c 73	14	93.3	228	49	US-09-534-846B-24527	Sequence 13, Appl	146	14	93.3	664	62	US-60-180-489-3756	Sequence 3756, Ap
c 74	14	93.3	231	12	US-08-843-950-124	Sequence 124, App	147	14	93.3	674	23	US-09-604-693A-287	Sequence 287, App
c 75	14	93.3	231	21	US-09-540-229-54274	Sequence 54274, A	148	14	93.3	708	29	US-09-604-693A-287	Sequence 287, App
c 76	14	93.3	231	45	US-60-015-716-124	Sequence 124, App	149	14	93.3	742	18	US-09-404-520-6574	Sequence 6574, Ap
c 77	14	93.3	242	15	US-09-113-753-325	Sequence 325, App	150	14	93.3	831	23	US-09-604-693A-285	Sequence 285, App
c 78	14	93.3	242	20	US-09-534-846B-24524	Sequence 24524, A	151	14	93.3	1062	57	US-60-138-103-2116	Sequence 2116, Ap
c 79	14	93.3	242	49	US-60-052-200-325	Sequence 325, App	152	14	93.3	1322	42	US-10-219-999-18257	Sequence 18257, A
c 80	14	93.3	248	15	US-09-114-053-1084	Sequence 1084, Ap	153	14	93.3	1371	80	US-60-360-039-27932	Sequence 27932, A
c 81	14	93.3	248	18	US-09-420-691-4257	Sequence 4257, Ap	154	14	93.3	1437	80	US-60-360-039-23840	Sequence 23840, A
c 82	14	93.3	248	20	US-09-534-846B-24522	Sequence 24522, A	155	14	93.3	1553	80	US-60-360-207-1581	Sequence 1581, Ap
c 83	14	93.3	253	16	US-09-250-002B-833	Sequence 833, App	156	14	93.3	1582	16	US-09-270-767-10487	Sequence 10487, A
c 84	14	93.3	253	20	US-09-534-846B-24525	Sequence 24525, A	157	14	93.3	1989	4	US-08-074-893-1	Sequence 1, Appli
c 85	14	93.3	255	15	US-09-112-577-248	Sequence 248, App	158	14	93.3	1992	4	US-08-074-893-3	Sequence 3, Appli
c 86	14	93.3	256	20	US-09-534-846B-24492	Sequence 24492, A	159	14	93.3	2036	23	US-09-614-150-14975	Sequence 14975, A
c 87	14	93.3	256	58	US-60-141-232-4377	Sequence 4377, Ap	160	14	93.3	2036	60	US-60-167-217-15041	Sequence 15041, A
c 88	14	93.3	258	17	US-09-304-517A-151972	Sequence 151972, A	161	14	93.3	2036	61	US-60-173-464-12259	Sequence 12259, A
c 89	14	93.3	258	17	US-09-371-146A-151972	Sequence 151972, A	162	14	93.3	2036	63	US-60-191-637-15019	Sequence 15019, A
c 90	14	93.3	258	37	US-09-985-678-151972	Sequence 151972, A	163	14	93.3	2036	63	US-60-191-681-11854	Sequence 11854, A
c 91	14	93.3	265	15	US-09-129-873-3790	Sequence 3790, Ap	164	14	93.3	2397	5	US-07-627-950A-5	Sequence 5, Appli
c 92	14	93.3	265	20	US-09-534-846B-24496	Sequence 24496, A	165	14	93.3	2397	5	US-08-187-634-1	Sequence 1, Appli
c 93	14	93.3	270	16	US-09-250-002B-526	Sequence 526, App	166	14	93.3	2397	13	US-08-912-332-5	Sequence 5, Appli
c 94	14	93.3	270	20	US-09-534-846B-24495	Sequence 24495, A	167	14	93.3	2397	13	US-08-912-332-5	Sequence 5, Appli

c 168	14	93.3	3478	80	US-60-360-207-10993	Sequence 10993, A	c 241	13	86.7	99	26	US-09-669-817A-834	Sequence 834, App
c 169	14	93.3	3675	80	US-60-360-207-8748	Sequence 8748, Ap	242	13	86.7	117	23	US-09-619-643-12724	Sequence 12724, A
c 170	14	93.3	4479	18	US-09-404-520-15283	Sequence 15283, A	243	13	86.7	117	25	US-09-654-617-340657	Sequence 340657, A
c 171	14	93.3	5031	23	US-09-614-150-14974	Sequence 14974, A	244	13	86.7	117	27	US-09-684-016-340857	Sequence 340857, A
c 172	14	93.3	5031	60	US-60-167-217-15040	Sequence 15040, A	245	13	86.7	117	58	US-60-145-485-7789	Sequence 7789, Ap
c 173	14	93.3	5031	61	US-60-174-464-12258	Sequence 12258, A	246	13	86.7	135	60	US-60-164-378-482	Sequence 482, App
c 174	14	93.3	5031	63	US-60-191-637-15058	Sequence 15058, A	247	13	86.7	160	16	US-09-270-849B-23230	Sequence 23230, A
c 175	14	93.3	5031	63	US-60-191-681-11853	Sequence 11853, A	248	13	86.7	197	25	US-09-654-617-237248	Sequence 237248, A
c 176	14	93.3	8005	64	US-60-207-361-6	Sequence 6, Appl1	249	13	86.7	197	27	US-09-684-016-237248	Sequence 237248, A
c 177	14	93.3	23369	24	US-09-620-392-21337	Sequence 21337, A	250	13	86.7	204	30	US-09-760-466-159	Sequence 159, App
c 178	14	93.3	28237	19	US-09-528-237A-692	Sequence 692, App	251	13	86.7	204	30	US-09-760-466-629	Sequence 629, App
c 179	14	93.3	32387	68	US-60-248-592-44	Sequence 44, Appl	252	13	86.7	204	30	US-09-760-495-444	Sequence 444, App
c 180	14	93.3	32768	67	US-60-234-446-211	Sequence 211, App	253	13	86.7	204	40	US-10-143-775-444	Sequence 444, App
c 181	14	93.3	35442	28	US-09-702-134-6392	Sequence 6392, A	254	13	86.7	204	42	US-10-212-083-159	Sequence 159, App
c 182	14	93.3	35442	31	US-09-815-264-80318	Sequence 80318, A	255	13	86.7	204	42	US-10-212-083-629	Sequence 629, App
c 183	14	93.3	45355	33	US-09-897-516-436	Sequence 436, App	256	13	86.7	223	33	US-09-865-439A-56447	Sequence 56447, A
c 184	14	93.3	45355	33	US-09-897-516-437	Sequence 437, App	257	13	86.7	223	33	US-09-865-439A-56447	Sequence 56447, A
c 185	14	93.3	45355	33	US-09-897-516-438	Sequence 438, App	258	13	86.7	224	31	US-09-821-837-6070	Sequence 6070, Ap
c 186	14	93.3	45355	33	US-09-897-516-3725	Sequence 3725, Ap	259	13	86.7	224	31	US-09-821-837-6070	Sequence 6070, Ap
c 187	14	93.3	45355	33	US-09-897-516-3726	Sequence 3726, Ap	260	13	86.7	224	31	US-09-821-837-6070	Sequence 6070, Ap
c 188	14	93.3	45355	33	US-09-897-516-3727	Sequence 3727, Ap	261	13	86.7	233	52	US-09-298-328A-751	Sequence 751, App
c 189	14	93.3	45355	33	US-09-897-516-3728	Sequence 3728, Ap	262	13	86.7	233	52	US-09-085-147-751	Sequence 751, App
c 190	14	93.3	45355	33	US-09-897-516-3729	Sequence 3729, Ap	263	13	86.7	234	34	US-09-362-510-24581	Sequence 24581, A
c 191	14	93.3	45355	33	US-09-897-516-3730	Sequence 3730, Ap	264	13	86.7	234	34	US-09-362-510-24581	Sequence 24581, A
c 192	14	93.3	45355	33	US-09-897-516-3731	Sequence 3731, Ap	265	13	86.7	250	21	US-09-540-212A-56729	Sequence 56729, A
c 193	14	93.3	45355	33	US-09-897-516-3732	Sequence 3732, Ap	266	13	86.7	250	21	US-09-540-212A-56729	Sequence 56729, A
c 194	14	93.3	45355	33	US-09-897-516-3733	Sequence 3733, Ap	267	13	86.7	258	16	US-09-270-849B-163161	Sequence 163161, A
c 195	14	93.3	45355	33	US-09-897-516-3734	Sequence 3734, Ap	268	13	86.7	262	14	US-09-092-505-2737	Sequence 2737, Ap
c 196	14	93.3	45355	33	US-09-897-516-3735	Sequence 3735, Ap	269	13	86.7	262	14	US-09-540-212A-31327	Sequence 31327, A
c 197	14	93.3	45355	33	US-09-897-516-3736	Sequence 3736, Ap	270	13	86.7	265	27	US-09-692-257A-9085	Sequence 9085, Ap
c 198	14	93.3	45355	33	US-09-897-516-3737	Sequence 3737, Ap	271	13	86.7	265	27	US-09-692-257A-9085	Sequence 9085, Ap
c 199	14	93.3	45355	33	US-09-897-516-3738	Sequence 3738, Ap	272	13	86.7	269	17	US-09-313-294A-3136	Sequence 3136, Ap
c 200	14	93.3	45355	33	US-09-897-516-3739	Sequence 3739, Ap	273	13	86.7	269	17	US-09-086-722-3136	Sequence 3136, Ap
c 201	14	93.3	45355	33	US-09-897-516-3740	Sequence 3740, Ap	274	13	86.7	272	26	US-09-663-779-7346	Sequence 7346, Ap
c 202	14	93.3	45355	33	US-09-897-516-3741	Sequence 3741, Ap	275	13	86.7	272	26	US-09-138-103-13500	Sequence 13500, A
c 203	14	93.3	45355	33	US-09-897-516-3742	Sequence 3742, Ap	276	13	86.7	278	62	US-09-185-215-4073	Sequence 4073, Ap
c 204	14	93.3	45355	33	US-09-897-516-3743	Sequence 3743, Ap	277	13	86.7	281	32	US-09-834-366-36983	Sequence 36983, A
c 205	14	93.3	45355	33	US-09-897-516-3744	Sequence 3744, Ap	278	13	86.7	281	63	US-09-197-873-36983	Sequence 36983, A
c 206	14	93.3	45355	65	US-60-215-161-436	Sequence 436, App	279	13	86.7	282	26	US-09-669-817A-24620	Sequence 24620, A
c 207	14	93.3	45355	65	US-60-215-161-437	Sequence 437, App	280	13	86.7	283	21	US-09-540-213-30696	Sequence 30696, A
c 208	14	93.3	45355	65	US-60-215-161-438	Sequence 438, App	281	13	86.7	283	69	US-09-256-867-1671	Sequence 1671, Ap
c 209	14	93.3	45355	65	US-60-215-161-3725	Sequence 3725, Ap	282	13	86.7	286	65	US-60-213-178-972	Sequence 972, App
c 210	14	93.3	45355	65	US-60-215-161-3726	Sequence 3726, Ap	283	13	86.7	286	65	US-60-213-178-1007	Sequence 1007, Ap
c 211	14	93.3	45355	65	US-60-215-161-3727	Sequence 3727, Ap	284	13	86.7	299	25	US-09-654-617-314284	Sequence 314284, A
c 212	14	93.3	45355	65	US-60-215-161-3728	Sequence 3728, Ap	285	13	86.7	299	27	US-09-684-016-314284	Sequence 314284, A
c 213	14	93.3	45355	65	US-60-215-161-3729	Sequence 3729, Ap	286	13	86.7	302	64	US-60-207-458-6136	Sequence 6136, Ap
c 214	14	93.3	45355	65	US-60-215-161-3730	Sequence 3730, Ap	287	13	86.7	308	27	US-09-654-617-280771	Sequence 280771, A
c 215	14	93.3	45355	65	US-60-215-161-3731	Sequence 3731, Ap	288	13	86.7	308	27	US-09-684-016-280771	Sequence 280771, A
c 216	14	93.3	45355	65	US-60-215-161-3732	Sequence 3732, Ap	289	13	86.7	310	17	US-09-394-745-324	Sequence 324, App
c 217	14	93.3	45355	65	US-60-215-161-3733	Sequence 3733, Ap	290	13	86.7	310	22	US-09-565-306-6	Sequence 6, Appl1
c 218	14	93.3	45355	65	US-60-215-161-3734	Sequence 3734, Ap	291	13	86.7	314	69	US-60-253-652-15165	Sequence 15165, A
c 219	14	93.3	45355	65	US-60-215-161-3735	Sequence 3735, Ap	292	13	86.7	339	69	US-60-256-867-1730	Sequence 1730, Ap
c 220	14	93.3	45355	65	US-60-215-161-3736	Sequence 3736, Ap	293	13	86.7	350	26	US-09-666-355A-5732	Sequence 5732, Ap
c 221	14	93.3	45355	65	US-60-215-161-3737	Sequence 3737, Ap	294	13	86.7	358	17	US-09-362-510A-13987	Sequence 13987, A
c 222	14	93.3	45355	65	US-60-215-161-3738	Sequence 3738, Ap	295	13	86.7	358	17	US-09-362-510A-13987	Sequence 13987, A
c 223	14	93.3	45355	65	US-60-215-161-3739	Sequence 3739, Ap	296	13	86.7	358	34	US-09-904-013-13987	Sequence 13987, A
c 224	14	93.3	45355	65	US-60-215-161-3740	Sequence 3740, Ap	297	13	86.7	361	17	US-09-397-424-2325	Sequence 2325, Ap
c 225	14	93.3	45355	65	US-60-215-161-3741	Sequence 3741, Ap	298	13	86.7	368	25	US-09-654-617-310872	Sequence 310872, A
c 226	14	93.3	45355	65	US-60-215-161-3742	Sequence 3742, Ap	299	13	86.7	368	27	US-09-684-016-310872	Sequence 310872, A
c 227	14	93.3	45355	65	US-60-215-161-3743	Sequence 3743, Ap	300	13	86.7	368	27	US-09-684-016-310872	Sequence 310872, A
c 228	14	93.3	45355	65	US-60-215-161-3744	Sequence 3744, Ap	301	13	86.7	374	1	PCT-US01-01354-24231	Sequence 24231, A
c 229	14	93.3	70665	1	PCT-US02-02176-850	Sequence 850, App	302	13	86.7	374	1	PCT-US01-01354-24231	Sequence 24231, A
c 230	14	93.3	264792	68	US-60-245-228-44	Sequence 44, Appl	303	13	86.7	374	16	US-09-235-076-37637	Sequence 37637, A
c 231	14	93.3	1090936	14	US-09-012-031B-308	Sequence 308, App	304	13	86.7	374	17	US-09-332-782-37637	Sequence 37637, A
c 232	14	93.3	1090936	14	US-09-012-031C-308	Sequence 308, App	305	13	86.7	374	29	US-09-737-223-37637	Sequence 37637, A
c 233	14	93.3	1090936	14	US-09-012-031C-308	Sequence 308, App	306	13	86.7	374	30	US-09-764-905-24230	Sequence 24230, A
c 234	14	93.3	1090936	17	US-09-335-032-12210	Sequence 12210, A	307	13	86.7	374	30	US-09-764-905-24230	Sequence 24230, A
c 235	13	86.7	24	42	US-10-239-316-561	Sequence 56, Appl	308	13	86.7	374	34	US-09-909-627-16269	Sequence 16269, A
c 236	13	86.7	25	36	US-09-954-427-66715	Sequence 66715, A	309	13	86.7	374	34	US-09-918-995-37637	Sequence 37637, A
c 237	13	86.7	25	67	US-60-233-166-66715	Sequence 66715, A	310	13	86.7	374	39	US-10-092-399-24230	Sequence 24230, A
c 238	13	86.7	25	79	US-60-353-987-809837	Sequence 809837, A	311	13	86.7	374	39	US-10-092-399-24231	Sequence 24231, A
c 239	13	86.7	70	33	US-09-874-708A-31751	Sequence 31751, A	312	13	86.7	379	19	US-09-521-640-63009	Sequence 63009, A
c 240	13	86.7	70	65	US-60-211-750-31307	Sequence 31307, A	313	13	86.7	379	23	US-09-605-698-8174	Sequence 8174, Ap

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315	13	86.7	386	29	US-09-724-866A-10979	Sequence 10979, A	c 388	13	86.7	483	16	US-09-287-618-29984	Sequence 29984, A
316	13	86.7	386	61	US-60-171-432-10979	Sequence 10979, A	c 389	13	86.7	483	22	US-09-572-409-26925	Sequence 26925, A
317	13	86.7	390	19	US-09-521-640-178471	Sequence 178471, A	390	13	86.7	484	19	US-09-528-409-110397	Sequence 110397, A
318	13	86.7	390	58	US-60-140-769-11531	Sequence 11531, A	391	13	86.7	484	35	US-09-933-524-110397	Sequence 110397, A
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320	13	86.7	391	11	US-08-798-074B-6050	Sequence 6050, Ap	c 393	13	86.7	485	18	US-09-400-122A-22	Sequence 22, Appl
321	13	86.7	393	16	US-09-248-797-22456	Sequence 22456, A	c 394	13	86.7	485	18	US-09-400-122A-22	Sequence 22, Appl
322	13	86.7	393	25	US-09-654-617-426485	Sequence 426485, A	395	13	86.7	488	24	US-09-521-640-205532	Sequence 205532, A
323	13	86.7	393	26	US-09-669-817A-27412	Sequence 27412, A	c 396	13	86.7	489	24	US-09-620-111B-1398	Sequence 1398, Ap
324	13	86.7	393	27	US-09-684-016-426485	Sequence 426485, A	c 397	13	86.7	489	62	US-60-182-467-1094	Sequence 1094, Ap
325	13	86.7	393	34	US-09-525-564-22456	Sequence 22456, A	c 398	13	86.7	491	18	US-09-400-122A-23	Sequence 23, Appl
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327	13	86.7	400	30	US-09-764-905-2126	Sequence 2126, Ap	c 400	13	86.7	496	64	US-60-207-458-137089	Sequence 137089, A
328	13	86.7	400	39	US-10-092-399-2126	Sequence 2126, Ap	c 401	13	86.7	497	18	US-09-400-122A-24	Sequence 24, Appl
329	13	86.7	402	31	US-09-821-837-6779	Sequence 6779, Ap	c 402	13	86.7	498	61	US-60-170-870-610	Sequence 29366, A
330	13	86.7	408	57	US-60-135-952-4795	Sequence 4795, Ap	c 403	13	86.7	499	26	US-09-669-817A-29366	Sequence 29366, A
331	13	86.7	414	27	US-09-692-257A-548	Sequence 548, App	c 404	13	86.7	501	28	US-09-710-282-336	Sequence 336, App
332	13	86.7	414	60	US-60-162-747-510	Sequence 510, App	c 405	13	86.7	501	38	US-10-029-386-11356	Sequence 11356, A
333	13	86.7	415	19	US-09-528-409-85841	Sequence 85841, A	c 406	13	86.7	503	38	US-10-029-386-11356	Sequence 11356, A
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335	13	86.7	415	35	US-09-933-524A-85841	Sequence 85841, A	c 408	13	86.7	505	25	US-09-654-617-454344	Sequence 454344, A
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338	13	86.7	416	56	US-60-128-436-112	Sequence 112, App	c 411	13	86.7	508	32	US-09-834-366-9089	Sequence 9089, Ap
339	13	86.7	416	26	US-09-669-817A-26056	Sequence 26056, A	c 412	13	86.7	508	32	US-60-197-873-9089	Sequence 9089, Ap
340	13	86.7	418	26	US-10-260-238-79	Sequence 79, Appl	c 413	13	86.7	510	25	US-09-654-617-127482	Sequence 127482, A
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343	13	86.7	420	69	US-60-325-448-79	Sequence 79, Appl	c 416	13	86.7	516	61	US-60-207-458-58762	Sequence 58762, A
344	13	86.7	420	76	US-09-540-215-1368	Sequence 1368, Ap	c 417	13	86.7	516	61	US-60-172-362-3004	Sequence 3004, Ap
345	13	86.7	421	21	US-09-540-215-1368	Sequence 1368, Ap	c 418	13	86.7	516	61	US-09-528-409-110705	Sequence 110705, A
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347	13	86.7	424	56	US-60-128-436-1168	Sequence 1168, Ap	c 420	13	86.7	520	35	US-09-933-524A-110705	Sequence 110705, A
348	13	86.7	424	56	US-60-128-436-1168	Sequence 1168, Ap	c 421	13	86.7	521	25	US-09-654-617-393123	Sequence 393123, A
349	13	86.7	426	17	US-09-397-022-1314	Sequence 1314, Ap	c 422	13	86.7	521	27	US-09-684-016-393123	Sequence 393123, A
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351	13	86.7	426	26	US-09-669-817A-9994	Sequence 9994, Ap	c 424	13	86.7	526	63	US-60-196-713-1031	Sequence 1031, Ap
352	13	86.7	426	26	US-09-675-784A-2644	Sequence 2644, Ap	c 425	13	86.7	526	63	US-60-196-713-1032	Sequence 1032, Ap
353	13	86.7	426	27	US-09-684-016-414050	Sequence 414050, A	c 426	13	86.7	526	63	US-60-196-713-1033	Sequence 1033, Ap
354	13	86.7	426	31	US-09-808-383-1314	Sequence 1314, Ap	c 427	13	86.7	526	63	US-60-196-713-1034	Sequence 1034, Ap
355	13	86.7	431	57	US-60-135-952-1314	Sequence 1314, Ap	c 428	13	86.7	526	63	US-60-196-714-147	Sequence 147, App
356	13	86.7	431	57	US-60-135-952-1314	Sequence 1314, Ap	c 429	13	86.7	526	63	US-60-196-714-303	Sequence 303, App
357	13	86.7	435	21	US-09-540-215-2493	Sequence 2493, Ap	c 430	13	86.7	531	19	US-09-526-263A-1118	Sequence 1118, App
358	13	86.7	435	25	US-09-654-617-417934	Sequence 417934, A	c 431	13	86.7	536	39	US-10-081-124-443	Sequence 443, App
359	13	86.7	435	26	US-09-669-817A-40152	Sequence 40152, A	c 432	13	86.7	536	39	US-60-196-714-362	Sequence 362, App
360	13	86.7	435	26	US-09-684-016-417934	Sequence 417934, A	c 433	13	86.7	536	39	US-10-256-174-300	Sequence 300, App
361	13	86.7	436	19	US-09-421-106-25908	Sequence 25908, A	c 434	13	86.7	544	52	US-60-082-300-21532	Sequence 21532, A
362	13	86.7	436	19	US-09-521-640-294539	Sequence 294539, A	c 435	13	86.7	544	52	US-60-082-300-19972	Sequence 19972, A
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366	13	86.7	439	63	US-60-197-872-55314	Sequence 55314, A	c 439	13	86.7	570	18	US-09-417-507-18190	Sequence 18190, A
367	13	86.7	441	18	US-09-417-507-18180	Sequence 18180, A	c 440	13	86.7	572	22	US-09-565-309A-8768	Sequence 8768, Ap
368	13	86.7	444	17	US-09-391-631-4198	Sequence 4198, Ap	c 441	13	86.7	580	61	US-60-172-375-8217	Sequence 8217, Ap
369	13	86.7	445	13	US-08-975-985-2116	Sequence 2116, Ap	c 442	13	86.7	580	61	US-60-172-375-8217	Sequence 8217, Ap
370	13	86.7	445	62	US-60-182-094-445	Sequence 445, App	c 443	13	86.7	582	22	US-09-565-309A-8766	Sequence 8766, Ap
371	13	86.7	446	30	US-09-785-276A-12050	Sequence 12050, A	c 444	13	86.7	586	62	US-09-480-489-3950	Sequence 3950, Ap
372	13	86.7	447	16	US-09-252-991A-11703	Sequence 11703, A	c 445	13	86.7	592	25	US-09-654-617-391883	Sequence 391883, A
373	13	86.7	448	26	US-09-669-817A-23637	Sequence 23637, A	c 446	13	86.7	594	52	US-09-684-016-391883	Sequence 391883, A
374	13	86.7	455	16	US-09-235-076-14723	Sequence 14723, A	c 447	13	86.7	606	18	US-09-417-507-11596	Sequence 11596, A
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378	13	86.7	455	34	US-09-918-995-14723	Sequence 14723, A	c 451	13	86.7	610	31	US-09-819-091A-17429	Sequence 17429, A
379	13	86.7	455	34	US-09-925-564-33261	Sequence 33261, A	c 452	13	86.7	612	63	US-60-195-136-696	Sequence 696, App
380	13	86.7	462	69	US-60-256-867-1724	Sequence 1724, Ap	c 453	13	86.7	624	63	US-60-196-718-1250	Sequence 1250, Ap
381	13	86.7	464	28	US-09-704-424-25504	Sequence 25504, A	c 454	13	86.7	624	63	US-60-207-458-26435	Sequence 26435, A
382	13	86.7	464	33	US-09-873-402A-75923	Sequence 75923, A	c 455	13	86.7	625	61	US-60-170-869-155	Sequence 155, App
383	13	86.7	466	25	US-09-654-617-185194	Sequence 185194, A	c 456	13	86.7	633	33	US-09-865-439A-85855	Sequence 85855, A
384	13	86.7	467	22	US-09-684-016-185194	Sequence 185194, A	c 457	13	86.7	633	34	US-60-207-458-129997	Sequence 129997, A
385	13	86.7	467	22	US-09-565-306-13369	Sequence 13369, A	c 458	13	86.7	635	60	US-60-162-242-141	Sequence 141, App
386	13	86.7	473	57	US-60-135-952-2006	Sequence 2006, Ap	c 459	13	86.7	635	60		

460	13	86.7	635	60	US-60-162-248-539	Sequence 539, App	533	13	86.7	1244	27	US-09-684-016-261872	Sequence 261872,
461	13	86.7	636	60	US-60-162-356-307	Sequence 307, App	534	13	86.7	1261	65	US-60-212-656-621	Sequence 621, App
462	13	86.7	636	60	US-60-163-232-430	Sequence 830, App	535	13	86.7	1261	67	US-60-230-435-2363	Sequence 2363, App
463	13	86.7	636	60	US-60-169-842-1562	Sequence 1562, App	536	13	86.7	1284	80	US-60-360-039-46583	Sequence 46583, A
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466	13	86.7	643	69	US-60-256-867-1769	Sequence 1769, App	539	13	86.7	1336	23	US-09-614-150-4055	Sequence 4055, App
467	13	86.7	644	69	US-60-256-867-1738	Sequence 1738, App	540	13	86.7	1336	23	US-09-619-049-227	Sequence 227, App
468	13	86.7	647	17	US-09-317-311C-117	Sequence 117, App	541	13	86.7	1336	61	US-60-171-627-332	Sequence 332, App
469	13	86.7	647	39	US-10-077-478-117	Sequence 117, App	542	13	86.7	1336	61	US-60-173-464-3388	Sequence 3388, App
c 470	13	86.7	650	25	US-09-654-617-271571	Sequence 271571, App	543	13	86.7	1336	63	US-60-191-637-4070	Sequence 4070, App
c 471	13	86.7	650	27	US-09-684-016-271571	Sequence 271571, App	544	13	86.7	1336	63	US-60-191-681-3254	Sequence 3254, App
472	13	86.7	655	38	US-10-021-323-229	Sequence 229, App	545	13	86.7	1380	16	US-09-252-991A-12957	Sequence 12957, A
473	13	86.7	655	69	US-60-255-619-229	Sequence 229, App	546	13	86.7	1414	38	US-10-029-386-20850	Sequence 20850, A
474	13	86.7	669	19	US-09-514-000-2385	Sequence 2385, App	547	13	86.7	1414	38	US-10-029-386-205068	Sequence 205068, A
475	13	86.7	684	18	US-09-417-507-11593	Sequence 11593, A	548	13	86.7	1420	67	US-60-230-435-2456	Sequence 2456, App
476	13	86.7	685	52	US-60-082-300-6301	Sequence 6301, App	549	13	86.7	1425	16	US-09-252-991A-11848	Sequence 11848, A
c 477	13	86.7	690	29	US-09-739-449-6263	Sequence 6263, App	550	13	86.7	1440	34	US-09-902-540-9640	Sequence 9640, App
c 478	13	86.7	690	31	US-09-803-110-6263	Sequence 6263, App	551	13	86.7	1446	16	US-09-252-991A-11593	Sequence 11593, A
c 479	13	86.7	702	80	US-60-360-207-33052	Sequence 33052, A	552	13	86.7	1501	31	US-09-815-264-25351	Sequence 25351, A
c 480	13	86.7	716	18	US-09-471-275-10264	Sequence 10264, A	553	13	86.7	1501	31	US-09-815-264-32361	Sequence 32361, A
c 481	13	86.7	738	1	PCT-US02-13142-2086	Sequence 2086, App	554	13	86.7	1530	28	US-09-708-427-36329	Sequence 36329, A
c 482	13	86.7	738	18	US-09-417-507-11581	Sequence 11581, A	555	13	86.7	1535	65	US-60-213-178-22	Sequence 22, Appl
c 483	13	86.7	738	40	US-10-128-714-2086	Sequence 2086, App	556	13	86.7	1548	30	US-09-770-175-7141	Sequence 7141, App
c 484	13	86.7	738	75	US-60-316-362-2086	Sequence 2086, App	557	13	86.7	1581	38	US-10-015-127-8942	Sequence 8942, App
c 485	13	86.7	740	18	US-09-404-520-25007	Sequence 25007, App	558	13	86.7	1584	80	US-60-360-039-41456	Sequence 41456, A
c 486	13	86.7	753	26	US-09-675-784A-2277	Sequence 2277, App	559	13	86.7	1599	18	US-09-417-507-8698	Sequence 8698, App
c 487	13	86.7	765	34	US-03-902-540-9484	Sequence 9484, App	560	13	86.7	1716	18	US-09-404-520-25338	Sequence 25338, App
c 488	13	86.7	796	1	PCT-US02-13142-1086	Sequence 1086, App	561	13	86.7	1717	19	US-09-513-996A-54344	Sequence 54344, A
c 489	13	86.7	796	40	US-10-128-714-1086	Sequence 1086, App	562	13	86.7	1721	19	US-09-513-996A-25105	Sequence 25105, A
c 490	13	86.7	796	75	US-60-316-362-1086	Sequence 1086, App	563	13	86.7	1721	25	US-09-649-866A-938	Sequence 938, App
c 491	13	86.7	805	23	US-09-614-150-3653	Sequence 3653, App	564	13	86.7	1779	80	US-60-360-207-37859	Sequence 37859, A
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c 493	13	86.7	808	60	US-60-167-217-3718	Sequence 3718, App	566	13	86.7	1880	66	US-60-229-515-1565	Sequence 1565, App
c 494	13	86.7	809	80	US-60-360-039-37023	Sequence 37023, A	567	13	86.7	1899	55	US-60-213-178-57	Sequence 57, Appl
c 495	13	86.7	815	18	US-09-404-520-21560	Sequence 21560, A	568	13	86.7	2001	18	US-08-951-984-4	Sequence 4, Appl
c 496	13	86.7	850	18	US-09-404-520-13362	Sequence 13362, A	569	13	86.7	2001	18	US-09-400-122-4	Sequence 4, Appl
c 497	13	86.7	850	18	US-09-404-520-21306	Sequence 21306, A	570	13	86.7	2001	18	US-09-400-122A-4	Sequence 4, Appl
c 498	13	86.7	851	24	US-09-620-392-29770	Sequence 29770, A	571	13	86.7	2023	12	US-08-886-333-6	Sequence 6, Appl
c 499	13	86.7	875	18	US-09-404-520-26174	Sequence 26174, A	572	13	86.7	2066	1	PCT-US01-08631-15472	Sequence 15472, A
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c 501	13	86.7	915	80	US-60-360-039-35401	Sequence 35401, A	574	13	86.7	2118	16	US-09-252-991A-11782	Sequence 11782, A
c 502	13	86.7	915	80	US-60-360-039-37915	Sequence 37915, A	575	13	86.7	2126	23	US-09-614-150-13685	Sequence 13685, A
c 503	13	86.7	915	80	US-60-360-039-38486	Sequence 38486, A	576	13	86.7	2126	60	US-60-167-217-13753	Sequence 13753, A
c 504	13	86.7	915	80	US-60-360-039-38660	Sequence 38660, A	577	13	86.7	2126	61	US-60-173-464-11185	Sequence 11185, A
c 505	13	86.7	924	19	US-09-514-000-3965	Sequence 3965, App	578	13	86.7	2168	28	US-09-708-427-76744	Sequence 76744, A
c 506	13	86.7	933	29	US-09-739-449-6367	Sequence 6367, App	579	13	86.7	2205	69	US-60-258-273-227	Sequence 227, App
c 507	13	86.7	933	31	US-09-803-110-6367	Sequence 6367, App	580	13	86.7	2224	63	US-60-191-637-13726	Sequence 13726, A
c 508	13	86.7	952	18	US-09-404-520-7813	Sequence 7813, App	581	13	86.7	2224	63	US-60-191-681-10819	Sequence 10819, A
c 509	13	86.7	956	28	US-09-708-427-92279	Sequence 92279, A	582	13	86.7	2250	1	PCT-US01-08631-15187	Sequence 5187, App
c 510	13	86.7	960	80	US-60-360-039-27084	Sequence 27084, A	583	13	86.7	2250	1	PCT-US01-08656-3711	Sequence 3711, App
c 511	13	86.7	1026	16	US-09-270-767-11786	Sequence 11786, A	584	13	86.7	2280	16	US-09-252-991A-12824	Sequence 12824, A
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c 513	13	86.7	1029	31	US-09-819-091A-32082	Sequence 32082, A	586	13	86.7	2292	31	US-09-826-509-398	Sequence 398, App
c 514	13	86.7	1049	19	US-09-513-996A-26435	Sequence 26435, A	587	13	86.7	2292	31	US-09-826-509-402	Sequence 402, App
c 515	13	86.7	1049	22	US-09-565-309A-55195	Sequence 55195, A	588	13	86.7	2292	31	US-09-826-509-406	Sequence 406, App
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c 520	13	86.7	1060	38	US-10-027-632-117808	Sequence 117808, App	593	13	86.7	2295	3	US-07-914-370A-1	Sequence 1, Appl
c 521	13	86.7	1060	38	US-10-027-632-117809	Sequence 117809, App	594	13	86.7	2385	16	US-09-252-991A-12517	Sequence 12517, A
c 522	13	86.7	1111	39	US-10-060-063-6846	Sequence 6846, App	595	13	86.7	2413	14	US-09-016-434-1469	Sequence 1469, App
c 523	13	86.7	1140	80	US-60-360-039-45095	Sequence 45095, A	596	13	86.7	2450	12	US-08-886-333-2	Sequence 2, Appl
c 524	13	86.7	1143	30	US-09-782-816A-55	Sequence 55, Appl	597	13	86.7	2469	3	US-07-722-620-38	Sequence 28, Appl
c 525	13	86.7	1173	33	US-09-887-272A-4693	Sequence 4693, App	598	13	86.7	2469	15	US-09-186-350A-54	Sequence 54, Appl
c 526	13	86.7	1182	41	US-10-155-881-23516	Sequence 23516, A	599	13	86.7	2512	38	US-09-417-507-18181	Sequence 18181, A
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c 529	13	86.7	1206	38	US-10-015-127-5712	Sequence 5712, App	602	13	86.7	2553	1	PCT-US01-14827-5132	Sequence 5132, App
c 530	13	86.7	1206	40	US-10-128-714-7086	Sequence 7086, App	603	13	86.7	2553	22	US-09-577-408-5994	Sequence 5994, App
c 531	13	86.7	1210	20	US-09-533-559-113	Sequence 113, App	604	13	86.7	2600	60	US-60-168-139-1655	Sequence 1655, App
c 532	13	86.7	1244	25	US-09-654-617-261872	Sequence 261872, App	605	13	86.7	2608	18	US-09-404-520-11473	Sequence 11473, A

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c 607	13	86.7	2668	24	US-09-634-3068-112100	Sequence 112100, Ap	680	13	86.7	3840	61	US-60-171-625-140	Sequence 140, Ap
c 608	13	86.7	2668	38	US-10-027-6332-112100	Sequence 112100, Ap	681	13	86.7	3840	61	US-60-171-625-140	Sequence 140, Ap
c 609	13	86.7	2694	18	US-09-404-520-3874	Sequence 3874, Ap	682	13	86.7	3867	22	US-09-577-410-7484	Sequence 7484, Ap
c 610	13	86.7	2708	34	US-09-102-540-2864	Sequence 2864, Ap	c 683	13	86.7	3882	68	US-60-245-228-588	Sequence 588, Ap
c 611	13	86.7	2733	61	US-60-173-464-7365	Sequence 7365, Ap	684	13	86.7	3915	60	US-60-167-245-293	Sequence 293, Ap
c 612	13	86.7	2736	60	US-60-167-217-9140	Sequence 9140, Ap	685	13	86.7	3985	1	PCT-US01-01354-40190	Sequence 40190, A
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c 615	13	86.7	2796	40	US-10-128-714-86	Sequence 86, Appl	688	13	86.7	3992	1	PCT-US01-08631-15470	Sequence 15470, A
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c 618	13	86.7	2827	65	US-60-213-178-1186	Sequence 1186, Ap	691	13	86.7	3992	18	US-09-442-384A-735	Sequence 735, Ap
c 619	13	86.7	2874	17	US-09-391-631-4197	Sequence 4197, Ap	692	13	86.7	3992	35	US-09-442-384B-735	Sequence 735, Ap
c 620	13	86.7	2897	80	US-60-360-207-13554	Sequence 13554, A	693	13	86.7	3992	38	US-09-944-807-9	Sequence 9, Appl
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c 624	13	86.7	2959	23	US-09-614-150-38845	Sequence 38845, A	697	13	86.7	4008	65	US-60-213-360-925	Sequence 925, Ap
c 625	13	86.7	2959	61	US-60-173-464-29325	Sequence 29325, A	c 698	13	86.7	4043	1	PCT-US01-08631-22364	Sequence 22364, A
c 626	13	86.7	2959	63	US-60-191-637-38471	Sequence 38471, A	699	13	86.7	4048	61	US-60-172-373-2381	Sequence 2381, Ap
c 627	13	86.7	2959	63	US-60-191-681-29834	Sequence 29834, A	700	13	86.7	4340	23	US-09-614-150-4388	Sequence 4288, Ap
c 628	13	86.7	3015	23	US-09-614-150-3652	Sequence 3652, Ap	701	13	86.7	4340	60	US-60-167-217-4376	Sequence 4376, Ap
c 629	13	86.7	3015	63	US-60-191-637-3664	Sequence 3664, Ap	702	13	86.7	4340	61	US-60-173-464-3567	Sequence 3567, Ap
c 630	13	86.7	3018	60	US-60-167-217-3717	Sequence 3717, Ap	703	13	86.7	4340	63	US-60-191-637-4303	Sequence 4303, Ap
c 631	13	86.7	3032	23	US-09-614-150-9077	Sequence 9077, Ap	704	13	86.7	4340	63	US-60-191-681-3418	Sequence 3418, Ap
c 632	13	86.7	3032	63	US-60-191-637-9106	Sequence 9106, Ap	705	13	86.7	4374	1	PCT-US01-04098A-847	Sequence 847, Ap
c 633	13	86.7	3032	63	US-60-191-681-7102	Sequence 7102, Ap	c 706	13	86.7	4402	23	US-09-614-150-2810	Sequence 2810, Ap
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c 635	13	86.7	3096	23	US-60-173-464-14968	Sequence 14968, A	c 708	13	86.7	4402	63	US-60-191-681-2255	Sequence 2255, Ap
c 636	13	86.7	3096	63	US-60-173-464-18229	Sequence 18229, A	709	13	86.7	4455	1	PCT-US01-04098A-846	Sequence 846, Ap
c 637	13	86.7	3096	63	US-60-191-681-14428	Sequence 14428, A	710	13	86.7	4471	24	US-09-620-392-56261	Sequence 56261, A
c 638	13	86.7	3099	60	US-60-167-217-18234	Sequence 18234, A	711	13	86.7	4471	60	US-60-168-139-1957	Sequence 1957, Ap
c 639	13	86.7	3168	80	US-60-360-207-11302	Sequence 11302, A	712	13	86.7	4490	60	US-60-167-217-1249	Sequence 1249, Ap
c 640	13	86.7	3215	23	US-09-614-150-21409	Sequence 21409, A	713	13	86.7	4490	61	US-60-173-464-994	Sequence 994, Ap
c 641	13	86.7	3215	63	US-60-191-637-21471	Sequence 21471, A	714	13	86.7	4495	1	PCT-US01-08631-22684	Sequence 22684, A
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c 643	13	86.7	3240	24	US-09-631-022-4	Sequence 4, Appl	c 716	13	86.7	4558	1	PCT-US01-01333-937	Sequence 937, Ap
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c 647	13	86.7	3338	23	US-09-614-150-7166	Sequence 7166, Ap	c 720	13	86.7	4558	39	US-10-074-095-937	Sequence 937, Ap
c 648	13	86.7	3338	63	US-60-191-637-7187	Sequence 7187, Ap	c 721	13	86.7	4558	42	US-10-212-872-937	Sequence 937, Ap
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c 652	13	86.7	3486	23	US-09-619-049-226	Sequence 226, Ap	c 725	13	86.7	4765	38	US-10-015-127-449	Sequence 449, Ap
c 653	13	86.7	3486	61	US-60-171-627-331	Sequence 331, Ap	c 726	13	86.7	4899	30	US-09-785-276A-23256	Sequence 23256, A
c 654	13	86.7	3486	61	US-60-173-464-3387	Sequence 3387, Ap	c 727	13	86.7	5068	61	US-60-173-464-7364	Sequence 7364, Ap
c 655	13	86.7	3486	63	US-60-191-637-4069	Sequence 4069, Ap	c 728	13	86.7	5071	60	US-60-167-217-9139	Sequence 9139, Ap
c 656	13	86.7	3486	63	US-60-191-681-3253	Sequence 3253, Ap	c 729	13	86.7	5299	23	US-09-614-150-9076	Sequence 9076, Ap
c 657	13	86.7	3537	1	PCT-US02-13142-6240	Sequence 6240, Ap	c 730	13	86.7	5299	63	US-60-191-637-9105	Sequence 9105, Ap
c 658	13	86.7	3537	40	US-10-128-714-6240	Sequence 6240, Ap	c 731	13	86.7	5299	63	US-60-191-681-7101	Sequence 7101, Ap
c 659	13	86.7	3537	40	US-10-128-714-6240	Sequence 7240, Ap	c 732	13	86.7	5494	23	US-09-614-150-18175	Sequence 18175, A
c 660	13	86.7	3537	40	US-10-128-714-7240	Sequence 7240, Ap	c 733	13	86.7	5494	61	US-60-173-464-14967	Sequence 14967, A
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c 662	13	86.7	3549	31	US-09-826-509-586	Sequence 586, Ap	735	13	86.7	5494	63	US-60-191-637-18228	Sequence 18228, A
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c 665	13	86.7	3549	65	US-60-219-005-281	Sequence 281, Ap	c 738	13	86.7	5537	40	US-10-128-714-5240	Sequence 5240, Ap
c 666	13	86.7	3564	23	US-09-614-150-26663	Sequence 26663, A	c 739	13	86.7	5537	18	US-09-430-029-1	Sequence 1, Appl
c 667	13	86.7	3564	63	US-60-191-637-26835	Sequence 26835, A	740	13	86.7	5828	23	US-09-614-150-13684	Sequence 13684, A
c 668	13	86.7	3564	63	US-60-191-681-21444	Sequence 21444, A	741	13	86.7	5902	60	US-60-167-217-13752	Sequence 13752, A
c 669	13	86.7	3564	65	US-60-219-005-278	Sequence 278, Ap	742	13	86.7	5902	61	US-60-173-464-11184	Sequence 11184, A
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c 671	13	86.7	3614	60	US-60-167-217-2859	Sequence 2859, Ap	744	13	86.7	5902	63	US-60-191-681-10818	Sequence 10818, A
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c 674	13	86.7	3671	18	US-09-471-275-6778	Sequence 6778, Ap	747	13	86.7	6390	1	PCT-US01-08631-20740	Sequence 20740, A
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c 676	13	86.7	3754	63	US-60-191-637-26841	Sequence 26841, A	c 749	13	86.7	6632	59	US-60-150-584-520	Sequence 520, Ap
c 677	13	86.7	3754	63	US-60-191-681-21450	Sequence 21450, A	c 750	13	86.7	6689	23	US-09-614-150-26668	Sequence 26668, A
c 678	13	86.7	3754	65	US-60-219-005-284	Sequence 284, Ap	c 751	13	86.7	6689	63	US-60-191-637-26840	Sequence 26840, A

c 752	13	86.7	6689	63	US-60-191-681-21449	Sequence 21449, A	825	13	86.7	24286	24	US-09-620-392-43064	Sequence 43064, A
c 753	13	86.7	6692	65	US-60-219-005-283	Sequence 283, App	826	13	86.7	24414	24	US-09-620-392-46782	Sequence 46782, A
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c 755	13	86.7	6720	24	US-09-620-392-29779	Sequence 29779, A	828	13	86.7	24414	31	US-09-815-264-65310	Sequence 65310, A
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ALIGNMENTS

RESULT 1
PCT-US00-35491-9
; Sequence 9, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David D.
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
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; ORGANISM: Homo sapiens
PCT-US00-35491-9

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-750-609-9
; Sequence 9, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.


```
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-9

Query Match      100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 3
US-60-173-682-9
; Sequence 9, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-9

Query Match      100.0%; Score 15; DB 61; Length 15;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 4
US-09-440-302A-470
; Sequence 470, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302A-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 5
US-09-440-302B-470
; Sequence 470, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 6
US-09-440-302-470
; Sequence 470, Application US/09440302
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302-470

Query Match      100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15
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```
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302A-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 5
US-09-440-302B-470
; Sequence 470, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 6
US-09-440-302-470
; Sequence 470, Application US/09440302
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302-470

Query Match      100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15
```

RESULT 7
US-09-442-366A-309
; Sequence 309, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-309

Query Match 100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
DB 45 CCTTCTCGCCCTGTT 59

RESULT 8
US-09-698-012-481/c
; Sequence 481, Application US/09698012
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2002-001
; CURRENT APPLICATION NUMBER: US/09/698,012
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,166
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 9719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-698-012-481

Query Match 100.0%; Score 15; DB 27; Length 472;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
DB 76 CCTTCTCGCCCTGTT 62

RESULT 9
US-09-534-856-18784/c
; Sequence 18784, Application US/09534856
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED, AND

; TITLE OF INVENTION: EXTRACELLULAR MOLECULES
; FILE REFERENCE: PD-1015 CIP
; CURRENT APPLICATION NUMBER: US/09/534,856
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 26334
; SOFTWARE: PERL Program
; SEQ ID NO 18784
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inceyte ID No: hu01124269
; NAME/KEY: unsure
; LOCATION: 488
; OTHER INFORMATION: a, t, c, g, or other
US-09-534-856-18784

Query Match 100.0%; Score 15; DB 20; Length 510;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
DB 185 CCTTCTCGCCCTGTT 171

RESULT 10
US-60-230-445-2923
; Sequence 2923, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL000765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2923
; LENGTH: 592
; TYPE: DNA
; ORGANISM: HUMAN
US-60-230-445-2923

Query Match 100.0%; Score 15; DB 67; Length 592;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
DB 44 CCTTCTCGCCCTGTT 58

RESULT 11
US-09-948-933-4005/c
; Sequence 4005, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4005
; LENGTH: 601

; TYPE: DNA
 ; ORGANISM: Human
 US-09-948-933-4005

```
Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CCTTCTCGCCCTGTT 15
| | | | | | | | | | | | | | |
Db 27 CCTTCTCGCCCTGTT 13

RESULT 12
US-09-948-933-4006/c

```

; sequence 4006, Application US/05948933
; GENERAL INFORMATION:
;
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; DETECTION AND USES THEREOF
;

```

```

, FILE REFERENCE: CL000787
, CURRENT APPLICATION NUMBER: US/09/948,933
, CURRENT FILING DATE: 2001-09-10
, PRIOR APPLICATION NUMBER: 60/231,399
, PRIOR FILING DATE: 2000-09-08
, NUMBER OF SEQ ID NOS: 6404
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 4006
, LENGTH: 601

```

Query Match	100.0%;	Score 15;	DB 35;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 56;		

Qy	1	CCTTCTCGCCCTGTT	15
Db	126	CCTTCTCGCCCTGTT	112

RESULT 13
US-09-948-933-4007/c

```

; sequence 4007, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; DETECTION AND USES THEREOF

```

```

; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/7231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4007
; LENGTH: 601

```

Query Match	100.0%;	Score 15;	DB 35;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 56;		

Qy 1 CCTCTCGCCCTGTT 15
db 226 CCTCTCGCCCTGTT 212

RESULT 1A

US-09-948-933-4008/c
; Sequence 4008, Application US/09948933

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; GENERAL INFORMATION:
;
; APPLICANT: VENTER, J. Craig et al.
;
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID
;
; TITLE OF INVENTION: DETECTION AND USES THEREOF
;
; FILE REFERENCE: 01/00787

```

```

? FILE REFERENCE: CLO000787
? CURRENT APPLICATION NUMBER: US/09/948,933
? CURRENT FILING DATE: 2001-09-10
? PRIOR APPLICATION NUMBER: 60/231,399
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 6404
? SOFTWARE: FastSEQ for Windows Version 4.0
? SEQ ID NO 4008
? LENGTH: 601
?

```

Query Match	100.0%	Score 15;	DB 35;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 56;		
Matches 15;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy 1 CCTTCTCGCCCTGTT 15
db 337 CCTTCTCGCCCTGTT 323

RESULT 15

US-09-634-306B-7016/c
; Sequence 7016, Application US/09634306B

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827, 129
; CREATION DATE: 2000-05-24 00:00

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Query Match 100.0%; Score 15; DB 24; Length 817;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 15: Conservative 0; Mismatches 0; Indels

Qy 1 CCTTCTCGCCCTGTT 15
|||||
Db 138 CCTTCTCGCCCTGTT 124

Search completed: December 11, 2002, 20:27:12
Job time : 2589 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:10:08 ; Search time 88.5 Seconds
(without alignments)
121.821 Million cell updates/sec

Title: US-09-750-609-9
Perfect score: 15
Sequence: 1'ccttctgcgcctgtt 15

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 407964 seqs, 359371392 residues

Word size : 0
Total number of hits satisfying chosen parameters: 815928

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/US06_PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	2876	5	US-09-724-676-47407 Sequence 47407, A
2	15	100.0	2876	5	US-09-724-676A-47407 Sequence 47407, A
3	15	100.0	4338	5	US-09-724-676-24273 Sequence 24273, A
4	15	100.0	4338	5	US-09-724-676A-24273 Sequence 24273, A
5	15	100.0	4848	5	US-09-724-676-24268 Sequence 24268, A
6	15	100.0	4848	5	US-09-724-676A-24268 Sequence 24268, A
7	15	100.0	5222	6	US-10-133-937-67 Sequence 67, Appl
8	15	100.0	5589	5	US-09-724-676A-24272 Sequence 24272, A
9	15	100.0	5589	5	US-09-724-676A-24272 Sequence 24272, A
10	15	100.0	5642	5	US-09-724-676-24271 Sequence 24271, A
11	15	100.0	5642	5	US-09-724-676A-24271 Sequence 24271, A
12	15	100.0	6099	5	US-09-724-676-24267 Sequence 24267, A
13	15	100.0	6099	5	US-09-724-676A-24267 Sequence 24267, A
14	15	100.0	6152	5	US-09-724-676-24266 Sequence 24266, A
15	15	100.0	6152	5	US-09-724-676A-24266 Sequence 24266, A
16	13	86.7	1936	5	US-09-724-676-32136 Sequence 32136, A
17	13	86.7	1936	5	US-09-724-676A-32136 Sequence 32136, A
18	13	86.7	3590	5	US-09-724-676-24360 Sequence 24360, A
19	13	86.7	3590	5	US-09-724-676A-24360 Sequence 24360, A
20	13	86.7	7430	1	PCT-US02-32727-4 Sequence 4, Appl
21	13	86.7	7430	6	US-10-057-498-4 Sequence 4, Appl
22	13	86.7	276820	1	PCT-US02-32700-9 Sequence 9, Appl
23	13	86.7	276820	6	US-10-271-416-9 Sequence 9, Appl
24	12	80.0	152	6	US-10-203-138A-5521 Sequence 5521, Ap
25	12	80.0	187	5	US-09-513-999C-18000 Sequence 18000, A
26	12	80.0	237	5	US-09-513-999C-35434 Sequence 35434, A

12	80.0	252	5	US-09-134-000C-1966 Sequence 1966, Ap
12	80.0	261	5	US-09-513-999C-35759 Sequence 35759, A
12	80.0	354	5	US-09-513-999C-3109 Sequence 3109, Ap
12	80.0	355	5	US-09-513-999C-32746 Sequence 32746, A
12	80.0	396	6	US-10-203-138A-3420 Sequence 3420, Ap
12	80.0	425	5	US-09-513-999C-27979 Sequence 27979, A
12	80.0	445	6	US-10-203-138A-338 Sequence 338, App
12	80.0	479	5	US-09-724-676-15535 Sequence 15535, A
12	80.0	479	5	US-09-724-676A-15535 Sequence 15535, A
12	80.0	480	5	US-09-724-676-45475 Sequence 45475, A
12	80.0	480	5	US-09-724-676A-45475 Sequence 45475, A
12	80.0	550	6	US-10-255-536-212 Sequence 212, App
12	80.0	565	5	US-09-724-676-23454 Sequence 23454, A
12	80.0	565	5	US-09-724-676A-23454 Sequence 23454, A
12	80.0	590	7	US-60-425-113-14 Sequence 14, Appl
12	80.0	600	5	US-09-724-676-23455 Sequence 23455, A
12	80.0	600	5	US-09-724-676A-23455 Sequence 23455, A
12	80.0	611	6	US-10-266-131-2335 Sequence 2335, Ap
12	80.0	638	5	US-09-724-676-11461 Sequence 11461, A
12	80.0	638	5	US-09-724-676A-11461 Sequence 11461, A
12	80.0	667	6	US-10-152-319A-1167 Sequence 1167, Ap
12	80.0	687	5	US-09-724-676-23441 Sequence 23441, A
12	80.0	687	5	US-09-724-676A-23441 Sequence 23441, A
12	80.0	722	5	US-09-724-676-23435 Sequence 23435, A
12	80.0	722	5	US-09-724-676A-23435 Sequence 23435, A
12	80.0	723	5	US-09-724-676-15534 Sequence 15534, A
12	80.0	723	5	US-09-724-676A-15534 Sequence 15534, A
12	80.0	746	5	US-09-724-676-39258 Sequence 39258, A
12	80.0	746	5	US-09-724-676A-39258 Sequence 39258, A
12	80.0	795	5	US-09-724-676-23451 Sequence 23451, A
12	80.0	795	5	US-09-724-676A-23451 Sequence 23451, A
12	80.0	819	5	US-09-724-676-45474 Sequence 45474, A
12	80.0	819	5	US-09-724-676A-45474 Sequence 45474, A
12	80.0	890	5	US-09-724-676-23452 Sequence 23452, A
12	80.0	890	5	US-09-724-676A-23452 Sequence 23452, A
12	80.0	915	5	US-09-724-676-23426 Sequence 23426, A
12	80.0	915	5	US-09-724-676A-23426 Sequence 23426, A
12	80.0	917	5	US-09-724-676-23438 Sequence 23438, A
12	80.0	917	5	US-09-724-676A-23438 Sequence 23438, A
12	80.0	928	5	US-09-724-676-35066 Sequence 35066, A
12	80.0	928	5	US-09-724-676A-35066 Sequence 35066, A
12	80.0	950	5	US-09-724-676-23427 Sequence 23427, A
12	80.0	950	5	US-09-724-676A-23427 Sequence 23427, A
12	80.0	974	5	US-09-724-676-23445 Sequence 23445, A
12	80.0	974	5	US-09-724-676A-23445 Sequence 23445, A
12	80.0	1012	5	US-09-724-676-23439 Sequence 23439, A
12	80.0	1012	5	US-09-724-676A-23439 Sequence 23439, A
12	80.0	1030	5	US-09-724-676-23453 Sequence 23453, A
12	80.0	1030	5	US-09-724-676A-23453 Sequence 23453, A
12	80.0	1037	5	US-09-724-676-23456 Sequence 23456, A
12	80.0	1037	5	US-09-724-676A-23456 Sequence 23456, A
12	80.0	1039	5	US-09-724-676-23449 Sequence 23449, A
12	80.0	1039	5	US-09-724-676A-23449 Sequence 23449, A
12	80.0	1069	5	US-09-724-676-23446 Sequence 23446, A
12	80.0	1069	5	US-09-724-676A-23446 Sequence 23446, A
12	80.0	1072	5	US-09-724-676-23413 Sequence 23413, A
12	80.0	1072	5	US-09-724-676A-23413 Sequence 23413, A
12	80.0	1096	5	US-09-724-676-23431 Sequence 23431, A
12	80.0	1096	5	US-09-724-676A-23431 Sequence 23431, A
12	80.0	1145	5	US-09-724-676-23423 Sequence 23423, A
12	80.0	1145	5	US-09-724-676A-23423 Sequence 23423, A
12	80.0	1152	5	US-09-724-676-23440 Sequence 23440, A
12	80.0	1152	5	US-09-724-676A-23440 Sequence 23440, A
12	80.0	1161	5	US-09-724-676-23436 Sequence 23436, A
12	80.0	1161	5	US-09-724-676A-23436 Sequence 23436, A
12	80.0	1191	5	US-09-724-676-23432 Sequence 23432, A
12	80.0	1191	5	US-09-724-676A-23432 Sequence 23432, A
12	80.0	1204	5	US-09-724-676-35054 Sequence 35054, A
12	80.0	1204	5	US-09-724-676A-35054 Sequence 35054, A
12	80.0	1209	5	US-09-724-676-23447 Sequence 23447, A
12	80.0	1209	5	US-09-724-676A-23447 Sequence 23447, A
12	80.0	1218	5	US-09-724-676-23443 Sequence 23443, A
12	80.0	1218	5	US-09-724-676A-23443 Sequence 23443, A

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101	12	80.0	1236	5	US-09-724-676A-23450	Sequence 23450, A	174	12	80.0	1765	5	US-09-724-676-23416	Sequence 23416, A
102	12	80.0	1240	5	US-09-724-676-23424	Sequence 23424, A	175	12	80.0	1765	5	US-09-724-676A-23416	Sequence 23416, A
103	12	80.0	1240	5	US-09-724-676A-23424	Sequence 23424, A	176	12	80.0	1781	5	US-09-724-676-23428	Sequence 23428, A
104	12	80.0	1267	5	US-09-724-676-23410	Sequence 23410, A	177	12	80.0	1781	5	US-09-724-676A-23428	Sequence 23428, A
105	12	80.0	1267	5	US-09-724-676A-23410	Sequence 23410, A	178	12	80.0	1830	5	US-09-724-676-23420	Sequence 23420, A
106	12	80.0	1295	5	US-09-724-676-39263	Sequence 39263, A	179	12	80.0	1830	5	US-09-724-676A-23420	Sequence 23420, A
107	12	80.0	1295	5	US-09-724-676A-39263	Sequence 39263, A	180	12	80.0	1870	5	US-09-724-676-7693	Sequence 7693, Ap
108	12	80.0	1324	5	US-09-724-676-23417	Sequence 23417, A	181	12	80.0	1870	5	US-09-724-676A-7693	Sequence 7693, Ap
109	12	80.0	1324	5	US-09-724-676A-23417	Sequence 23417, A	182	12	80.0	1934	5	US-09-724-676-35064	Sequence 35064, A
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112	12	80.0	1331	5	US-09-724-676-23433	Sequence 23433, A	185	12	80.0	1952	5	US-09-724-676A-23407	Sequence 23407, A
113	12	80.0	1331	5	US-09-724-676-39262	Sequence 39262, A	186	12	80.0	1954	6	US-10-203-138A-4807	Sequence 4807, Ap
114	12	80.0	1331	5	US-09-724-676-39262	Sequence 39262, A	187	12	80.0	1955	5	US-09-724-676-35065	Sequence 35065, A
115	12	80.0	1331	5	US-09-724-676A-23433	Sequence 23433, A	188	12	80.0	1955	5	US-09-724-676A-35065	Sequence 35065, A
116	12	80.0	1331	5	US-09-724-676A-39262	Sequence 39262, A	189	12	80.0	1983	5	US-09-724-676-35057	Sequence 35057, A
117	12	80.0	1331	5	US-09-724-676A-39262	Sequence 39262, A	190	12	80.0	1983	5	US-09-724-676A-35057	Sequence 35057, A
118	12	80.0	1340	5	US-09-724-676-23429	Sequence 23429, A	191	12	80.0	2009	5	US-09-724-676-23414	Sequence 23414, A
119	12	80.0	1340	5	US-09-724-676A-23429	Sequence 23429, A	192	12	80.0	2009	5	US-09-724-676A-23414	Sequence 23414, A
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121	12	80.0	1358	5	US-09-724-676A-23437	Sequence 23437, A	194	12	80.0	2031	5	US-09-724-676A-35058	Sequence 35058, A
122	12	80.0	1362	5	US-09-724-676-23411	Sequence 23411, A	195	12	80.0	2163	5	US-09-724-676-17044	Sequence 17044, A
123	12	80.0	1362	5	US-09-724-676-39265	Sequence 39265, A	196	12	80.0	2163	5	US-09-724-676A-17044	Sequence 17044, A
124	12	80.0	1362	5	US-09-724-676-39267	Sequence 39267, A	197	12	80.0	2247	6	US-10-240-965-271	Sequence 271, App
125	12	80.0	1362	5	US-09-724-676A-23411	Sequence 23411, A	198	12	80.0	2319	5	US-09-724-676-17043	Sequence 17043, A
126	12	80.0	1362	5	US-09-724-676A-39265	Sequence 39265, A	199	12	80.0	2319	5	US-09-724-676A-17043	Sequence 17043, A
127	12	80.0	1362	5	US-09-724-676A-39267	Sequence 39267, A	200	12	80.0	2326	5	US-09-724-676-35060	Sequence 35060, A
128	12	80.0	1362	5	US-09-724-676A-39267	Sequence 39267, A	201	12	80.0	2326	5	US-09-724-676A-35060	Sequence 35060, A
129	12	80.0	1380	5	US-09-724-676A-23425	Sequence 23425, A	202	12	80.0	2347	5	US-09-724-676-35061	Sequence 35061, A
130	12	80.0	1389	5	US-09-724-676-23421	Sequence 23421, A	203	12	80.0	2347	5	US-09-724-676A-35061	Sequence 35061, A
131	12	80.0	1389	5	US-09-724-676A-23421	Sequence 23421, A	204	12	80.0	2451	5	US-09-724-676-7694	Sequence 7694, Ap
132	12	80.0	1415	5	US-09-724-676-23444	Sequence 23444, A	205	12	80.0	2451	5	US-09-724-676A-7694	Sequence 7694, Ap
133	12	80.0	1415	5	US-09-724-676A-23444	Sequence 23444, A	206	12	80.0	2454	6	US-10-240-965-108	Sequence 108, App
134	12	80.0	1419	5	US-09-724-676-23418	Sequence 23418, A	207	12	80.0	2485	6	US-10-152-319A-1901	Sequence 1901, Ap
135	12	80.0	1419	5	US-09-724-676A-23418	Sequence 23418, A	208	12	80.0	2856	6	US-10-240-965-202	Sequence 202, App
136	12	80.0	1467	5	US-09-724-676-39287	Sequence 39287, A	209	12	80.0	2793	6	US-10-152-319A-1649	Sequence 1649, Ap
137	12	80.0	1467	5	US-09-724-676A-39287	Sequence 39287, A	210	12	80.0	2976	6	US-10-194-163-36	Sequence 36, Appl
138	12	80.0	1480	5	US-09-724-676-23448	Sequence 23448, A	211	12	80.0	3010	5	US-09-724-676-7222	Sequence 7222, Ap
139	12	80.0	1480	5	US-09-724-676A-23448	Sequence 23448, A	212	12	80.0	3010	5	US-09-724-676A-7222	Sequence 7222, Ap
140	12	80.0	1498	5	US-09-724-676-39260	Sequence 39260, A	213	12	80.0	3063	5	US-09-724-676-33577	Sequence 33577, A
141	12	80.0	1498	5	US-09-724-676A-39260	Sequence 39260, A	214	12	80.0	3063	5	US-09-724-676A-33579	Sequence 33579, A
142	12	80.0	1502	5	US-09-724-676-23412	Sequence 23412, A	215	12	80.0	3067	5	US-09-724-676-33579	Sequence 33579, A
143	12	80.0	1502	5	US-09-724-676A-23412	Sequence 23412, A	216	12	80.0	3102	5	US-09-724-676A-7225	Sequence 7225, Ap
144	12	80.0	1503	5	US-09-724-676-39286	Sequence 39286, A	217	12	80.0	3102	5	US-09-724-676A-7225	Sequence 7225, Ap
145	12	80.0	1503	5	US-09-724-676-39286	Sequence 39286, A	218	12	80.0	3105	5	US-09-724-676-35040	Sequence 35040, A
146	12	80.0	1503	5	US-09-724-676A-39286	Sequence 39286, A	219	12	80.0	3105	5	US-09-724-676A-35040	Sequence 35040, A
147	12	80.0	1511	5	US-09-724-676A-39288	Sequence 39288, A	220	12	80.0	3289	5	US-09-724-676-35078	Sequence 35078, A
148	12	80.0	1511	5	US-09-724-676-23408	Sequence 23408, A	221	12	80.0	3289	5	US-09-724-676A-35078	Sequence 35078, A
149	12	80.0	1511	5	US-09-724-676A-23408	Sequence 23408, A	222	12	80.0	3629	6	US-10-289-757-9	Sequence 9, Appl1
150	12	80.0	1534	5	US-09-724-676-39259	Sequence 39259, A	223	12	80.0	3629	6	US-10-289-757-130	Sequence 130, App
151	12	80.0	1534	5	US-09-724-676-39261	Sequence 39261, A	224	12	80.0	3633	6	US-10-289-757-11	Sequence 11, Appl
152	12	80.0	1534	5	US-09-724-676A-39259	Sequence 39259, A	225	12	80.0	3735	6	US-10-289-757-132	Sequence 132, App
153	12	80.0	1537	5	US-09-724-676-23430	Sequence 23430, A	226	12	80.0	3735	6	US-09-724-676-33578	Sequence 33578, A
154	12	80.0	1537	5	US-09-724-676A-23430	Sequence 23430, A	227	12	80.0	3888	5	US-09-724-676A-33578	Sequence 33578, A
155	12	80.0	1537	5	US-09-724-676-23419	Sequence 23419, A	228	12	80.0	3888	5	US-09-724-676-35074	Sequence 35074, A
156	12	80.0	1559	5	US-09-724-676-23419	Sequence 23419, A	229	12	80.0	3952	5	US-09-724-676A-35074	Sequence 35074, A
157	12	80.0	1559	5	US-09-724-676A-23419	Sequence 23419, A	230	12	80.0	3952	5	US-09-724-676-35075	Sequence 35075, A
158	12	80.0	1568	5	US-09-724-676-23415	Sequence 23415, A	231	12	80.0	4000	5	US-09-724-676-35075	Sequence 35075, A
159	12	80.0	1568	5	US-09-724-676A-23415	Sequence 23415, A	232	12	80.0	4000	5	US-09-724-676A-35075	Sequence 35075, A
160	12	80.0	1586	5	US-09-724-676-23422	Sequence 23422, A	233	12	80.0	4117	6	US-10-152-319A-1994	Sequence 1994, Ap
161	12	80.0	1586	5	US-09-724-676A-23422	Sequence 23422, A	234	12	80.0	4295	5	US-09-724-676-35076	Sequence 35076, A
162	12	80.0	1591	5	US-09-724-676-35062	Sequence 35062, A	235	12	80.0	4295	5	US-09-724-676A-35076	Sequence 35076, A
163	12	80.0	1591	5	US-09-724-676A-35062	Sequence 35062, A	236	12	80.0	4316	5	US-09-724-676-35077	Sequence 35077, A
164	12	80.0	1602	5	US-09-724-676-23434	Sequence 23434, A	237	12	80.0	4316	5	US-09-724-676A-35077	Sequence 35077, A
165	12	80.0	1602	5	US-09-724-676A-23434	Sequence 23434, A	238	12	80.0	4344	5	US-09-724-676-35069	Sequence 35069, A
166	12	80.0	1622	5	US-09-724-676-27210	Sequence 27210, A	239	12	80.0	4344	5	US-09-724-676A-35069	Sequence 35069, A
167	12	80.0	1622	5	US-09-724-676A-27210	Sequence 27210, A	240	12	80.0	4392	5	US-09-724-676-35071	Sequence 35071, A
168	12	80.0	1639	5	US-09-724-676-35063	Sequence 35063, A	241	12	80.0	4392	5	US-09-724-676A-35071	Sequence 35071, A
169	12	80.0	1639	5	US-09-724-676A-35063	Sequence 35063, A	242	12	80.0	4336	5	US-09-724-676-24735	Sequence 24735, A
170	12	80.0	1659	5	US-09-724-676-23442	Sequence 23442, A	243	12	80.0	4336	5	US-09-724-676A-24735	Sequence 24735, A
171	12	80.0	1659	5	US-09-724-676A-23442	Sequence 23442, A	244	12	80.0	4687	5	US-09-724-676-35072	Sequence 35072, A
172	12	80.0	1708	5	US-09-724-676-23409	Sequence 23409, A	245	12	80.0	4687	5	US-09-724-676A-35072	Sequence 35072, A

c 246	12	80.0	4708	5	US-09-724-676-35073	Sequence 35073, A	319	11	73.3	874	5	US-09-724-676-11829	Sequence 11829, A
c 247	12	80.0	4708	5	US-09-724-676-35073	Sequence 35073, A	320	11	73.3	874	5	US-09-724-676A-11829	Sequence 11829, A
c 248	12	80.0	4733	5	US-09-724-676-17573	Sequence 17573, A	321	11	73.3	883	5	US-09-724-676-11824	Sequence 11824, A
c 249	12	80.0	4733	5	US-09-724-676A-17573	Sequence 17573, A	322	11	73.3	883	5	US-09-724-676A-11824	Sequence 11824, A
c 250	12	80.0	4942	5	US-09-724-676-17571	Sequence 17571, A	c 323	11	73.3	896	5	US-09-724-676-45866	Sequence 45866, A
c 251	12	80.0	4942	5	US-09-724-676A-17571	Sequence 17571, A	c 324	11	73.3	896	5	US-09-724-676A-45866	Sequence 45866, A
c 252	12	80.0	5343	5	US-09-724-676-17572	Sequence 17572, A	c 325	11	73.3	903	5	US-09-724-676-45852	Sequence 45852, A
c 253	12	80.0	5343	5	US-09-724-676A-17572	Sequence 17572, A	c 326	11	73.3	903	5	US-09-724-676A-45852	Sequence 45852, A
c 254	12	80.0	5648	6	US-10-152-319A-1694	Sequence 1694, Ap	c 327	11	73.3	937	5	US-09-724-676-10938	Sequence 10938, A
c 255	12	80.0	7753	5	US-09-724-676-42420	Sequence 42420, A	c 328	11	73.3	937	5	US-09-724-676A-10938	Sequence 10938, A
c 256	12	80.0	7753	5	US-09-724-676A-42420	Sequence 42420, A	c 329	11	73.3	956	5	US-09-724-676-45854	Sequence 45854, A
c 257	12	80.0	7791	5	US-09-724-676-42419	Sequence 42419, A	c 330	11	73.3	956	5	US-09-724-676A-45854	Sequence 45854, A
c 258	12	80.0	7791	5	US-09-724-676A-42419	Sequence 42419, A	c 331	11	73.3	978	5	US-09-724-676-34072	Sequence 34072, A
c 259	12	80.0	7880	5	US-09-724-676-42422	Sequence 42422, A	c 332	11	73.3	978	5	US-09-724-676A-34072	Sequence 34072, A
c 260	12	80.0	7880	5	US-09-724-676A-42422	Sequence 42422, A	c 333	11	73.3	992	5	US-09-724-676-18324	Sequence 18324, A
c 261	12	80.0	7918	5	US-09-724-676-42421	Sequence 42421, A	c 334	11	73.3	992	5	US-09-724-676A-18324	Sequence 18324, A
c 262	12	80.0	7918	5	US-09-724-676A-42421	Sequence 42421, A	c 335	11	73.3	1009	1	PCT-US02-32727-215	Sequence 215, App
c 263	12	80.0	9589	5	US-09-724-676-42416	Sequence 42416, A	c 336	11	73.3	1009	6	US-10-057-498-215	Sequence 215, App
c 264	12	80.0	9589	5	US-09-724-676A-42416	Sequence 42416, A	c 337	11	73.3	1038	5	US-09-724-676-11828	Sequence 11828, A
c 265	12	80.0	9716	5	US-09-724-676-42418	Sequence 42418, A	c 338	11	73.3	1038	5	US-09-724-676A-11828	Sequence 11828, A
c 266	12	80.0	9716	5	US-09-724-676A-42418	Sequence 42418, A	c 339	11	73.3	1047	5	US-09-724-676-11823	Sequence 11823, A
c 267	12	80.0	9754	5	US-09-724-676-42417	Sequence 42417, A	c 340	11	73.3	1047	5	US-09-724-676A-11823	Sequence 11823, A
c 268	12	80.0	9754	5	US-09-724-676A-42417	Sequence 42417, A	c 341	11	73.3	1056	5	US-09-724-676-18322	Sequence 18322, A
c 269	12	80.0	9905	6	US-10-270-144-3	Sequence 3, Appl	c 342	11	73.3	1056	5	US-09-724-676A-18322	Sequence 18322, A
c 270	12	80.0	18522	1	PCT-US02-32727-55	Sequence 55, Appl	c 343	11	73.3	1058	6	US-10-264-237-839	Sequence 839, App
c 271	12	80.0	18522	6	US-10-057-498-55	Sequence 55, Appl	c 344	11	73.3	1092	5	US-09-724-676-18321	Sequence 18321, A
c 272	11	73.3	139	6	US-10-203-138A-9135	Sequence 9135, Ap	c 345	11	73.3	1092	5	US-09-724-676A-18321	Sequence 18321, A
c 273	11	73.3	161	5	US-09-513-999C-17838	Sequence 17838, A	c 346	11	73.3	1139	5	US-09-724-676-10940	Sequence 10940, A
c 274	11	73.3	161	5	US-09-513-999C-17841	Sequence 17841, A	c 347	11	73.3	1139	5	US-09-724-676A-10940	Sequence 10940, A
c 275	11	73.3	164	5	US-09-513-999C-17419	Sequence 17419, A	c 348	11	73.3	1150	6	US-10-125-923A-519	Sequence 519, App
c 276	11	73.3	170	5	US-09-513-999C-18312	Sequence 18312, A	c 349	11	73.3	1150	6	US-10-205-892-519	Sequence 519, App
c 277	11	73.3	183	5	US-09-513-999C-16261	Sequence 16261, A	c 350	11	73.3	1150	6	US-10-174-575-519	Sequence 519, App
c 278	11	73.3	207	5	US-09-134-000C-2208	Sequence 2208, Ap	c 351	11	73.3	1154	5	US-09-724-676-11827	Sequence 11827, A
c 279	11	73.3	208	6	US-10-266-131-1622	Sequence 1062, Ap	c 352	11	73.3	1154	5	US-09-724-676A-11827	Sequence 11827, A
c 280	11	73.3	214	5	US-09-513-999C-18050	Sequence 18050, A	c 353	11	73.3	1156	5	US-09-724-676-18323	Sequence 18323, A
c 281	11	73.3	228	6	US-10-203-138A-9011	Sequence 9011, Ap	c 354	11	73.3	1156	5	US-09-724-676A-18323	Sequence 18323, A
c 282	11	73.3	236	6	US-10-284-499-14	Sequence 14, Appl	c 355	11	73.3	1163	5	US-09-724-676-11822	Sequence 11822, A
c 283	11	73.3	245	5	US-09-513-999C-31986	Sequence 31986, A	c 356	11	73.3	1163	5	US-09-724-676A-11822	Sequence 11822, A
c 284	11	73.3	251	5	US-09-513-999C-8420	Sequence 8420, Ap	c 357	11	73.3	1198	5	US-09-724-676-10939	Sequence 10939, A
c 285	11	73.3	276	5	US-09-513-999C-3085	Sequence 3085, Ap	c 358	11	73.3	1198	5	US-09-724-676A-10939	Sequence 10939, A
c 286	11	73.3	280	5	US-09-513-999C-27084	Sequence 27084, A	c 359	11	73.3	1237	5	US-09-724-676-11602	Sequence 11602, A
c 287	11	73.3	358	5	US-09-513-999C-27013	Sequence 27013, A	c 360	11	73.3	1237	5	US-09-724-676A-11602	Sequence 11602, A
c 288	11	73.3	362	6	US-10-203-138A-3875	Sequence 3875, Ap	c 361	11	73.3	1340	5	US-09-724-676-10937	Sequence 10937, A
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c 296	11	73.3	426	5	US-09-513-999C-16404	Sequence 16404, A	c 369	11	73.3	1429	5	US-09-724-676-34071	Sequence 34071, A
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c 303	11	73.3	560	5	US-09-724-676A-45863	Sequence 45863, A	c 376	11	73.3	1564	6	US-10-237-021-61	Sequence 61, Appl
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c 306	11	73.3	570	5	US-09-724-676A-44825	Sequence 44825, A	c 379	11	73.3	1608	1	PCT-US02-06147-6	Sequence 6, Appl
c 307	11	73.3	578	5	US-09-724-676-45860	Sequence 45860, A	c 380	11	73.3	1616	5	US-09-724-676-41734	Sequence 41734, A
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c 429	11	73.3	2271	5	US-09-724-676A-24692	Sequence 24692, A	c 502	11	73.3	3314	5	US-09-724-676A-47854	Sequence 47854, A
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c 559	11	73.3	4070	5	US-09-724-676-32170	Sequence 32170, A	c 632	11	73.3	5329	5	US-09-724-676-7104	Sequence 7104, Ap
c 560	11	73.3	4070	5	US-09-724-676A-32170	Sequence 32170, A	c 633	11	73.3	5329	5	US-09-724-676-7110	Sequence 7110, Ap
c 561	11	73.3	4072	5	US-09-724-676-41732	Sequence 41732, A	c 634	11	73.3	5329	5	US-09-724-676A-7104	Sequence 7104, Ap
c 562	11	73.3	4072	5	US-09-724-676A-41732	Sequence 41732, A	c 635	11	73.3	5329	5	US-09-724-676A-7110	Sequence 7110, Ap
c 563	11	73.3	4084	5	US-09-724-676-32179	Sequence 32179, A	c 636	11	73.3	5369	6	US-10-257-166-31	Sequence 31, Appl
c 564	11	73.3	4084	5	US-09-724-676A-32179	Sequence 32179, A	c 637	11	73.3	5506	5	US-09-724-676-7038	Sequence 7038, Ap
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c 566	11	73.3	4107	5	US-09-724-676A-45543	Sequence 45543, A	c 639	11	73.3	5542	5	US-09-724-676-7035	Sequence 7035, Ap
c 567	11	73.3	4134	5	US-09-724-676-7108	Sequence 7108, Ap	c 640	11	73.3	5542	5	US-09-724-676-7041	Sequence 7041, Ap
c 568	11	73.3	4134	5	US-09-724-676A-7108	Sequence 7108, Ap	c 641	11	73.3	5542	5	US-09-724-676A-7035	Sequence 7035, Ap
c 569	11	73.3	4147	5	US-09-724-676-32194	Sequence 32194, A	c 642	11	73.3	5542	5	US-09-724-676A-7041	Sequence 7041, Ap
c 570	11	73.3	4147	5	US-09-724-676A-32194	Sequence 32194, A	c 643	11	73.3	5576	6	US-10-240-453-136	Sequence 136, App
c 571	11	73.3	4157	5	US-09-404-026-9	Sequence 9, Appl	c 644	11	73.3	5626	5	US-09-724-676-7083	Sequence 7083, Ap
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c 573	11	73.3	4166	5	US-09-724-676-45538	Sequence 45538, A	c 646	11	73.3	5662	5	US-09-724-676-7022	Sequence 7022, Ap
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c 577	11	73.3	4170	5	US-09-724-676-7111	Sequence 7111, Ap	c 650	11	73.3	5705	5	US-09-724-676-7049	Sequence 7049, Ap
c 578	11	73.3	4170	5	US-09-724-676A-7105	Sequence 7111, Ap	c 651	11	73.3	5705	5	US-09-724-676A-7049	Sequence 7049, Ap
c 579	11	73.3	4170	5	US-09-724-676A-7111	Sequence 7111, Ap	c 652	11	73.3	5741	5	US-09-724-676-7046	Sequence 7046, Ap
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c 595	11	73.3	4345	5	US-09-724-676A-23240	Sequence 23240, A	c 668	11	73.3	6063	6	US-10-240-453-268	Sequence 268, App
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c 692	11	73.3	6900	5	US-09-724-676A-7051	Sequence 7051, App	c 765	10	66.7	262	5	US-09-513-999C-22885	Sequence 22885, A
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c 706	11	73.3	7474	5	US-09-724-676A-7050	Sequence 7050, App	c 779	10	66.7	337	5	US-09-513-999C-30472	Sequence 30472, A
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c 753	10	66.7	173	5	US-09-513-999C-34463	Sequence 34463, A	c 826	10	66.7	495	6	US-10-145-016A-191	Sequence 191, App
c 754	10	66.7	175	5	US-09-513-999C-20097	Sequence 20097, A	c 827	10	66.7	495	6	US-10-145-088A-191	Sequence 191, App
c 755	10	66.7	190	5	US-09-513-999C-10050	Sequence 10050, A	c 828	10	66.7	495	6	US-10-145-129A-191	Sequence 191, App
c 756	10	66.7	196	5	US-09-513-999C-25501	Sequence 25501, A	c 829	10	66.7	495	6	US-10-145-129A-191	Sequence 191, App

c 830	10	66.7	495	6	US-10-165-353A-191	Sequence 191, App	c 903	10	66.7	729	5	US-09-724-676A-6638	Sequence 6638, Ap
c 831	10	66.7	496	6	US-10-240-425-15	Sequence 15, App1	c 904	10	66.7	730	5	US-09-513-999C-762	Sequence 762, App
c 832	10	66.7	498	6	US-10-266-131-2148	Sequence 2148, Ap	c 905	10	66.7	732	5	US-09-724-676-6655	Sequence 6655, Ap
c 833	10	66.7	500	5	US-09-724-676-40442	Sequence 40442, A	c 906	10	66.7	732	5	US-09-724-676A-6655	Sequence 6655, Ap
c 834	10	66.7	500	5	US-09-724-676A-40442	Sequence 40442, A	c 907	10	66.7	735	5	US-09-134-000C-574	Sequence 574, App
c 835	10	66.7	505	6	US-10-194-163-376	Sequence 376, App	c 908	10	66.7	737	5	US-09-724-676-6669	Sequence 6669, Ap
c 836	10	66.7	509	5	US-09-724-676-38721	Sequence 38721, A	c 909	10	66.7	737	5	US-09-724-676A-6669	Sequence 6669, Ap
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c 892	10	66.7	691	5	US-09-724-676-21190	Sequence 21190, A	c 965	10	66.7	840	5	US-09-724-676-5177	Sequence 5177, Ap
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c 894	10	66.7	692	6	US-10-240-425-466	Sequence 466, App	c 967	10	66.7	841	5	US-09-724-676-42739	Sequence 42739, A
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c 980 10 66.7 848 5 US-09-724-676-6614 Sequence 6614, Ap
c 981 10 66.7 848 5 US-09-724-676A-6612 Sequence 6612, Ap
c 982 10 66.7 848 5 US-09-724-676A-6614 Sequence 6614, Ap
c 983 10 66.7 851 5 US-09-724-676-6610 Sequence 6610, Ap
c 984 10 66.7 851 5 US-09-724-676-6629 Sequence 6629, Ap
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c 987 10 66.7 851 5 US-09-724-676A-6610 Sequence 6610, Ap
c 988 10 66.7 851 5 US-09-724-676A-6629 Sequence 6629, Ap
c 989 10 66.7 851 5 US-09-724-676A-6631 Sequence 6631, Ap
c 990 10 66.7 851 5 US-09-724-676A-6675 Sequence 6675, Ap
c 991 10 66.7 854 5 US-09-724-676-6625 Sequence 6625, Ap
c 992 10 66.7 854 5 US-09-724-676-6627 Sequence 6627, Ap
c 993 10 66.7 854 5 US-09-724-676-14961 Sequence 14961, A
c 994 10 66.7 854 5 US-09-724-676A-6625 Sequence 6625, Ap
c 995 10 66.7 854 5 US-09-724-676A-6627 Sequence 6627, Ap
c 996 10 66.7 854 5 US-09-724-676A-14961 Sequence 14961, A
c 997 10 66.7 863 5 US-09-724-676-72 Sequence 72, Appl
c 998 10 66.7 863 5 US-09-724-676A-72 Sequence 72, Appl
c 999 10 66.7 864 5 US-09-724-676-6633 Sequence 6633, Ap
c1000 10 66.7 864 5 US-09-724-676-6635 Sequence 6635, Ap

ALIGNMENTS

RESULT 1
US-09-724-676-47407
; Sequence 47407, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47407
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-47407

Query Match 100.0%; Score 15; DB 5; Length 2876;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
Db 1422 CCTTCTCGCCCTGTT 1436
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RESULT 2
US-09-724-676A-47407
; Sequence 47407, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47407
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-47407

Query Match 100.0%; Score 15; DB 5; Length 2876;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
Db 1422 CCTTCTCGCCCTGTT 1436
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RESULT 3
US-09-724-676-24273/c
; Sequence 24273, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24273
; LENGTH: 4338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24273

Query Match 100.0%; Score 15; DB 5; Length 4338;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
Db 2821 CCTTCTCGCCCTGTT 2807
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RESULT 4
US-09-724-676A-24273/c
; Sequence 24273, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24273
; LENGTH: 4338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24273

Query Match 100.0%; Score 15; DB 5; Length 4338;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
Db 2821 CCTTCTCGCCCTGTT 2807
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RESULT 5
US-09-724-676-24268/c
; Sequence 24268, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24268

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; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24268

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 6
US-09-724-676A-24268/c
; Sequence 24268, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24268
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24268

Query Match      100.0%; Score 15; DB 5; Length 4848;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 7
US-10-133-937-67/c
; Sequence 67, Application US/10133937
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 5222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-67

Query Match      100.0%; Score 15; DB 6; Length 5222;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-09-724-676-24272/c
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; Sequence 24272, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24272
; LENGTH: 5589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24272

Query Match      100.0%; Score 15; DB 5; Length 5589;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 9
US-09-724-676A-24272/c
; Sequence 24272, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24272
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24272

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; Sequence 24271, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
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; SEQ ID NO 24271
; LENGTH: 5642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24271

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 11

US-09-724-676A-24271/c
; Sequence 24271, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24271
; LENGTH: 5642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24271

Query Match 100.0%; Score 15; DB 5; Length 5642;

Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 12

US-09-724-676-24267/c
; Sequence 24267, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24267
; LENGTH: 6099
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;

Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 13

US-09-724-676A-24267/c
; Sequence 24267, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24267
; LENGTH: 6099
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;

Best Local Similarity 100.0%; Pred. No. 1.7;
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US-09-724-676-24266/c
; Sequence 24266, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24266
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24266

Query Match

100.0%; Score 15; DB 5; Length 6152;

Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 15

US-09-724-676A-24266/c
; Sequence 24266, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
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; ORGANISM: Homo sapiens
US-09-724-676A-24266

Query Match

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3331 CCTTCTCGCCCTGTT 3317

Search completed: December 11, 2002, 20:30:07
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:30:57 ; Search time 2560.5 Seconds
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Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 ccttcctccctgtt 15

Scoring table: IDENTITY_NUC
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	15	100.0	15	61	US-60-173-682-10	Sequence 10, Appl
4	15	100.0	41	1	PCT-US00-35491-5	Sequence 5, Appl
5	15	100.0	41	1	PCT-US00-35491-6	Sequence 6, Appl
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-35491-10

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Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCTGTT 15
Db 1 CCTTCTCCCTGTT 15

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; Sequence 10, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27-2
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456

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; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-10

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Query Match 100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCTGTT 15
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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-10

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Query Match 100.0%; Score 15; DB 61; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
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; Sequence 5, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.0%; Pred. No. 3e+03;

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PCT-US00-35491-6/c

; Sequence 6, Application PC/TUS0035491

; GENERAL INFORMATION:

; APPLICANT: Robertson, David

; APPLICANT: Blakely, Randy D.

; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND

; FILE REFERENCE: Attorney Docket No. 1242-27 PCT

; CURRENT APPLICATION NUMBER: PCT/US00/35491

; PRIOR FILING DATE: 2000-12-28

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; PRIOR APPLICATION NUMBER: 60/173,682

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; SOFTWARE: PatentIn Ver. 2.0

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; TYPE: DNA

; ORGANISM: Homo sapiens

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Query Match 100.0%; Score 15; DB 1; Length 41;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application US/09750609

; GENERAL INFORMATION:

; APPLICANT: Robertson, David

; APPLICANT: Blakely, Randy D.

; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND

; FILE REFERENCE: Attorney Docket No. 1242-27-2-2

; CURRENT APPLICATION NUMBER: US/09/750,609

; PRIOR FILING DATE: 2000-12-28

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; NUMBER OF SEQ ID NOS: 40

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; SEQ ID NO 5

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; TYPE: DNA

; ORGANISM: Homo sapiens

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; Sequence 6, Application US/09750609

; GENERAL INFORMATION:

; APPLICANT: Robertson, David

; APPLICANT: Blakely, Randy D.

; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND

; FILE REFERENCE: Attorney Docket No. 1242-27-2-2

; CURRENT APPLICATION NUMBER: US/09/750,609

; CURRENT FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: 60/175,456

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: 60/173,682

; PRIOR FILING DATE: 1999-12-29

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 41

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-750-609-6

Query Match 100.0%; Score 15; DB 29; Length 41;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||
Db 28 CCTTCTCCCTGTT 14

RESULT 8

US-60-173-682-5

; Sequence 5, Application US/60173682

; GENERAL INFORMATION:

; APPLICANT: Robertson, David

; APPLICANT: Blakely, Randy D.

; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND

; FILE REFERENCE: Attorney Docket No. 1242-27

; CURRENT APPLICATION NUMBER: US/60/173,682

; CURRENT FILING DATE: 1999-12-29

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 41

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-173-682-5

Query Match 100.0%; Score 15; DB 61; Length 41;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
|||||
Db 14 CCTTCTCCCTGTT 28

RESULT 9

US-60-173-682-6/c

; Sequence 6, Application US/60173682

; GENERAL INFORMATION:

; APPLICANT: Robertson, David

; APPLICANT: Blakely, Randy D.

; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND

; FILE REFERENCE: Attorney Docket No. 1242-27

; CURRENT APPLICATION NUMBER: US/60/173,682

; CURRENT FILING DATE: 1999-12-29

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 41

; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-6

Query Match 100.0%; Score 15; DB 61; Length 41;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCTGTT 15
Db 28 CCTTCTCCCTGTT 14

RESULT 10
US-09-306-349-2932
; Sequence 2932, Application US/09306349
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15367)B
; CURRENT APPLICATION NUMBER: US/09/306,349
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 53893
; SEQ ID NO 2932
; LENGTH: 197
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 701040886H1
US-09-306-349-2932

Query Match 100.0%; Score 15; DB 17; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCTGTT 15
Db 3 CCTTCTCCCTGTT 17

RESULT 11
US-09-960-481-2932
; Sequence 2932, Application US/09960481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15367)C
; CURRENT APPLICATION NUMBER: US/09/960,481
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/306,349
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 53893
; SEQ ID NO 2932
; LENGTH: 197
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1).(197)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 701040886H1
US-09-960-481-2932

Query Match 100.0%; Score 15; DB 36; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCTGTT 15
Db 3 CCTTCTCCCTGTT 17

RESULT 12
US-09-076-667-2907
; Sequence 2907, Application US/09076667
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: HUMAN BRAIN
; NUMBER OF SEQUENCES: 4483
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,667
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0370P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 2907:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 3268389H1
US-09-076-667-2907

Query Match 100.0%; Score 15; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCTGTT 15
Db 75 CCTTCTCCCTGTT 89

RESULT 13
US-09-540-229-47840
; Sequence 47840, Application US/09540229
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.

```
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
; FILE REFERENCE: PD-1033 CIP
; CURRENT APPLICATION NUMBER: US/09/540,229
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 193582
; SOFTWARE: PERL Program
; SEQ ID NO 47840
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00535318
; NAME/KEY: unsure
; LOCATION: 211
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-229-47840

Query Match      100.0%; Score 15; DB 21; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCTGTT 15
Db 75 CCTTCTCCCCCTGTT 89

RESULT 14
US-60-048-002-2907
; Sequence 2907, Application US/60048002
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: HUMAN BRAIN
; NUMBER OF SEQUENCES: 4483
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/048,002
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0370P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 2907:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 3268389H1
US-60-048-002-2907

Query Match      100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
Db 75 CCTTCTCCCCCTGTT 89

RESULT 15
US-09-637-890-4668/c
; Sequence 4668, Application US/09637890
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine A.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Vasicek, Tom
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Villevall, Jean-Luc M. G.
; APPLICANT: Cepada, Mario
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1152-001
; CURRENT APPLICATION NUMBER: US/09/637,890
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,939
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 10217
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4668
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-637-890-4668

Query Match      100.0%; Score 15; DB 24; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
Db 168 CCTTCTCCCCCTGTT 154

Search completed: December 11, 2002, 16:56:15
Job time : 2561.5 secs
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;; PRIOR APPLICATION NUMBER: US 60/205,515
;; PRIOR FILING DATE: 2000-05-19
;; NUMBER OF SEQ ID NOS: 2876
;; SOFTWARE: PatentIn Ver. 3.1
;; SEQ ID NO 1036
;; LENGTH: 2520
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (99)-(99)
;; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1036

Query Match 100.0%; Score 15; DB 6; Length 2520;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
| | | | | | | | | | | | | | |
DB 1062 CCTTCTCCCCCTGTT 1076

RESULT 3
US-09-620-607B-1245/C
; Sequence 1245, Application US/09620607B
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0032-USA
; CURRENT APPLICATION NUMBER: US/09/620,607B
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/144942
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 1848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1245
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-620-607B-1245

Query Match 93.3%; Score 14; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCTCCCCCTGTT 15
| | | | | | | | | | | | | | |
DB 88 CTCTCTCCCCCTGTT 75

RESULT 4
US-09-724-676-38339
; Sequence 38339, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38339
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-38339

Query Match 93.3%; Score 14; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCCCCCTGT 14
| | | | | | | | | | | | | | |
DB 444 CCTTCTCCCCCTGT 457

RESULT 5
US-09-724-676A-38339
; Sequence 38339, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38339
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-38339

Query Match 93.3%; Score 14; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
| | | | | | | | | | | | | | |
DB 444 CCTTCTCCCCCTGT 457

RESULT 6
US-09-724-676-24274/C
; Sequence 24274, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24274
; LENGTH: 1030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24274

Query Match 93.3%; Score 14; DB 5; Length 1030;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
| | | | | | | | | | | | | | |
DB 692 CCTTCTCCCCCTGT 679

RESULT 7
US-09-724-676A-24274/C
; Sequence 24274, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24274
; LENGTH: 1030
; TYPE: DNA
US-09-724-676A-24274

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; ORGANISM: Homo sapiens
US-09-724-676A-24274

Query Match          93.3%; Score 14; DB 5; Length 1030;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
    |||||
Db 692 CCTTCTCCCCCTGT 679

RESULT 8
US-09-724-676-2247/c
; Sequence 2247, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2247

Query Match          93.3%; Score 14; DB 5; Length 1509;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
    |||||
Db 831 CCTTCTCCCCCTGT 818

RESULT 9
US-09-724-676A-2247/c
; Sequence 2247, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2247

Query Match          93.3%; Score 14; DB 5; Length 1509;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
    |||||
Db 831 CCTTCTCCCCCTGT 818

RESULT 10
US-09-724-676-2234/c
; Sequence 2234, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2234
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2234

Query Match          93.3%; Score 14; DB 5; Length 1667;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
    |||||
Db 989 CCTTCTCCCCCTGT 976

RESULT 11
US-09-724-676A-2234/c
; Sequence 2234, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2234
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2234

Query Match          93.3%; Score 14; DB 5; Length 1667;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
    |||||
Db 989 CCTTCTCCCCCTGT 976

RESULT 12
US-09-724-676-2221/c
; Sequence 2221, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2221
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2221

Query Match          93.3%; Score 14; DB 5; Length 1712;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
    |||||
Db 1034 CCTTCTCCCCCTGT 1021

RESULT 13
US-09-724-676A-2221/c
; Sequence 2221, Application US/09724676A
; GENERAL INFORMATION:
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;; APPLICANT: Compugen LTD
;; TITLE OF INVENTION: Variants of alternative splicing
;; FILE REFERENCE: 129181.4 Compugen
;; CURRENT APPLICATION NUMBER: US/09/724,676A
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 97222
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2221
;; LENGTH: 1712
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-724-676A-2221

Query Match 93.3%; Score 14; DB 5; Length 1712;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
| | | | | | | | | |
Db 1034 CCTTCTCCCCCTGT 1021

RESULT 14
US-09-724-676-2240/c
; Sequence 2240, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2240
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
| | | | | | | | | |
Db 831 CCTTCTCCCCCTGT 818

RESULT 15
US-09-724-676A-2240/c
; Sequence 2240, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2240
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
| | | | | | | | | |
Db 831 CCTTCTCCCCCTGT 818

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:01:38 ; Search time 2560 Seconds
(without alignments)
147.319 Million cell updates/sec

Title: US-09-750-609-10
Perfect score: 15
Sequence: 1 cttctcccccgttt 15

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15	100.0	15	29	US-09-750-609-10
3	15	100.0	15	61	US-60-173-682-10
4	15	100.0	41	1	PCT-US00-35491-5
5	15	100.0	41	1	PCT-US00-35491-6
6	15	100.0	41	29	US-09-750-609-5
7	15	100.0	41	29	US-09-750-609-6
8	15	100.0	41	61	US-60-173-682-5
9	15	100.0	41	61	US-60-173-682-6
10	15	100.0	197	17	US-09-306-349-2932
11	15	100.0	197	36	US-09-960-481-2932
12	15	100.0	248	14	US-09-076-667-2907
13	15	100.0	248	21	US-09-540-229-47840
14	15	100.0	248	48	US-60-048-002-2907
15	15	100.0	327	24	US-09-637-890-4668
16	15	100.0	327	25	US-09-652-918-2311
17	15	100.0	355	33	US-09-865-439A-106084
18	15	100.0	355	64	US-60-207-458-150004
19	15	100.0	376	22	US-09-552-086-8529
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21	15	100.0	393	16	US-09-293-972-23661

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	23	15	100.0	395	22	US-09-565-240-8098	Sequence 8098, Ap	c	96	15	100.0	4215	30	US-09-785-276A-22739	Sequence 22739, A
	24	15	100.0	400	18	US-09-465-877-11236	Sequence 11236, A	c	97	15	100.0	4215	30	US-09-785-276A-228587	Sequence 228587, A
	25	15	100.0	400	34	US-09-906-555-11236	Sequence 11236, A	c	98	15	100.0	4364	65	US-60-213-359-651	Sequence 651, App
	26	15	100.0	410	31	US-09-804-730-2488	Sequence 2488, Ap	c	99	15	100.0	4364	76	US-60-324-185-11950	Sequence 11950, A
	27	15	100.0	410	62	US-60-189-657-2488	Sequence 2488, Ap	c	100	15	100.0	4366	28	US-09-705-426-396	Sequence 396, App
c	28	15	100.0	416	25	US-09-652-918-2079	Sequence 2079, Ap	c	101	15	100.0	4366	61	US-60-172-360-18466	Sequence 18466, A
	29	15	100.0	432	18	US-09-465-877-13056	Sequence 13056, A	c	102	15	100.0	15857	1	PCT-US01-01341-1704	Sequence 1704, Ap
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	35	15	100.0	452	34	US-09-906-555-10936	Sequence 10936, A	c	108	15	100.0	13311	65	US-60-212-664-230	Sequence 230, App
	36	15	100.0	456	20	US-09-534-846B-25592	Sequence 25592, A	c	109	15	100.0	391912	69	US-60-258-251-25	Sequence 25, Appl1
	37	15	100.0	463	29	US-09-726-806-1928	Sequence 1928, Ap	c	110	14	93.3	25	79	US-60-353-987-723033	Sequence 723033, A
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c 184	14	93.3	486	19	US-09-521-640-27966	Sequence 27966,	c 257	14	93.3	2658	27	US-09-698-010-14027	Sequence 14027, A
c 185	14	93.3	490	29	US-09-726-807-1149	Sequence 1149, Ap	c 258	14	93.3	2658	29	US-09-721-589-6200	Sequence 6200, Ap
c 186	14	93.3	491	24	US-09-634-306B-287701	Sequence 287701,	c 259	14	93.3	2658	29	US-09-726-788-6727	Sequence 6727, Ap
c 187	14	93.3	491	38	US-10-027-632-287701	Sequence 287701,	c 260	14	93.3	2658	29	US-09-726-807-3209	Sequence 3209, Ap
c 188	14	93.3	496	34	US-09-920-953-8229	Sequence 8229, Ap	c 261	14	93.3	2740	80	US-09-629-469A-10598	Sequence 74, Appl
c 189	14	93.3	497	6	US-08-276-163B-7505	Sequence 7505, Ap	c 262	14	93.3	2775	24	US-09-629-469A-10598	Sequence 10998, A
c 190	14	93.3	497	6	US-08-276-163B-7505	Sequence 7505, Ap	c 263	14	93.3	2951	61	US-09-172-373-7893	Sequence 7893, Ap
c 191	14	93.3	497	32	US-09-840-145-7505	Sequence 7505, Ap	c 264	14	93.3	2953	24	US-09-634-306B-112395	Sequence 112395,
c 192	14	93.3	509	25	US-09-649-161-7119	Sequence 7119, Ap	c 265	14	93.3	2953	38	US-10-027-632-112395	Sequence 112395,
c 193	14	93.3	509	25	US-09-649-161-7119	Sequence 7119, Ap	c 266	14	93.3	2977	29	US-09-758-455-99	Sequence 99, Appl
c 194	14	93.3	561	15	US-09-154-625-220	Sequence 220, App	c 267	14	93.3	2977	42	US-10-231-351-99	Sequence 99, Appl
c 195	14	93.3	561	25	US-09-644-873-6239	Sequence 6239, Ap	c 268	14	93.3	3250	80	US-09-360-207-40578	Sequence 40578, A
c 196	14	93.3	561	32	US-09-836-373-230	Sequence 230, App	c 269	14	93.3	3286	38	US-10-043-487-99	Sequence 99, Appl
c 197	14	93.3	574	38	US-10-029-386-12679	Sequence 12679, A	c 270	14	93.3	3308	24	US-09-620-392-24732	Sequence 24732, A
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c 203	14	93.3	594	33	US-09-864-761-13104	Sequence 13104, A	c 276	14	93.3	3983	42	US-10-212-054-1615	Sequence 1615, Ap
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c 214	14	93.3	658	24	US-09-634-306B-142204	Sequence 142204,	c 287	14	93.3	5928	61	US-09-620-392-8503	Sequence 8503, Ap
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c 317	14	93.3	13169	28	US-09-702-134-25267	Sequence 25267, A	390	13	86.7	209	1	PCT-US01-00663-24656	Sequence 24656, A
c 318	14	93.3	13169	31	US-09-815-364-64690	Sequence 64690, A	391	13	86.7	209	33	US-09-864-761-23557	Sequence 23557, A
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c 323	14	93.3	16877	30	US-09-764-874-12825	Sequence 12825, A	396	13	86.7	209	42	US-10-203-135-23512	Sequence 23512, A
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c 463	13	86.7	273	13	US-08-937-142-1291	Sequence 1291, Ap	536	13	86.7	335	29	US-09-733-811A-20037	Sequence 20037, A
c 464	13	86.7	273	14	US-09-035-172-6664	Sequence 6664, Ap	537	13	86.7	335	33	US-09-898-888-42231	Sequence 42231, A
c 465	13	86.7	273	15	US-09-189-834-337	Sequence 337, App	538	13	86.7	335	33	US-09-898-888A-42231	Sequence 42231, A
c 466	13	86.7	273	15	US-09-189-834A-337	Sequence 337, App	539	13	86.7	335	36	US-09-975-640-20037	Sequence 20037, A
c 467	13	86.7	273	20	US-09-534-840-3042	Sequence 3042, Ap	540	13	86.7	335	36	US-09-975-640A-20037	Sequence 20037, A
c 468	13	86.7	273	20	US-09-535-896-15584	Sequence 15584, A	c 541	13	86.7	337	17	US-09-332-782-11470	Sequence 11470, A
c 469	13	86.7	273	21	US-09-540-2108-8735	Sequence 8735, Ap	542	13	86.7	337	17	US-09-362-510-32072	Sequence 32072, A
c 470	13	86.7	273	34	US-09-912-292-18493	Sequence 18493, A	543	13	86.7	337	17	US-09-362-510A-32072	Sequence 32072, A
c 471	13	86.7	276	20	US-09-534-840-3044	Sequence 3044, Ap	c 544	13	86.7	337	19	US-09-515-694-11470	Sequence 11470, A
c 472	13	86.7	276	20	US-09-535-896-1824	Sequence 1824, Ap	545	13	86.7	337	29	US-09-724-750-7131	Sequence 7131, Ap
c 473	13	86.7	281	21	US-09-540-222-155393	Sequence 155393, A	c 546	13	86.7	337	33	US-09-867-701-10110	Sequence 10110, A
c 474	13	86.7	281	58	US-60-141-232-1591	Sequence 1591, Ap	547	13	86.7	337	33	US-09-867-701-10110	Sequence 10110, A
c 475	13	86.7	283	20	US-09-534-840-3041	Sequence 3041, Ap	548	13	86.7	337	61	US-60-171-431-7131	Sequence 32072, A
c 476	13	86.7	283	21	US-09-540-768-56324	Sequence 56324, A	c 549	13	86.7	337	61	US-60-171-431-7131	Sequence 32072, A
c 477	13	86.7	285	18	US-09-417-507-9590	Sequence 9590, Ap	c 550	13	86.7	337	64	US-09-207-484-10110	Sequence 10110, A
c 478	13	86.7	285	33	US-09-867-701-4769	Sequence 4769, Ap	c 551	13	86.7	340	14	US-09-076-897-1595	Sequence 1595, Ap
c 479	13	86.7	285	64	US-60-207-484-4769	Sequence 4769, Ap	c 552	13	86.7	340	14	US-09-076-897A-1595	Sequence 1595, Ap
c 480	13	86.7	286	14	US-09-070-695A-2154	Sequence 2154, Ap	c 553	13	86.7	340	14	US-09-076-897B-1595	Sequence 1595, Ap
c 481	13	86.7	286	20	US-09-534-858-4461	Sequence 4461, Ap	c 554	13	86.7	340	63	US-09-197-872-25027	Sequence 25027, A
c 482	13	86.7	286	20	US-09-535-896-15618	Sequence 15618, A	555	13	86.7	342	29	US-09-724-750-4861	Sequence 4861, Ap
c 483	13	86.7	286	54	US-60-108-282-1281	Sequence 1281, Ap	556	13	86.7	342	61	US-60-171-431-4861	Sequence 4861, Ap
c 484	13	86.7	289	34	US-09-920-953-11	Sequence 11, Appl	c 557	13	86.7	343	19	US-09-521-640-261885	Sequence 261885, A
c 485	13	86.7	292	19	US-09-522-304-522	Sequence 522, App	c 558	13	86.7	343	58	US-60-140-769-47671	Sequence 47671, A
c 486	13	86.7	292	21	US-09-540-213-30950	Sequence 30950, A	c 559	13	86.7	343	63	US-60-197-872-13522	Sequence 13522, A
c 487	13	86.7	292	29	US-09-724-750-9042	Sequence 9042, Ap	c 560	13	86.7	344	6	US-08-221-623A-305	Sequence 305, App
c 488	13	86.7	292	61	US-60-171-431-9042	Sequence 9042, Ap	561	13	86.7	344	6	US-08-221-623B-305	Sequence 305, App
c 489	13	86.7	292	69	US-60-253-652-26104	Sequence 26104, A	562	13	86.7	344	6	US-08-221-623D-305	Sequence 305, App
c 490	13	86.7	294	21	US-09-540-212A-58952	Sequence 58952, A	563	13	86.7	344	14	US-09-076-897-1504	Sequence 1504, Ap
c 491	13	86.7	297	21	US-09-540-212A-49890	Sequence 49890, A	564	13	86.7	344	14	US-09-076-897A-1504	Sequence 1504, Ap
c 492	13	86.7	297	29	US-09-724-750-715	Sequence 715, App	565	13	86.7	344	14	US-09-076-897B-1504	Sequence 1504, Ap
c 493	13	86.7	297	61	US-60-171-431-715	Sequence 715, App	566	13	86.7	344	14	US-09-076-897C-1504	Sequence 1504, Ap
c 494	13	86.7	301	20	US-09-534-840-13234	Sequence 13234, A	567	13	86.7	344	34	US-09-912-293-2624	Sequence 2624, Ap
c 495	13	86.7	303	29	US-09-724-547-376	Sequence 376, App	c 568	13	86.7	345	62	US-60-180-489-4911	Sequence 4911, A
c 496	13	86.7	306	29	US-09-732-630-2622	Sequence 2622, Ap	569	13	86.7	346	18	US-09-436-762A-37703	Sequence 37703, A
c 497	13	86.7	309	56	US-60-125-818-8823	Sequence 8823, Ap	c 570	13	86.7	346	63	US-60-192-746-1026	Sequence 1026, Ap
c 498	13	86.7	310	69	US-60-253-456-26307	Sequence 26307, A	c 571	13	86.7	346	63	US-60-194-109-746	Sequence 746, App
c 499	13	86.7	311	18	US-09-489-036-25930	Sequence 25930, A	c 572	13	86.7	347	19	US-09-515-128-14929	Sequence 14929, A
c 500	13	86.7	311	19	US-09-528-409-57546	Sequence 57546, A	573	13	86.7	347	25	US-09-654-617-374866	Sequence 374866, A
c 501	13	86.7	311	35	US-09-933-524-57546	Sequence 57546, A	574	13	86.7	347	27	US-09-684-016-374866	Sequence 374866, A
c 502	13	86.7	311	35	US-09-933-524A-57546	Sequence 57546, A	c 575	13	86.7	347	29	US-09-721-544-14929	Sequence 14929, A
c 503	13	86.7	311	35	US-09-943-143-25930	Sequence 25930, A	c 576	13	86.7	347	31	US-09-823-241-3154	Sequence 3154, Ap
c 504	13	86.7	315	28	US-09-712-363-96	Sequence 96, Appl	c 577	13	86.7	351	19	US-09-321-640-192443	Sequence 192443, A
c 505	13	86.7	316	25	US-09-684-617-307305	Sequence 307305, A	c 578	13	86.7	351	58	US-60-140-769-19699	Sequence 19699, A
c 506	13	86.7	316	27	US-09-684-016-307305	Sequence 307305, A	c 579	13	86.7	353	38	US-10-050-759-384	Sequence 384, App
c 507	13	86.7	317	19	US-09-521-640-257731	Sequence 257731, A	c 580	13	86.7	353	63	US-60-197-872-20890	Sequence 20890, A
c 508	13	86.7	317	19	US-09-521-640-250714	Sequence 250714, A	c 581	13	86.7	353	26	US-09-663-779-3580	Sequence 3580, Ap
c 509	13	86.7	317	58	US-60-140-769-45112	Sequence 45112, A	c 582	13	86.7	355	23	US-09-619-643-20235	Sequence 20235, A
c 510	13	86.7	317	58	US-60-140-769-45112	Sequence 45112, A	c 583	13	86.7	359	58	US-60-145-148-3817	Sequence 3817, Ap
c 511	13	86.7	320	23	US-09-606-977-50854	Sequence 50854, A	c 584	13	86.7	360	17	US-09-359-067-7964	Sequence 7964, Ap
c 512	13	86.7	322	1	PCR-US01-01349-6313	Sequence 6313, App	c 585	13	86.7	360	60	US-60-169-840-150	Sequence 150, App
c 513	13	86.7	322	1	PCR-US01-01345-618	Sequence 618, App	c 586	13	86.7	363	20	US-09-535-896-1823	Sequence 1823, Ap
c 514	13	86.7	322	17	US-09-342-069-3983	Sequence 3983, Ap	c 587	13	86.7	363	61	US-60-172-375-7395	Sequence 7395, Ap
c 515	13	86.7	322	17	US-09-342-069A-3983	Sequence 3983, Ap	c 588	13	86.7	363	17	US-09-371-805-3643	Sequence 3643, Ap
c 516	13	86.7	322	30	US-09-764-891-6313	Sequence 6313, Ap	c 589	13	86.7	364	17	US-09-371-805-3643	Sequence 3643, Ap
c 517	13	86.7	322	30	US-09-764-892-618	Sequence 618, App	c 590	13	86.7	364	19	US-09-528-409-92789	Sequence 92789, A
c 518	13	86.7	322	32	US-09-834-366-33738	Sequence 33738, A	c 591	13	86.7	364	35	US-09-933-524-92789	Sequence 92789, A
c 519	13	86.7	322	42	US-10-205-428-618	Sequence 618, App	c 592	13	86.7	364	35	US-09-933-524A-92789	Sequence 92789, A
c 520	13	86.7	322	63	US-60-197-873-33738	Sequence 33738, A	c 593	13	86.7	365	17	US-09-362-510-29944	Sequence 29944, A
c 521	13	86.7	324	18	US-09-436-762A-31898	Sequence 31898, A	c 594	13	86.7	365	19	US-09-362-510A-29944	Sequence 29944, A
c 522	13	86.7	324	19	US-09-521-640-126599	Sequence 126599, A	c 595	13	86.7	365	17	US-09-521-640-237689	Sequence 237689, A
c 523	13	86.7	325	8	US-08-401-791A-14322	Sequence 14322, A	c 596	13	86.7	365	34	US-09-904-013-29944	Sequence 29944, A
c 524	13	86.7	325	8	US-08-401-791B-14322	Sequence 14322, A	c 597	13	86.7	365	58	US-60-140-769-32438	Sequence 32438, A
c 525	13	86.7	327	28	US-09-710-281-3084	Sequence 3084, Ap	c 598	13	86.7	366	25	US-09-654-617-369258	Sequence 369258, A
c 526	13	86.7	329	32	US-09-834-366-51421	Sequence 51421, A	c 599	13	86.7	366	25	US-09-684-016-369258	Sequence 369258, A
c 527	13	86.7	329	63	US-60-197-873-51421	Sequence 51421, A	c 600	13	86.7	367	24	US-09-637-086A-43691	Sequence 43691, A
c 528	13	86.7	330	18	US-09-489-036-25995	Sequence 25995, A	c 601	13	86.7	369	24	US-09-637-086B-43691	Sequence 43691, A
c 529	13	86.7	330	35	US-09-943-143-25995	Sequence 25995, A	c 602	13	86.7	369	25	US-09-654-617-227387	Sequence 227387, A
c 530	13	86.7	335	16	US-09-205-070-42231	Sequence 42231, A	c 603	13	86.7	369	27	US-09-684-016-227387	Sequence 227387, A
c 531	13	86.7	335	17	US-09-321-214-20037	Sequence 20037, A	c 604	13	86.7	371	32	US-09-849-526A-14850	Sequence 14850, A
c 532	13	86.7	335	17	US-09-340-623-42231	Sequence 42231, A	c 605	13	86.7	371	64	US-60-202-214-14605	Sequence 14605, A

c 606	13	86.7	372	19	US-09-519-705-748	Sequence 748, App	679	13	86.7	401	1	PCT-US01-03800A-115	Sequence 115, App
c 607	13	86.7	372	19	US-09-519-705-1257	Sequence 1257, App	680	13	86.7	401	16	US-09-293-972-30063	Sequence 30063, A
c 608	13	86.7	372	22	US-09-574-454-748	Sequence 748, App	681	13	86.7	401	16	US-09-496-914A-1464	Sequence 1464, Ap
c 609	13	86.7	372	22	US-09-574-454-1257	Sequence 1257, Ap	682	13	86.7	401	22	US-09-560-875A-1464	Sequence 1464, Ap
c 610	13	86.7	372	42	US-10-221-279-739	Sequence 739, App	683	13	86.7	401	34	US-09-904-939-30063	Sequence 30063, A
c 611	13	86.7	372	42	US-10-221-279-1241	Sequence 1241, Ap	c 684	13	86.7	403	23	US-09-606-977-54854	Sequence 54854, A
c 612	13	86.7	373	1	PCT-US01-01354-1599	Sequence 1599, Ap	685	13	86.7	404	25	US-09-606-977-54854	Sequence 3241, Ap
c 613	13	86.7	373	30	US-09-764-905-1599	Sequence 1599, Ap	686	13	86.7	405	16	US-09-644-871-3241	Sequence 33009, A
c 614	13	86.7	373	39	US-10-092-399-1599	Sequence 1599, Ap	687	13	86.7	405	16	US-09-235-076-33009	Sequence 33009, A
c 615	13	86.7	373	41	US-10-155-881-12327	Sequence 12327, Ap	688	13	86.7	405	16	US-09-277-227-414	Sequence 414, App
c 616	13	86.7	373	63	US-60-197-872-43332	Sequence 43332, A	689	13	86.7	405	29	US-09-332-782-33009	Sequence 33009, A
c 617	13	86.7	374	23	US-09-606-977-35488	Sequence 35488, A	690	13	86.7	405	34	US-09-737-223-33009	Sequence 33009, A
c 618	13	86.7	374	31	US-09-824-559-7669	Sequence 7669, Ap	691	13	86.7	406	34	US-09-909-627-414	Sequence 414, App
c 619	13	86.7	375	5	US-08-196-363-10397	Sequence 10397, A	692	13	86.7	406	34	US-09-909-627-414	Sequence 33009, A
c 620	13	86.7	375	5	US-08-196-363A-10397	Sequence 10397, A	693	13	86.7	406	35	US-09-918-995-33009	Sequence 33096, A
c 621	13	86.7	375	5	US-08-196-363-10397	Sequence 10397, A	694	13	86.7	406	35	US-09-933-524-93096	Sequence 93096, A
c 622	13	86.7	375	32	US-09-859-490-10397	Sequence 10397, A	695	13	86.7	406	35	US-09-933-524-93096	Sequence 93096, A
c 623	13	86.7	377	64	US-60-207-458-46645	Sequence 46645, A	696	13	86.7	408	14	US-09-076-897-5037	Sequence 5037, Ap
c 624	13	86.7	378	23	US-09-606-977-43452	Sequence 43452, A	697	13	86.7	408	14	US-09-076-897B-5037	Sequence 5037, Ap
c 625	13	86.7	379	19	US-09-521-640-43101	Sequence 43101, A	698	13	86.7	408	14	US-09-076-897C-5037	Sequence 5037, Ap
c 626	13	86.7	379	22	US-09-552-087-13068	Sequence 13068, A	699	13	86.7	408	16	US-09-293-972-20833	Sequence 20833, A
c 627	13	86.7	379	22	US-09-552-087B-13068	Sequence 13068, A	700	13	86.7	408	16	US-09-293-972-20833	Sequence 49143, A
c 628	13	86.7	381	1	PCT-US01-08631-119	Sequence 119, App	c 701	13	86.7	408	17	US-09-362-510-49143	Sequence 49143, A
c 629	13	86.7	381	11	US-08-790-774-1258	Sequence 1258, Ap	c 702	13	86.7	408	17	US-09-362-510A-49143	Sequence 49143, A
c 630	13	86.7	382	19	US-09-528-409-77283	Sequence 77283, Ap	c 703	13	86.7	408	34	US-09-362-510A-49143	Sequence 20833, A
c 631	13	86.7	382	35	US-09-933-524-77283	Sequence 77283, A	704	13	86.7	409	17	US-09-362-510A-28800	Sequence 28800, A
c 632	13	86.7	382	35	US-09-933-524A-77283	Sequence 77283, A	705	13	86.7	409	17	US-09-421-106-14696	Sequence 14696, A
c 633	13	86.7	383	1	PCT-US02-25766-2100	Sequence 2100, App	706	13	86.7	409	18	US-09-521-640-282947	Sequence 282947, A
c 634	13	86.7	383	16	US-09-271-122-928	Sequence 928, App	707	13	86.7	409	25	US-09-652-121-112	Sequence 112, App
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c 636	13	86.7	383	33	US-09-880-1077-1077	Sequence 1077, Ap	c 710	13	86.7	410	19	US-09-521-640-143677	Sequence 143677, A
c 637	13	86.7	383	34	US-09-927-875-928	Sequence 928, App	711	13	86.7	411	19	US-09-521-640-5491	Sequence 5491, Ap
c 638	13	86.7	383	34	US-09-927-875A-928	Sequence 928, App	712	13	86.7	411	20	US-09-535-896-1842	Sequence 1842, Ap
c 639	13	86.7	383	36	US-09-954-456-892	Sequence 892, App	713	13	86.7	411	20	US-09-534-844A-2206	Sequence 2206, Ap
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c 641	13	86.7	385	27	US-09-684-016-161559	Sequence 161559, A	c 716	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 642	13	86.7	386	16	US-09-274-861-11212	Sequence 11212, A	c 717	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 643	13	86.7	386	29	US-09-726-176-1055	Sequence 1055, Ap	c 718	13	86.7	418	17	US-09-394-745-13919	Sequence 13919, A
c 644	13	86.7	386	34	US-09-915-738-11212	Sequence 11212, A	c 719	13	86.7	418	17	US-09-399-932-3616	Sequence 3616, Ap
c 645	13	86.7	387	17	US-09-362-510-41372	Sequence 41372, A	c 720	13	86.7	418	17	US-09-436-762A-25967	Sequence 25967, A
c 646	13	86.7	387	17	US-09-362-510A-41372	Sequence 41372, A	c 721	13	86.7	418	18	US-09-436-762A-25967	Sequence 35702, A
c 647	13	86.7	387	20	US-09-606-977-9521	Sequence 9521, Ap	c 722	13	86.7	418	22	US-09-565-306-35702	Sequence 35702, A
c 648	13	86.7	387	34	US-09-904-013-41372	Sequence 41372, A	c 723	13	86.7	418	25	US-09-565-306-35702	Sequence 1081, Ap
c 649	13	86.7	388	19	US-09-528-409-10539	Sequence 10539, A	c 724	13	86.7	418	26	US-09-663-784-296	Sequence 296, App
c 650	13	86.7	388	24	US-09-637-086A-44592	Sequence 44592, A	c 725	13	86.7	418	26	US-09-667-760-414	Sequence 414, App
c 651	13	86.7	388	24	US-09-637-086D-44592	Sequence 44592, A	c 726	13	86.7	418	26	US-09-667-760-414	Sequence 414, App
c 652	13	86.7	388	25	US-09-654-617-251588	Sequence 251588, A	c 727	13	86.7	418	37	US-09-985-678-87573	Sequence 87573, A
c 653	13	86.7	388	27	US-09-684-016-251588	Sequence 251588, A	c 728	13	86.7	419	19	US-09-528-409-65784	Sequence 65784, A
c 654	13	86.7	388	35	US-09-933-524-10539	Sequence 10539, A	c 729	13	86.7	419	25	US-09-528-409-65784	Sequence 307749, A
c 655	13	86.7	388	39	US-10-050-759-501	Sequence 501, App	c 730	13	86.7	419	26	US-09-669-817A-13194	Sequence 415511, A
c 656	13	86.7	390	38	US-10-021-323-7873	Sequence 7873, Ap	c 731	13	86.7	419	26	US-09-669-817A-13194	Sequence 13194, A
c 657	13	86.7	390	69	US-60-255-619-7873	Sequence 7873, Ap	c 732	13	86.7	419	25	US-09-654-617-415511	Sequence 307749, A
c 658	13	86.7	391	16	US-09-248-797-5920	Sequence 5920, Ap	c 733	13	86.7	419	27	US-09-684-016-10998	Sequence 10998, A
c 659	13	86.7	391	16	US-09-271-490-6581	Sequence 6581, Ap	c 734	13	86.7	419	27	US-09-684-016-415511	Sequence 415511, A
c 660	13	86.7	391	17	US-09-346-956-3257	Sequence 3257, Ap	c 735	13	86.7	419	35	US-09-692-257A-10998	Sequence 10998, A
c 661	13	86.7	391	34	US-09-904-703-3257	Sequence 3257, Ap	c 736	13	86.7	419	35	US-09-933-524-65784	Sequence 65784, A
c 662	13	86.7	391	34	US-09-925-552-6581	Sequence 6581, Ap	c 737	13	86.7	419	35	US-09-933-524A-65784	Sequence 65784, A
c 663	13	86.7	391	34	US-09-925-564-5920	Sequence 5920, Ap	c 738	13	86.7	420	17	US-09-162-747-10189	Sequence 10189, A
c 664	13	86.7	391	34	US-09-925-564-5920	Sequence 5920, Ap	c 739	13	86.7	420	17	US-09-340-517A-249692	Sequence 249692, A
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c 668	13	86.7	392	27	US-09-684-016-368146	Sequence 368146, A	c 743	13	86.7	422	33	US-09-985-678-249692	Sequence 1762, Ap
c 669	13	86.7	395	17	US-09-332-782-14760	Sequence 14760, A	c 744	13	86.7	422	33	US-09-804-730-1762	Sequence 68909, A
c 670	13	86.7	395	17	US-09-366-691A-1211	Sequence 1211, Ap	c 745	13	86.7	422	33	US-09-804-730-1762	Sequence 1858, Ap
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c 672	13	86.7	396	27	US-09-698-013-5019	Sequence 5019, Ap	c 747	13	86.7	422	33	US-09-865-439A-68909	Sequence 113069, A
c 673	13	86.7	397	17	US-09-394-745-14832	Sequence 14832, A	c 748	13	86.7	422	62	US-60-189-657-1858	Sequence 113069, A
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C 822	13	86.7	447	37	US-09-985-678-261621	Sequence 261621, A	C 895	13	86.7	469	41	US-10-182-997-570
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; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-10

Query Match      100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
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RESULT 3
US-60-173-682-10
; Sequence 10, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-10

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RESULT 4
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; Sequence 5, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
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US-09-750-609-5

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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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; TYPE: DNA
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PCT-US00-35491-5

Query Match      100.0%; Score 15; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
PCT-US00-35491-6/C
; Sequence 6, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
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; ORGANISM: Homo sapiens
PCT-US00-35491-6

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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-750-609-5
; Sequence 5, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
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US-09-750-609-5

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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
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RESULT 9
US-80-173-682-6/c
; Sequence 6, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION
; TITLE OF INVENTION: DIAGNOSTIC AND
; FILE REFERENCE: Attorney Docket No.

T T T T T T T T T T T T T T T T T

; LOCATION: (1)..(197)

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; LOCATION: (1)..(197)
; OTHER INFORMATION: unsure at all n locations
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OTHER INFORMATION: Clone ID: 701040886H1
US-09-960-481-2932

Query Match 100.0%; Score 15; DB 36; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 CCTTCTCCCCCTGTT 17

RESULT 12

US-09-076-667-2907
Sequence 2907, Application US/09076667

GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: HUMAN BRAIN
NUMBER OF SEQUENCES: 4483

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166

INFORMATION FOR SEQ ID NO: 2907:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 3268389H1
US-09-076-667-2907

Query Match 100.0%; Score 15; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
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Db 75 CCTTCTCCCCCTGTT 89

RESULT 13

US-09-540-229-47840
Sequence 47840, Application US/09540229

GENERAL INFORMATION:
APPLICANT: Seilbamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
FILE REFERENCE: PD-1033 CIP
CURRENT APPLICATION NUMBER: US/09/540,229
CURRENT FILING DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 193582
SOFTWARE: PERL Program
SEQ ID NO 47840
LENGTH: 248
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu00535318
NAME/KEY: unsure
LOCATION: 211
OTHER INFORMATION: a, t, c, g, or other
US-09-540-229-47840

Query Match

100.0%; Score 15; DB 21; Length 248;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
| | | | | | | | | | | | | | | | | | | | |
Db 75 CCTTCTCCCCCTGTT 89

RESULT 14

US-60-048-002-2907

Sequence 2907, Application US/60048002

GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: HUMAN BRAIN
NUMBER OF SEQUENCES: 4483

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/048,002
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166

INFORMATION FOR SEQ ID NO: 2907:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 3268389H1
US-60-048-002-2907

Query Match 100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
DB 75 CCTTCTCCCCCTGTT 89

RESULT 15
US-09-637-890-4668/c
Sequence 4668, Application US/09637890
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine
APPLICANT: Culpepper, Janice A.
APPLICANT: Leiby, Kevin R.
APPLICANT: Vasicek, Tom
APPLICANT: MacBeth, Kyle J.
APPLICANT: Villeval, Jean-Luc M. G.
APPLICANT: Cepada, Mario
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1152-001
CURRENT APPLICATION NUMBER: US/09/637,890
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,939
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 10217
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4668
LENGTH: 327
TYPE: DNA
ORGANISM: Homo sapiens
US-09-637-890-4668

Query Match 100.0%; Score 15; DB 24; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
|||||
DB 168 CCTTCTCCCCCTGTT 154

Search completed: December 11, 2002, 20:27:36
Job time : 2584 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:10:08 ; Search time 88.5 Seconds
(without alignments)
121.821 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cttctccccctgtt 15

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 407964 seqs, 359371392 residues

Word size : 0

Total number of hits satisfying chosen parameters: 815928

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	15	100.0	352	US-09-513-999C-13316	Sequence 13316, A
c 2	15	100.0	2520	US-10-264-237-1036	Sequence 1036, Ap
c 3	14	93.3	248	US-09-620-607B-1245	Sequence 1245, Ap
c 4	14	93.3	908	US-09-724-676-38339	Sequence 38339, A
c 5	14	93.3	908	US-09-724-676A-38339	Sequence 38339, A
c 6	14	93.3	1030	US-09-724-676-24274	Sequence 24274, A
c 7	14	93.3	1030	US-09-724-676A-24274	Sequence 24274, A
c 8	14	93.3	1509	US-09-724-676-2247	Sequence 2247, Ap
c 9	14	93.3	1509	US-09-724-676A-2247	Sequence 2247, Ap
c 10	14	93.3	1667	US-09-724-676-2234	Sequence 2234, Ap
c 11	14	93.3	1667	US-09-724-676A-2234	Sequence 2234, Ap
c 12	14	93.3	1712	US-09-724-676-2221	Sequence 2221, Ap
c 13	14	93.3	1712	US-09-724-676A-2221	Sequence 2221, Ap
c 14	14	93.3	1755	US-09-724-676-2240	Sequence 2240, Ap
c 15	14	93.3	1755	US-09-724-676A-2240	Sequence 2240, Ap
c 16	14	93.3	1825	US-09-724-676-2246	Sequence 2246, Ap
c 17	14	93.3	1825	US-09-724-676A-2246	Sequence 2246, Ap
c 18	14	93.3	1871	US-09-724-676-2245	Sequence 2245, Ap
c 19	14	93.3	1871	US-09-724-676A-2245	Sequence 2245, Ap
c 20	14	93.3	1913	US-09-724-676-2227	Sequence 2227, Ap
c 21	14	93.3	1913	US-09-724-676A-2227	Sequence 2227, Ap
c 22	14	93.3	1958	US-09-724-676-2214	Sequence 2214, Ap
c 23	14	93.3	1958	US-09-724-676A-2214	Sequence 2214, Ap
c 24	14	93.3	1983	US-09-724-676-2233	Sequence 2233, Ap
c 25	14	93.3	1983	US-09-724-676A-2233	Sequence 2233, Ap
c 26	14	93.3	2028	US-09-724-676-2220	Sequence 2220, Ap

Sequence 2220, Ap
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Sequence 2232, Ap
Sequence 2239, Ap
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Sequence 2163, Ap
Sequence 2163, Ap
Sequence 2183, Ap
Sequence 2183, Ap

c 100	14	93.3	4902	5	US-09-724-676-2202	Sequence 2202, Ap	c 173	14	93.3	6525	5	US-09-724-676A-2192	Sequence 2192, Ap
c 101	14	93.3	4902	5	US-09-724-676A-2202	Sequence 2202, Ap	c 174	14	93.3	6527	5	US-09-724-676-2159	Sequence 2159, Ap
c 102	14	93.3	4947	5	US-09-724-676-2189	Sequence 2189, Ap	c 175	14	93.3	6527	5	US-09-724-676A-2159	Sequence 2159, Ap
c 103	14	93.3	4947	5	US-09-724-676A-2189	Sequence 2189, Ap	c 176	14	93.3	6570	5	US-09-724-676-2179	Sequence 2179, Ap
c 104	14	93.3	4948	5	US-09-724-676-2201	Sequence 2201, Ap	c 177	14	93.3	6570	5	US-09-724-676A-2179	Sequence 2179, Ap
c 105	14	93.3	4948	5	US-09-724-676A-2201	Sequence 2201, Ap	c 178	14	93.3	6728	5	US-09-724-676-2166	Sequence 2166, Ap
c 106	14	93.3	4993	5	US-09-724-676A-2188	Sequence 2188, Ap	c 179	14	93.3	6728	5	US-09-724-676A-2166	Sequence 2166, Ap
c 107	14	93.3	4993	5	US-09-724-676A-2188	Sequence 2188, Ap	c 180	14	93.3	6773	5	US-09-724-676-2230	Sequence 2230, Ap
c 108	14	93.3	5035	5	US-09-724-676-2170	Sequence 2170, Ap	c 181	14	93.3	6773	5	US-09-724-676A-2230	Sequence 2230, Ap
c 109	14	93.3	5035	5	US-09-724-676-2170	Sequence 2170, Ap	c 182	14	93.3	8424	5	US-09-724-676-6845	Sequence 6845, Ap
c 110	14	93.3	5080	5	US-09-724-676A-2157	Sequence 2157, Ap	c 183	14	93.3	8424	5	US-09-724-676A-6845	Sequence 6845, Ap
c 111	14	93.3	5080	5	US-09-724-676A-2157	Sequence 2157, Ap	c 184	14	93.3	9367	5	US-09-724-676-6847	Sequence 6847, Ap
c 112	14	93.3	5105	5	US-09-724-676A-2175	Sequence 2175, Ap	c 185	14	93.3	9367	5	US-09-724-676A-6847	Sequence 6847, Ap
c 113	14	93.3	5105	5	US-09-724-676-2195	Sequence 2195, Ap	c 186	14	93.3	9415	5	US-09-724-676-6836	Sequence 6836, Ap
c 114	14	93.3	5148	5	US-09-724-676A-2195	Sequence 2195, Ap	c 187	14	93.3	9415	5	US-09-724-676A-6836	Sequence 6836, Ap
c 115	14	93.3	5148	5	US-09-724-676-2162	Sequence 2162, Ap	c 188	14	93.3	9499	5	US-09-724-676-6841	Sequence 6841, Ap
c 116	14	93.3	5150	5	US-09-724-676A-2162	Sequence 2162, Ap	c 189	14	93.3	9499	5	US-09-724-676A-6841	Sequence 6841, Ap
c 117	14	93.3	5150	5	US-09-724-676-2174	Sequence 2174, Ap	c 190	14	93.3	135259	6	US-10-240-425-1585	Sequence 1585, Ap
c 118	14	93.3	5151	5	US-09-724-676A-2174	Sequence 2174, Ap	c 191	14	93.3	135259	7	US-10-240-425-1585	Sequence 1585, Ap
c 119	14	93.3	5151	5	US-09-724-676-2182	Sequence 2182, Ap	c 192	14	93.3	337	5	US-09-513-999C-15597	Sequence 24, Appl
c 120	14	93.3	5193	5	US-09-724-676-2182	Sequence 2182, Ap	c 193	13	86.7	469	6	US-09-513-999C-15597	Sequence 15597, A
c 121	14	93.3	5193	5	US-09-724-676A-2182	Sequence 2182, Ap	c 194	13	86.7	1400	5	US-10-203-138A-562	Sequence 562, App
c 122	14	93.3	5194	5	US-09-724-676-2194	Sequence 2194, Ap	c 195	13	86.7	1400	5	US-09-724-676-1020	Sequence 1020, Ap
c 123	14	93.3	5194	5	US-09-724-676A-2194	Sequence 2194, Ap	c 196	13	86.7	1400	5	US-09-724-676A-1020	Sequence 1020, Ap
c 124	14	93.3	5196	5	US-09-724-676-2161	Sequence 2161, Ap	c 197	13	86.7	1959	5	US-09-724-676-1015	Sequence 1015, Ap
c 125	14	93.3	5196	5	US-09-724-676A-2161	Sequence 2161, Ap	c 198	13	86.7	2244	5	US-09-724-676A-1015	Sequence 1015, Ap
c 126	14	93.3	5239	5	US-09-724-676-2181	Sequence 2181, Ap	c 199	13	86.7	2244	5	US-09-543-293C-35	Sequence 35, Appl
c 127	14	93.3	5239	5	US-09-724-676A-2181	Sequence 2181, Ap	c 200	13	86.7	2244	5	US-09-724-676A-1014	Sequence 1014, Ap
c 128	14	93.3	5351	5	US-09-724-676-2169	Sequence 2169, Ap	c 201	13	86.7	2431	6	US-09-724-676A-1014	Sequence 1014, Ap
c 129	14	93.3	5351	5	US-09-724-676A-2169	Sequence 2169, Ap	c 202	13	86.7	2601	5	US-10-194-163-351	Sequence 351, App
c 130	14	93.3	5396	5	US-09-724-676-2156	Sequence 2156, Ap	c 203	13	86.7	2601	5	US-09-724-676-1018	Sequence 1018, Ap
c 131	14	93.3	5396	5	US-09-724-676A-2156	Sequence 2156, Ap	c 204	13	86.7	2759	5	US-09-724-676-1016	Sequence 1016, Ap
c 132	14	93.3	5397	5	US-09-724-676-2168	Sequence 2168, Ap	c 205	13	86.7	2759	5	US-09-724-676A-1016	Sequence 1016, Ap
c 133	14	93.3	5397	5	US-09-724-676A-2168	Sequence 2168, Ap	c 206	13	86.7	2842	5	US-09-724-676-1019	Sequence 1019, Ap
c 134	14	93.3	5397	5	US-09-724-676-2155	Sequence 2155, Ap	c 207	13	86.7	2842	5	US-09-724-676A-1019	Sequence 1019, Ap
c 135	14	93.3	5442	5	US-09-724-676-2155	Sequence 2155, Ap	c 208	13	86.7	3000	5	US-09-724-676-1017	Sequence 1017, Ap
c 136	14	93.3	5442	5	US-09-724-676A-2155	Sequence 2155, Ap	c 209	13	86.7	3000	5	US-09-724-676A-1017	Sequence 1017, Ap
c 137	14	93.3	5921	5	US-09-724-676-2197	Sequence 2197, Ap	c 210	13	86.7	14537	6	US-10-240-425-1342	Sequence 41, Appl
c 138	14	93.3	5921	5	US-09-724-676A-2197	Sequence 2197, Ap	c 211	13	86.7	24740	1	PCT-US02-36465-41	Sequence 41, Appl
c 139	14	93.3	5966	5	US-09-724-676-2184	Sequence 2184, Ap	c 212	13	86.7	24740	1	PCT-US02-36465-41	Sequence 6, Appl1
c 140	14	93.3	5966	5	US-09-724-676A-2184	Sequence 2184, Ap	c 213	13	86.7	26729	1	PCT-US02-34708-6	Sequence 6, Appl1
c 141	14	93.3	5984	5	US-09-724-676-2200	Sequence 2200, Ap	c 214	13	86.7	26729	1	PCT-US02-34708-6	Sequence 3, Appl1
c 142	14	93.3	6029	5	US-09-724-676A-2200	Sequence 2200, Ap	c 215	13	86.7	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 143	14	93.3	6029	5	US-09-724-676-2186	Sequence 2186, Ap	c 216	13	86.7	70383	6	US-10-283-247-3	Sequence 6334, Ap
c 144	14	93.3	6124	5	US-09-724-676-2171	Sequence 2171, Ap	c 217	12	80.0	114	6	US-10-203-138A-8801	Sequence 8801, Ap
c 145	14	93.3	6124	5	US-09-724-676A-2171	Sequence 2171, Ap	c 218	12	80.0	134	6	US-09-513-999C-8801	Sequence 9015, Ap
c 146	14	93.3	6167	5	US-09-724-676-2191	Sequence 2191, Ap	c 219	12	80.0	174	6	US-10-203-138A-9015	Sequence 3354, A
c 147	14	93.3	6167	5	US-09-724-676A-2191	Sequence 2191, Ap	c 220	12	80.0	245	5	US-09-513-999C-3354	Sequence 16967, A
c 148	14	93.3	6169	5	US-09-724-676-2158	Sequence 2158, Ap	c 221	12	80.0	268	5	US-09-513-999C-3354	Sequence 23234, A
c 149	14	93.3	6169	5	US-09-724-676A-2158	Sequence 2158, Ap	c 222	12	80.0	376	5	US-09-513-999C-24005	Sequence 24005, A
c 150	14	93.3	6187	5	US-09-724-676-2173	Sequence 2173, Ap	c 223	12	80.0	397	5	US-09-513-999C-13701	Sequence 13701, A
c 151	14	93.3	6187	5	US-09-724-676A-2173	Sequence 2173, Ap	c 224	12	80.0	410	6	US-10-203-138A-1201	Sequence 1201, Ap
c 152	14	93.3	6212	5	US-09-724-676-2178	Sequence 2178, Ap	c 225	12	80.0	512	6	US-10-203-138A-6521	Sequence 6521, Ap
c 153	14	93.3	6212	5	US-09-724-676A-2178	Sequence 2178, Ap	c 226	12	80.0	522	6	US-10-264-237-275	Sequence 275, App
c 154	14	93.3	6230	5	US-09-724-676-2193	Sequence 2193, Ap	c 227	12	80.0	733	5	US-09-724-676-16244	Sequence 16244, A
c 155	14	93.3	6230	5	US-09-724-676A-2193	Sequence 2193, Ap	c 228	12	80.0	733	5	US-09-724-676A-16244	Sequence 16244, A
c 156	14	93.3	6232	5	US-09-724-676-2160	Sequence 2160, Ap	c 229	12	80.0	1012	6	US-10-203-138A-5888	Sequence 5888, Ap
c 157	14	93.3	6232	5	US-09-724-676A-2160	Sequence 2160, Ap	c 230	12	80.0	1149	1	PCT-US02-32727-273	Sequence 41, Appl
c 158	14	93.3	6275	5	US-09-724-676-2180	Sequence 2180, Ap	c 231	12	80.0	1389	1	PCT-US02-32727-273	Sequence 273, App
c 159	14	93.3	6275	5	US-09-724-676A-2180	Sequence 2180, Ap	c 232	12	80.0	1389	6	US-10-057-498-273	Sequence 16243, A
c 160	14	93.3	6279	5	US-09-724-676-2199	Sequence 2199, Ap	c 233	12	80.0	1553	5	US-09-724-676-16243	Sequence 16243, A
c 161	14	93.3	6294	5	US-09-724-676A-2199	Sequence 2199, Ap	c 234	12	80.0	1553	5	US-09-724-676-31339	Sequence 31339, A
c 162	14	93.3	6324	5	US-09-724-676-2185	Sequence 2185, Ap	c 235	12	80.0	1593	5	US-09-724-676A-31339	Sequence 31339, A
c 163	14	93.3	6324	5	US-09-724-676-2185	Sequence 2185, Ap	c 236	12	80.0	1619	5	US-09-724-676-16238	Sequence 16238, A
c 164	14	93.3	6370	5	US-09-724-676-2164	Sequence 2164, Ap	c 237	12	80.0	1619	5	US-09-724-676-16238	Sequence 16238, A
c 165	14	93.3	6370	5	US-09-724-676A-2164	Sequence 2164, Ap	c 238	12	80.0	1619	5	US-09-724-676A-16238	Sequence 16238, A
c 166	14	93.3	6433	5	US-09-724-676-2167	Sequence 2167, Ap	c 239	12	80.0	1890	5	US-09-724-676-34793	Sequence 34793, A
c 167	14	93.3	6433	5	US-09-724-676A-2167	Sequence 2167, Ap	c 240	12	80.0	1890	5	US-09-724-676-34793	Sequence 34793, A
c 168	14	93.3	6478	5	US-09-724-676-2241	Sequence 2241, Ap	c 241	12	80.0	1890	5	US-09-724-676A-34793	Sequence 34793, A
c 169	14	93.3	6478	5	US-09-724-676A-2241	Sequence 2241, Ap	c 242	12	80.0	1869	5	US-09-724-676-16228	Sequence 16228, A
c 170	14	93.3	6482	5	US-09-724-676-2172	Sequence 2172, Ap	c 243	12	80.0	1869	5	US-09-724-676A-16228	Sequence 16228, A
c 171	14	93.3	6482	5	US-09-724-676A-2172	Sequence 2172, Ap	c 244	12	80.0	1936	5	US-09-724-676-34790	Sequence 34790, A
c 172	14	93.3	6525	5	US-09-724-676-2192	Sequence 2192, Ap	c 245	12	80.0	1936	5	US-09-724-676A-34790	Sequence 34790, A

c 246	12	80.0	2057	6	US-10-366-829-15	Sequence 15, Appl	319	12	80.0	3496	5	US-09-724-676A-31329	Sequence 31329, A
247	12	80.0	2230	5	US-09-724-676A-16240	Sequence 16240, A	320	12	80.0	3512	5	US-09-724-676A-44419	Sequence 44419, A
248	12	80.0	2230	5	US-09-724-676A-16240	Sequence 16240, A	321	12	80.0	3512	5	US-09-724-676A-44419	Sequence 44419, A
249	12	80.0	2245	5	US-09-724-676A-16242	Sequence 16242, A	322	12	80.0	3592	5	US-09-724-676A-13824	Sequence 13824, A
250	12	80.0	2245	5	US-09-724-676A-16242	Sequence 16242, A	323	12	80.0	3592	5	US-09-724-676A-13824	Sequence 13824, A
251	12	80.0	2349	5	US-09-724-676A-16241	Sequence 16241, A	324	12	80.0	3617	5	US-09-724-676A-44417	Sequence 44417, A
252	12	80.0	2349	5	US-09-724-676A-16241	Sequence 16241, A	325	12	80.0	3617	5	US-09-724-676A-44417	Sequence 44417, A
c 253	12	80.0	2354	6	US-10-194-163-275	Sequence 275, App	326	12	80.0	3702	5	US-09-724-676A-31302	Sequence 31302, A
254	12	80.0	2380	5	US-09-724-676A-31338	Sequence 31338, A	327	12	80.0	3702	5	US-09-724-676A-31302	Sequence 31302, A
255	12	80.0	2380	5	US-09-724-676A-31338	Sequence 31338, A	c 328	12	80.0	3711	5	US-09-724-676A-40182	Sequence 40182, A
c 256	12	80.0	2574	5	US-09-724-676A-40184	Sequence 40184, A	c 329	12	80.0	3711	5	US-09-724-676A-40182	Sequence 40182, A
c 257	12	80.0	2574	5	US-09-724-676A-40184	Sequence 40184, A	c 330	12	80.0	3749	5	US-09-724-676A-40179	Sequence 40179, A
c 258	12	80.0	2577	5	US-09-724-676A-40177	Sequence 40177, A	c 331	12	80.0	3749	5	US-09-724-676A-40179	Sequence 40179, A
c 259	12	80.0	2577	5	US-09-724-676A-40177	Sequence 40177, A	c 332	12	80.0	3779	5	US-09-724-676A-31298	Sequence 31298, A
c 260	12	80.0	2612	5	US-09-724-676A-40181	Sequence 40181, A	c 333	12	80.0	3779	5	US-09-724-676A-31298	Sequence 31298, A
c 261	12	80.0	2612	5	US-09-724-676A-40181	Sequence 40181, A	c 334	12	80.0	3816	5	US-09-724-676A-40170	Sequence 40170, A
c 262	12	80.0	2679	5	US-09-724-676A-40172	Sequence 40172, A	c 335	12	80.0	3816	5	US-09-724-676A-40170	Sequence 40170, A
c 263	12	80.0	2679	5	US-09-724-676A-40172	Sequence 40172, A	c 336	12	80.0	3838	5	US-09-724-676A-25355	Sequence 25355, A
c 264	12	80.0	2682	5	US-09-724-676A-40165	Sequence 40165, A	c 337	12	80.0	3838	5	US-09-724-676A-25355	Sequence 25355, A
c 265	12	80.0	2682	5	US-09-724-676A-40165	Sequence 40165, A	c 338	12	80.0	3839	5	US-09-724-676A-40183	Sequence 40183, A
c 266	12	80.0	2717	5	US-09-724-676A-40169	Sequence 40169, A	c 339	12	80.0	3839	5	US-09-724-676A-40183	Sequence 40183, A
c 267	12	80.0	2717	5	US-09-724-676A-40169	Sequence 40169, A	c 340	12	80.0	3854	5	US-09-724-676A-40166	Sequence 40166, A
c 268	12	80.0	2733	5	US-09-724-676A-40160	Sequence 40160, A	c 341	12	80.0	3854	5	US-09-724-676A-40166	Sequence 40166, A
c 269	12	80.0	2736	5	US-09-724-676A-40154	Sequence 40154, A	c 342	12	80.0	3870	5	US-09-724-676A-40158	Sequence 40158, A
c 270	12	80.0	2736	5	US-09-724-676A-40154	Sequence 40154, A	c 343	12	80.0	3870	5	US-09-724-676A-40158	Sequence 40158, A
c 271	12	80.0	2736	5	US-09-724-676A-40154	Sequence 40154, A	c 344	12	80.0	3877	5	US-09-724-676A-40180	Sequence 40180, A
c 272	12	80.0	2741	5	US-09-724-676A-16219	Sequence 16219, A	c 345	12	80.0	3877	5	US-09-724-676A-40180	Sequence 40180, A
c 273	12	80.0	2741	5	US-09-724-676A-16219	Sequence 16219, A	c 346	12	80.0	3882	5	US-09-724-676A-31313	Sequence 31313, A
c 274	12	80.0	2754	5	US-09-724-676A-40176	Sequence 40176, A	c 347	12	80.0	3882	5	US-09-724-676A-31313	Sequence 31313, A
c 275	12	80.0	2754	5	US-09-724-676A-40176	Sequence 40176, A	c 348	12	80.0	3891	5	US-09-724-676A-40174	Sequence 40174, A
c 276	12	80.0	2764	5	US-09-724-676A-16224	Sequence 16224, A	c 349	12	80.0	3891	5	US-09-724-676A-40174	Sequence 40174, A
c 277	12	80.0	2764	5	US-09-724-676A-16224	Sequence 16224, A	c 350	12	80.0	3908	5	US-09-724-676A-40155	Sequence 40155, A
c 278	12	80.0	2771	5	US-09-724-676A-40157	Sequence 40157, A	c 351	12	80.0	3908	5	US-09-724-676A-40155	Sequence 40155, A
c 279	12	80.0	2771	5	US-09-724-676A-40157	Sequence 40157, A	c 352	12	80.0	3927	1	PCT-US02-04915-228	Sequence 228, App
c 280	12	80.0	2779	5	US-09-724-676A-40173	Sequence 40173, A	c 353	12	80.0	3944	5	US-09-724-676A-40171	Sequence 40171, A
c 281	12	80.0	2791	5	US-09-724-676A-40173	Sequence 40173, A	c 354	12	80.0	3944	5	US-09-724-676A-40171	Sequence 40171, A
c 282	12	80.0	2791	5	US-09-724-676A-16221	Sequence 16221, A	c 355	12	80.0	3959	5	US-09-724-676A-31309	Sequence 31309, A
c 283	12	80.0	2807	5	US-09-724-676A-16221	Sequence 16221, A	c 356	12	80.0	3959	5	US-09-724-676A-31309	Sequence 31309, A
c 284	12	80.0	2807	5	US-09-979-603A-1	Sequence 1, Appl	c 357	12	80.0	3982	5	US-09-724-676A-40168	Sequence 40168, A
c 285	12	80.0	2807	5	US-09-979-603A-1	Sequence 1, Appl	c 358	12	80.0	3982	5	US-09-724-676A-40168	Sequence 40168, A
c 286	12	80.0	2841	5	US-09-724-676A-40197	Sequence 40197, A	c 359	12	80.0	3996	5	US-09-724-676A-40162	Sequence 40162, A
c 287	12	80.0	2841	5	US-09-724-676A-40197	Sequence 40197, A	c 360	12	80.0	3996	5	US-09-724-676A-40162	Sequence 40162, A
c 288	12	80.0	2859	5	US-09-724-676A-40164	Sequence 40164, A	c 361	12	80.0	3998	5	US-09-724-676A-40159	Sequence 40159, A
c 289	12	80.0	2859	5	US-09-724-676A-40164	Sequence 40164, A	c 362	12	80.0	3998	5	US-09-724-676A-40159	Sequence 40159, A
c 290	12	80.0	2876	5	US-09-724-676A-40230	Sequence 40230, A	c 363	12	80.0	4013	5	US-09-724-676A-40208	Sequence 40208, A
c 291	12	80.0	2876	5	US-09-724-676A-40230	Sequence 40230, A	c 364	12	80.0	4013	5	US-09-724-676A-40208	Sequence 40208, A
c 292	12	80.0	2884	5	US-09-724-676A-40161	Sequence 40161, A	c 365	12	80.0	4019	5	US-09-724-676A-40175	Sequence 40175, A
c 293	12	80.0	2884	5	US-09-724-676A-40161	Sequence 40161, A	c 366	12	80.0	4019	5	US-09-724-676A-40175	Sequence 40175, A
c 294	12	80.0	2913	5	US-09-724-676A-40153	Sequence 40153, A	c 367	12	80.0	4026	5	US-09-724-676A-31322	Sequence 31322, A
c 295	12	80.0	2913	5	US-09-724-676A-40153	Sequence 40153, A	c 368	12	80.0	4026	5	US-09-724-676A-31322	Sequence 31322, A
c 296	12	80.0	2938	5	US-09-724-676A-40150	Sequence 40150, A	c 369	12	80.0	4036	5	US-09-724-676A-40156	Sequence 40156, A
c 297	12	80.0	2938	5	US-09-724-676A-40150	Sequence 40150, A	c 370	12	80.0	4036	5	US-09-724-676A-40156	Sequence 40156, A
c 298	12	80.0	3018	5	US-09-724-676A-40189	Sequence 40189, A	c 371	12	80.0	4044	5	US-09-724-676A-25346	Sequence 25346, A
c 299	12	80.0	3018	5	US-09-724-676A-40189	Sequence 40189, A	c 372	12	80.0	4044	5	US-09-724-676A-25346	Sequence 25346, A
c 300	12	80.0	3027	5	US-09-724-676A-31336	Sequence 31336, A	c 373	12	80.0	4050	5	US-09-724-676A-40151	Sequence 40151, A
c 301	12	80.0	3027	5	US-09-724-676A-31336	Sequence 31336, A	c 374	12	80.0	4050	5	US-09-724-676A-40151	Sequence 40151, A
c 302	12	80.0	3051	5	US-09-724-676A-31337	Sequence 31337, A	c 375	12	80.0	4103	5	US-09-724-676A-31318	Sequence 31318, A
c 303	12	80.0	3051	5	US-09-724-676A-31337	Sequence 31337, A	c 376	12	80.0	4103	5	US-09-724-676A-31318	Sequence 31318, A
c 304	12	80.0	3239	5	US-09-724-676A-31323	Sequence 31323, A	c 377	12	80.0	4124	5	US-09-724-676A-40163	Sequence 40163, A
c 305	12	80.0	3239	5	US-09-724-676A-31323	Sequence 31323, A	c 378	12	80.0	4124	5	US-09-724-676A-40163	Sequence 40163, A
c 306	12	80.0	3266	5	US-09-724-676A-34792	Sequence 34792, A	c 379	12	80.0	4141	5	US-09-724-676A-40219	Sequence 40219, A
c 307	12	80.0	3266	5	US-09-724-676A-34792	Sequence 34792, A	c 380	12	80.0	4141	5	US-09-724-676A-40219	Sequence 40219, A
c 308	12	80.0	3316	5	US-09-724-676A-31319	Sequence 31319, A	c 381	12	80.0	4155	5	US-09-724-676A-40167	Sequence 40167, A
c 309	12	80.0	3316	5	US-09-724-676A-31319	Sequence 31319, A	c 382	12	80.0	4155	5	US-09-724-676A-40167	Sequence 40167, A
c 310	12	80.0	3350	5	US-09-724-676A-34791	Sequence 34791, A	c 383	12	80.0	4178	5	US-09-724-676A-40152	Sequence 40152, A
c 311	12	80.0	3350	5	US-09-724-676A-34791	Sequence 34791, A	c 384	12	80.0	4178	5	US-09-724-676A-40152	Sequence 40152, A
c 312	12	80.0	3374	5	US-09-724-676A-44420	Sequence 44420, A	c 385	12	80.0	4204	5	US-09-724-676A-12933	Sequence 12933, A
c 313	12	80.0	3374	5	US-09-724-676A-44420	Sequence 44420, A	c 386	12	80.0	4204	5	US-09-724-676A-12933	Sequence 12933, A
c 314	12	80.0	3419	5	US-09-724-676A-31333	Sequence 31333, A	c 387	12	80.0	4206	5	US-09-724-676A-31332	Sequence 31332, A
c 315	12	80.0	3419	5	US-09-724-676A-31333	Sequence 31333, A	c 388	12	80.0	4206	5	US-09-724-676A-31332	Sequence 31332, A
c 316	12	80.0	3479	5	US-09-724-676A-44418	Sequence 44418, A	c 389	12	80.0	4258	5	US-09-724-676A-12931	Sequence 12931, A
c 317	12	80.0	3479	5	US-09-724-676A-44418	Sequence 44418, A	c 390	12	80.0	4258	5	US-09-724-676A-12931	Sequence 12931, A
c 318	12	80.0	3496	5	US-09-724-676A-31329	Sequence 31329, A	c 391	12	80.0	4265	5	US-09-724-676A-12937	Sequence 12937, A

392	12	80.0	4265	5	US-09-724-676A-12937	Sequence 12937, A	c 465	12	80.0	4706	5	US-09-724-676-25348	Sequence 25348, A
393	12	80.0	4283	5	US-09-724-676-31328	Sequence 31328, A	c 466	12	80.0	4706	5	US-09-724-676A-12937	Sequence 25348, A
c 394	12	80.0	4283	5	US-09-724-676-40178	Sequence 40178, A	467	12	80.0	4720	5	US-09-724-676A-12971	Sequence 12971, A
395	12	80.0	4283	5	US-09-724-676A-31328	Sequence 31328, A	468	12	80.0	4732	5	US-09-724-676A-12926	Sequence 12926, A
c 396	12	80.0	4283	5	US-09-724-676A-40178	Sequence 40178, A	469	12	80.0	4732	5	US-09-724-676A-12926	Sequence 12926, A
397	12	80.0	4298	5	US-09-724-676-12941	Sequence 12941, A	470	12	80.0	4734	5	US-09-724-676A-12981	Sequence 12981, A
398	12	80.0	4298	5	US-09-724-676A-12941	Sequence 12941, A	471	12	80.0	4734	5	US-09-724-676A-12981	Sequence 12981, A
399	12	80.0	4319	5	US-09-724-676-12935	Sequence 12935, A	472	12	80.0	4741	5	US-09-724-676-12987	Sequence 12987, A
400	12	80.0	4319	5	US-09-724-676A-12935	Sequence 12935, A	473	12	80.0	4741	5	US-09-724-676A-12987	Sequence 12987, A
401	12	80.0	4352	5	US-09-724-676-12939	Sequence 12939, A	474	12	80.0	4746	5	US-09-724-676-31308	Sequence 31308, A
402	12	80.0	4352	5	US-09-724-676A-12939	Sequence 12939, A	475	12	80.0	4746	5	US-09-724-676-31308	Sequence 31308, A
403	12	80.0	4374	5	US-09-724-676-12932	Sequence 12932, A	476	12	80.0	4750	5	US-09-724-676-31316	Sequence 31316, A
404	12	80.0	4374	5	US-09-724-676A-12932	Sequence 12932, A	477	12	80.0	4750	5	US-09-724-676A-31316	Sequence 31316, A
405	12	80.0	4388	5	US-09-724-676-44416	Sequence 44416, A	478	12	80.0	4774	5	US-09-724-676-12969	Sequence 12969, A
406	12	80.0	4388	5	US-09-724-676A-44416	Sequence 44416, A	479	12	80.0	4774	5	US-09-724-676-12969	Sequence 12969, A
407	12	80.0	4414	5	US-09-724-676-12978	Sequence 12978, A	480	12	80.0	4774	5	US-09-724-676-31317	Sequence 31317, A
408	12	80.0	4414	5	US-09-724-676A-12978	Sequence 12978, A	481	12	80.0	4774	5	US-09-724-676-31317	Sequence 31317, A
409	12	80.0	4428	5	US-09-724-676-12930	Sequence 12930, A	482	12	80.0	4774	5	US-09-724-676A-12992	Sequence 12992, A
410	12	80.0	4428	5	US-09-724-676A-12930	Sequence 12930, A	483	12	80.0	4774	5	US-09-724-676A-12992	Sequence 12992, A
411	12	80.0	4435	5	US-09-724-676-12936	Sequence 12936, A	484	12	80.0	4781	5	US-09-724-676-12975	Sequence 12975, A
412	12	80.0	4435	5	US-09-724-676A-12936	Sequence 12936, A	485	12	80.0	4781	5	US-09-724-676-12975	Sequence 12975, A
413	12	80.0	4468	5	US-09-724-676-12940	Sequence 12940, A	486	12	80.0	4781	5	US-09-724-676-12975	Sequence 12975, A
414	12	80.0	4468	5	US-09-724-676-12940	Sequence 12940, A	487	12	80.0	4795	5	US-09-724-676A-12985	Sequence 12985, A
415	12	80.0	4468	5	US-09-724-676A-12940	Sequence 12940, A	488	12	80.0	4795	5	US-09-724-676A-12985	Sequence 12985, A
416	12	80.0	4468	5	US-09-724-676A-12956	Sequence 12956, A	489	12	80.0	4814	5	US-09-724-676A-12980	Sequence 12980, A
417	12	80.0	4475	5	US-09-724-676-12995	Sequence 12995, A	490	12	80.0	4814	5	US-09-724-676A-12980	Sequence 12980, A
418	12	80.0	4475	5	US-09-724-676A-12995	Sequence 12995, A	491	12	80.0	4814	5	US-09-724-676A-12980	Sequence 12980, A
419	12	80.0	4489	5	US-09-724-676-12934	Sequence 12934, A	492	12	80.0	4828	5	US-09-724-676A-12990	Sequence 12990, A
420	12	80.0	4489	5	US-09-724-676-12934	Sequence 12934, A	493	12	80.0	4828	5	US-09-724-676A-12990	Sequence 12990, A
421	12	80.0	4489	5	US-09-724-676A-12934	Sequence 12934, A	494	12	80.0	4835	5	US-09-724-676A-12990	Sequence 12990, A
422	12	80.0	4489	5	US-09-724-676A-1301	Sequence 1301, A	495	12	80.0	4835	5	US-09-724-676A-12990	Sequence 12990, A
c 423	12	80.0	4500	5	US-09-724-676-25354	Sequence 25354, A	496	12	80.0	4853	5	US-09-724-676A-12977	Sequence 12977, A
c 424	12	80.0	4500	5	US-09-724-676A-25354	Sequence 25354, A	497	12	80.0	4853	5	US-09-724-676A-12977	Sequence 12977, A
425	12	80.0	4508	5	US-09-724-676-12929	Sequence 12929, A	498	12	80.0	4868	5	US-09-724-676A-12977	Sequence 12977, A
426	12	80.0	4508	5	US-09-724-676A-12929	Sequence 12929, A	499	12	80.0	4877	5	US-09-724-676A-31331	Sequence 31331, A
427	12	80.0	4510	5	US-09-724-676-12984	Sequence 12984, A	500	12	80.0	4877	5	US-09-724-676A-31331	Sequence 31331, A
428	12	80.0	4510	5	US-09-724-676A-12984	Sequence 12984, A	501	12	80.0	4880	5	US-09-724-676-12970	Sequence 12970, A
429	12	80.0	4522	5	US-09-724-676-12938	Sequence 12938, A	502	12	80.0	4880	5	US-09-724-676-12970	Sequence 12970, A
430	12	80.0	4522	5	US-09-724-676A-12938	Sequence 12938, A	503	12	80.0	4890	5	US-09-724-676A-1326	Sequence 31326, A
431	12	80.0	4526	5	US-09-724-676-44415	Sequence 44415, A	504	12	80.0	4930	5	US-09-724-676A-1326	Sequence 31326, A
432	12	80.0	4526	5	US-09-724-676A-44415	Sequence 44415, A	505	12	80.0	4930	5	US-09-724-676A-1326	Sequence 31326, A
433	12	80.0	4529	5	US-09-724-676-12989	Sequence 12989, A	506	12	80.0	4944	5	US-09-724-676-12968	Sequence 12968, A
434	12	80.0	4529	5	US-09-724-676A-12989	Sequence 12989, A	507	12	80.0	4944	5	US-09-724-676-12968	Sequence 12968, A
435	12	80.0	4562	5	US-09-724-676-12927	Sequence 12927, A	508	12	80.0	4951	5	US-09-724-676A-12974	Sequence 12974, A
436	12	80.0	4562	5	US-09-724-676A-12927	Sequence 12927, A	509	12	80.0	4951	5	US-09-724-676A-12974	Sequence 12974, A
437	12	80.0	4564	5	US-09-724-676-12982	Sequence 12982, A	510	12	80.0	4954	5	US-09-724-676A-31327	Sequence 31327, A
438	12	80.0	4564	5	US-09-724-676A-12982	Sequence 12982, A	511	12	80.0	4954	5	US-09-724-676A-31327	Sequence 31327, A
439	12	80.0	4566	5	US-09-724-676-31297	Sequence 31297, A	512	12	80.0	4984	5	US-09-724-676-12979	Sequence 12979, A
440	12	80.0	4566	5	US-09-724-676A-31297	Sequence 31297, A	513	12	80.0	4984	5	US-09-724-676-12979	Sequence 12979, A
441	12	80.0	4567	5	US-09-724-676-13820	Sequence 13820, A	514	12	80.0	5005	5	US-09-724-676-12972	Sequence 12972, A
442	12	80.0	4567	5	US-09-724-676A-13820	Sequence 13820, A	515	12	80.0	5005	5	US-09-724-676-12972	Sequence 12972, A
443	12	80.0	4571	5	US-09-724-676-12988	Sequence 12988, A	516	12	80.0	5038	5	US-09-724-676A-12976	Sequence 12976, A
444	12	80.0	4571	5	US-09-724-676A-12988	Sequence 12988, A	517	12	80.0	5038	5	US-09-724-676A-12976	Sequence 12976, A
445	12	80.0	4584	5	US-09-724-676-12967	Sequence 12967, A	518	12	80.0	5136	5	US-09-724-676-31299	Sequence 31299, A
446	12	80.0	4584	5	US-09-724-676A-12967	Sequence 12967, A	519	12	80.0	5136	5	US-09-724-676-31299	Sequence 31299, A
447	12	80.0	4604	5	US-09-724-676-12993	Sequence 12993, A	520	12	80.0	5160	5	US-09-724-676A-31300	Sequence 31300, A
448	12	80.0	4604	5	US-09-724-676A-12993	Sequence 12993, A	521	12	80.0	5160	5	US-09-724-676A-31300	Sequence 31300, A
449	12	80.0	4625	5	US-09-724-676-12986	Sequence 12986, A	522	12	80.0	5213	5	US-09-724-676A-31295	Sequence 31295, A
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451	12	80.0	4645	5	US-09-724-676-12994	Sequence 12994, A	524	12	80.0	5237	5	US-09-724-676A-31296	Sequence 31296, A
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453	12	80.0	4658	5	US-09-724-676-12991	Sequence 12991, A	526	12	80.0	5316	5	US-09-724-676-31310	Sequence 31310, A
454	12	80.0	4658	5	US-09-724-676A-12991	Sequence 12991, A	527	12	80.0	5316	5	US-09-724-676-31310	Sequence 31310, A
455	12	80.0	4659	5	US-09-724-676-31312	Sequence 31312, A	528	12	80.0	5340	5	US-09-724-676A-31311	Sequence 31311, A
456	12	80.0	4659	5	US-09-724-676A-31312	Sequence 31312, A	c 529	12	80.0	5340	5	US-09-724-676A-31311	Sequence 31311, A
457	12	80.0	4673	5	US-09-724-676-31320	Sequence 31320, A	530	12	80.0	5391	6	US-10-257-166-19	Sequence 19, Appl
458	12	80.0	4673	5	US-09-724-676A-31320	Sequence 31320, A	531	12	80.0	5393	5	US-09-724-676A-31305	Sequence 31305, A
459	12	80.0	4678	5	US-09-724-676-12928	Sequence 12928, A	532	12	80.0	5393	5	US-09-724-676A-31305	Sequence 31305, A
460	12	80.0	4680	5	US-09-724-676A-12928	Sequence 12928, A	533	12	80.0	5417	5	US-09-724-676-31307	Sequence 31307, A
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462	12	80.0	4680	5	US-09-724-676A-12983	Sequence 12983, A	c 535	12	80.0	5578	5	US-09-724-676A-12762	Sequence 12762, A
463	12	80.0	4697	5	US-09-724-676-31321	Sequence 31321, A	536	12	80.0	5578	5	US-09-724-676A-12762	Sequence 12762, A
464	12	80.0	4697	5	US-09-724-676A-31321	Sequence 31321, A	c 537	12	80.0	6079	5	US-09-724-676-25347	Sequence 25347, A
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c 538	12	80.0	6167	6	US-10-240-453-46	Sequence 46, Appl	c 611	11	73.3	208	5	US-09-513-999C-12545	Sequence 12545, A
c 539	12	80.0	6252	5	US-09-724-676-25358	Sequence 25358, A	612	11	73.3	209	6	US-10-203-138A-9916	Sequence 9916, Ap
c 540	12	80.0	6252	5	US-09-724-676A-25358	Sequence 25358, A	613	11	73.3	216	5	US-09-513-999C-16728	Sequence 16728, A
c 541	12	80.0	6257	5	US-09-724-676-25357	Sequence 25357, A	614	11	73.3	229	6	US-10-266-131-828	Sequence 828, App
c 542	12	80.0	6257	5	US-09-724-676A-25357	Sequence 25357, A	615	11	73.3	229	6	PCT-US02-36628-26	Sequence 26, Appl
c 543	12	80.0	6403	5	US-09-724-676-12763	Sequence 12763, A	616	11	73.3	258	5	US-09-513-999C-29796	Sequence 29796, A
c 544	12	80.0	6403	5	US-09-724-676A-12763	Sequence 12763, A	617	11	73.3	261	1	PCT-US02-34777-405	Sequence 405, App
c 545	12	80.0	6430	5	US-09-724-676-25356	Sequence 25356, A	618	11	73.3	261	6	US-10-283-017-405	Sequence 405, App
c 546	12	80.0	6430	5	US-09-724-676A-25356	Sequence 25356, A	619	11	73.3	261	5	US-09-513-999C-2281	Sequence 2281, Ap
c 547	12	80.0	7647	5	US-09-724-676-31283	Sequence 31283, A	620	11	73.3	270	5	US-09-513-999C-984	Sequence 984, App
c 548	12	80.0	7647	5	US-09-724-676A-31283	Sequence 31283, A	621	11	73.3	276	5	US-09-513-999C-28905	Sequence 28905, A
c 549	12	80.0	7724	5	US-09-724-676-31279	Sequence 31279, A	622	11	73.3	277	5	US-09-513-999C-27150	Sequence 27150, A
c 550	12	80.0	7724	5	US-09-724-676A-31279	Sequence 31279, A	623	11	73.3	283	5	US-09-513-999C-28528	Sequence 28528, A
c 551	12	80.0	7802	6	US-10-240-453-58	Sequence 58, Appl	624	11	73.3	296	6	US-10-240-425-1393	Sequence 1393, Ap
c 552	12	80.0	7827	5	US-09-724-676-31292	Sequence 31292, A	625	11	73.3	328	5	US-09-513-999C-33809	Sequence 33809, A
c 553	12	80.0	7827	5	US-09-724-676A-31292	Sequence 31292, A	626	11	73.3	343	5	US-09-513-999C-25726	Sequence 25726, A
c 554	12	80.0	7904	5	US-09-724-676-31288	Sequence 31288, A	627	11	73.3	347	5	US-09-513-999C-2258	Sequence 2258, Ap
c 555	12	80.0	7904	5	US-09-724-676A-31288	Sequence 31288, A	628	11	73.3	355	6	US-10-060-069-13	Sequence 13, Appl
c 556	12	80.0	8434	5	US-09-724-676-31282	Sequence 31282, A	629	11	73.3	356	5	US-09-606-397A-55	Sequence 55, Appl
c 557	12	80.0	8434	5	US-09-724-676A-31282	Sequence 31282, A	630	11	73.3	369	6	US-10-266-131-2738	Sequence 2738, Ap
c 558	12	80.0	8511	5	US-09-724-676-31278	Sequence 31278, A	631	11	73.3	374	5	US-09-513-999C-8247	Sequence 8247, Ap
c 559	12	80.0	8511	5	US-09-724-676A-31278	Sequence 31278, A	632	11	73.3	383	5	US-09-513-999C-20772	Sequence 20772, A
c 560	12	80.0	8614	5	US-09-724-676-31291	Sequence 31291, A	633	11	73.3	389	5	US-09-513-999C-33847	Sequence 33847, A
c 561	12	80.0	8614	5	US-09-724-676A-31291	Sequence 31291, A	634	11	73.3	419	6	US-10-203-138A-310	Sequence 310, App
c 562	12	80.0	8691	5	US-09-724-676-31287	Sequence 31287, A	635	11	73.3	426	6	US-10-203-138A-4803	Sequence 4803, App
c 563	12	80.0	8691	5	US-09-724-676A-31287	Sequence 31287, A	636	11	73.3	428	5	US-09-513-999C-1494	Sequence 1494, Ap
c 564	12	80.0	9081	5	US-09-724-676-31280	Sequence 31280, A	637	11	73.3	439	5	US-09-513-999C-27925	Sequence 27925, A
c 565	12	80.0	9081	5	US-09-724-676A-31280	Sequence 31280, A	638	11	73.3	445	6	US-10-203-138A-4972	Sequence 4972, Ap
c 566	12	80.0	9105	5	US-09-724-676-31281	Sequence 31281, A	639	11	73.3	454	5	US-09-724-676-29158	Sequence 29158, A
c 567	12	80.0	9105	5	US-09-724-676A-31281	Sequence 31281, A	640	11	73.3	454	5	US-09-724-676A-29158	Sequence 29158, A
c 568	12	80.0	9158	5	US-09-724-676-31340	Sequence 31340, A	641	11	73.3	454	6	US-10-203-138A-600	Sequence 600, App
c 569	12	80.0	9158	5	US-09-724-676A-31340	Sequence 31340, A	642	11	73.3	456	6	US-10-203-138A-2571	Sequence 2571, Ap
c 570	12	80.0	9182	5	US-09-724-676-31277	Sequence 31277, A	643	11	73.3	463	6	US-10-203-138A-2604	Sequence 2604, Ap
c 571	12	80.0	9182	5	US-09-724-676A-31277	Sequence 31277, A	644	11	73.3	468	6	US-10-280-864-3	Sequence 3, Appl
c 572	12	80.0	9261	5	US-09-724-676-31289	Sequence 31289, A	645	11	73.3	475	5	US-09-724-676-7925	Sequence 7925, Ap
c 573	12	80.0	9261	5	US-09-724-676A-31289	Sequence 31289, A	646	11	73.3	475	5	US-09-724-676A-7925	Sequence 7925, Ap
c 574	12	80.0	9285	5	US-09-724-676-31290	Sequence 31290, A	647	11	73.3	475	6	US-10-203-138A-1393	Sequence 1393, Ap
c 575	12	80.0	9285	5	US-09-724-676A-31290	Sequence 31290, A	648	11	73.3	478	6	US-10-203-138A-2011	Sequence 2011, Ap
c 576	12	80.0	9338	5	US-09-724-676-31285	Sequence 31285, A	649	11	73.3	479	6	US-10-203-138A-10296	Sequence 10296, A
c 577	12	80.0	9338	5	US-09-724-676A-31285	Sequence 31285, A	650	11	73.3	481	6	US-10-203-138A-1169	Sequence 1169, Ap
c 578	12	80.0	9362	5	US-09-724-676-31286	Sequence 31286, A	651	11	73.3	485	6	US-10-203-138A-3241	Sequence 3241, Ap
c 579	12	80.0	9362	5	US-09-724-676A-31286	Sequence 31286, A	652	11	73.3	488	6	US-10-203-138A-5762	Sequence 5762, Ap
c 580	12	80.0	11330	1	PCT-US02-32727-39	Sequence 39, Appl	653	11	73.3	493	6	US-10-203-138A-7703	Sequence 7703, Ap
c 581	12	80.0	11330	6	US-10-057-498-39	Sequence 39, Appl	654	11	73.3	502	5	US-09-724-676-14559	Sequence 14559, A
c 582	12	80.0	14127	5	US-09-724-676-33734	Sequence 33734, A	655	11	73.3	502	5	US-09-724-676A-14559	Sequence 14559, A ^e
c 583	12	80.0	14127	5	US-09-724-676A-33734	Sequence 33734, A	656	11	73.3	504	5	US-09-724-676-7920	Sequence 7920, Ap
c 584	12	80.0	14800	5	US-09-724-676-33732	Sequence 33732, A	657	11	73.3	504	5	US-09-724-676A-7920	Sequence 7920, Ap
c 585	12	80.0	14800	5	US-09-724-676A-33732	Sequence 33732, A	658	11	73.3	546	1	PCT-US02-34777-936	Sequence 936, App
c 586	12	80.0	14835	5	US-09-724-676-33733	Sequence 33733, A	659	11	73.3	546	6	US-10-283-017-936	Sequence 936, App
c 587	12	80.0	14835	5	US-09-724-676A-33733	Sequence 33733, A	660	11	73.3	547	6	US-10-152-319A-248	Sequence 248, App
c 588	12	80.0	15645	6	US-10-085-198-111	Sequence 111, App	661	11	73.3	570	6	US-10-266-131-182	Sequence 182, App
c 589	12	80.0	18073	5	US-09-728-552-12	Sequence 12, Appl	662	11	73.3	605	5	US-09-724-676-3673	Sequence 3673, Ap
c 590	12	80.0	45450	1	PCT-US02-32700-7	Sequence 7, Appl	663	11	73.3	605	5	US-09-724-676A-3673	Sequence 3673, Ap
c 591	12	80.0	45450	6	US-10-271-416-7	Sequence 7, Appl	664	11	73.3	625	6	US-10-203-138A-8372	Sequence 8372, Ap
c 592	12	80.0	53500	6	US-10-267-255-76	Sequence 76, Appl	665	11	73.3	628	5	US-09-724-676-14557	Sequence 14557, A
c 593	12	80.0	133760	6	US-10-240-425-1101	Sequence 1101, Ap	666	11	73.3	628	5	US-09-724-676A-14557	Sequence 14557, A
c 594	12	80.0	207433	6	US-10-277-216-5	Sequence 5, Appl	667	11	73.3	636	5	US-09-724-676-26486	Sequence 26486, A
c 595	12	80.0	659158	6	US-09-771-208A-20	Sequence 20, Appl	668	11	73.3	636	5	US-09-724-676A-26486	Sequence 26486, A
c 596	11	73.3	19	6	US-10-293-338-7137	Sequence 7137, Ap	669	11	73.3	638	5	US-09-724-676-14544	Sequence 14544, A
c 597	11	73.3	81	5	US-09-513-999C-23685	Sequence 23685, A	670	11	73.3	638	5	US-09-724-676A-14544	Sequence 14544, A
c 598	11	73.3	87	5	US-09-513-999C-23553	Sequence 23553, A	671	11	73.3	659	5	US-09-724-676-42343	Sequence 42343, A
c 599	11	73.3	93	5	US-09-513-999C-33619	Sequence 33619, A	672	11	73.3	659	5	US-09-724-676A-42343	Sequence 42343, A
c 600	11	73.3	118	5	US-09-513-999C-33625	Sequence 33625, A	673	11	73.3	673	6	US-10-152-319A-1340	Sequence 1340, Ap
c 601	11	73.3	121	6	US-10-209-787-349	Sequence 349, App	674	11	73.3	687	1	PCT-US02-32432-43	Sequence 43, Appl
c 602	11	73.3	121	6	US-10-209-787-350	Sequence 350, App	675	11	73.3	693	5	US-09-724-676-29604	Sequence 29604, A
c 603	11	73.3	130	5	US-09-513-999C-24744	Sequence 24744, A	676	11	73.3	693	5	US-09-724-676A-29604	Sequence 29604, A
c 604	11	73.3	130	5	US-09-606-397A-24	Sequence 24, Appl	677	11	73.3	700	6	US-10-203-138A-5915	Sequence 5915, Ap
c 605	11	73.3	150	5	US-09-513-999C-26415	Sequence 26415, A	678	11	73.3	711	5	US-09-724-676-14556	Sequence 14556, A
c 606	11	73.3	153	6	US-10-203-138A-7944	Sequence 7944, Ap	679	11	73.3	711	5	US-09-724-676A-14556	Sequence 14556, A
c 607	11	73.3	161	5	US-09-513-999C-16217	Sequence 16217, A	680	11	73.3	744	5	US-09-620-607B-644	Sequence 644, App
c 608	11	73.3	164	6	US-10-266-131-1868	Sequence 1686, Ap	681	11	73.3	744	5	US-09-724-676-7068	Sequence 7068, Ap
c 609	11	73.3	171	6	US-10-203-138A-7128	Sequence 7128, Ap	682	11	73.3	744	5	US-09-724-676A-7068	Sequence 7068, Ap
c 610	11	73.3	180	6	US-10-203-138A-5496	Sequence 5496, Ap	683	11	73.3	758	5	US-09-724-676-6144	Sequence 6144, Ap

c 684	11	73.3	758	5	US-09-724-676A-6144	Sequence 6144, Ap	757	11	73.3	999	5	US-09-724-676A-14541	Sequence 14541, A
c 685	11	73.3	776	5	US-09-724-676-14543	Sequence 14543, A	758	11	73.3	1001	5	US-09-724-676-14515	Sequence 14515, A
c 686	11	73.3	776	5	US-09-724-676A-14543	Sequence 14543, A	759	11	73.3	1001	5	US-09-724-676A-14515	Sequence 14515, A
c 687	11	73.3	776	5	US-09-724-676A-14543	Sequence 14543, A	759	11	73.3	1001	5	US-09-724-676A-14515	Sequence 14515, A
c 688	11	73.3	780	5	US-09-724-676-7066	Sequence 7066, Ap	c 760	11	73.3	1006	5	US-09-724-676-17582	Sequence 17582, A
c 689	11	73.3	780	5	US-09-724-676A-7066	Sequence 7066, Ap	c 761	11	73.3	1006	5	US-09-724-676A-17582	Sequence 17582, A
c 690	11	73.3	780	5	US-09-724-676A-7071	Sequence 7071, Ap	c 762	11	73.3	1010	5	US-09-724-676A-3680	Sequence 3680, Ap
c 691	11	73.3	780	5	US-09-724-676A-7071	Sequence 7071, Ap	c 763	11	73.3	1010	5	US-09-724-676A-3680	Sequence 3680, Ap
c 692	11	73.3	794	5	US-09-724-676-14519	Sequence 14519, A	c 764	11	73.3	1017	5	US-09-724-676-14517	Sequence 14517, A
c 693	11	73.3	794	5	US-09-724-676A-14519	Sequence 14519, A	c 765	11	73.3	1017	5	US-09-724-676-24664	Sequence 24664, A
c 694	11	73.3	803	5	US-09-724-676-14558	Sequence 14558, A	c 766	11	73.3	1017	5	US-09-724-676A-14517	Sequence 14517, A
c 695	11	73.3	803	5	US-09-724-676A-14558	Sequence 14558, A	c 767	11	73.3	1017	5	US-09-724-676A-24664	Sequence 24664, A
c 696	11	73.3	815	5	US-09-724-676-14548	Sequence 14548, A	c 768	11	73.3	1020	5	US-09-724-676-14530	Sequence 14530, A
c 697	11	73.3	815	5	US-09-724-676A-14548	Sequence 14548, A	c 769	11	73.3	1020	5	US-09-724-676A-14530	Sequence 14530, A
c 698	11	73.3	817	6	US-10-264-237-801	Sequence 801, App	c 770	11	73.3	1020	6	US-10-069-626-7	Sequence 7, Appl
c 699	11	73.3	827	5	US-09-724-676-35661	Sequence 35661, A	c 771	11	73.3	1024	5	US-09-724-676-18519	Sequence 18519, A
c 700	11	73.3	827	5	US-09-724-676A-35661	Sequence 35661, A	c 772	11	73.3	1024	5	US-09-724-676A-18519	Sequence 18519, A
c 701	11	73.3	837	5	US-09-724-676-13422	Sequence 13422, A	c 773	11	73.3	1025	5	US-09-724-676-47370	Sequence 47370, A
c 702	11	73.3	837	5	US-09-724-676A-13422	Sequence 13422, A	c 774	11	73.3	1025	5	US-09-724-676A-47370	Sequence 47370, A
c 703	11	73.3	843	5	US-09-724-676-18517	Sequence 18517, A	c 775	11	73.3	1026	5	US-09-724-676-26461	Sequence 26461, A
c 704	11	73.3	843	5	US-09-724-676A-18517	Sequence 18517, A	c 776	11	73.3	1026	5	US-09-724-676-26461	Sequence 26461, A
c 705	11	73.3	844	5	US-10-264-237-415	Sequence 415, App	c 777	11	73.3	1026	5	US-09-724-676-26470	Sequence 26470, A
c 706	11	73.3	844	5	US-09-724-676-14555	Sequence 14555, A	c 778	11	73.3	1026	5	US-09-724-676A-26461	Sequence 26461, A
c 707	11	73.3	845	5	US-09-724-676A-14555	Sequence 14555, A	c 779	11	73.3	1026	5	US-09-724-676A-26464	Sequence 26464, A
c 708	11	73.3	850	5	US-09-724-676-38090	Sequence 38090, A	c 780	11	73.3	1026	5	US-09-724-676A-26470	Sequence 26470, A
c 709	11	73.3	850	5	US-09-724-676A-38090	Sequence 38090, A	c 781	11	73.3	1026	5	US-09-724-676A-18522	Sequence 18522, A
c 710	11	73.3	852	5	US-09-724-676-18520	Sequence 18520, A	c 782	11	73.3	1027	5	US-09-724-676A-18522	Sequence 18522, A
c 711	11	73.3	853	5	US-09-724-676A-18520	Sequence 18520, A	c 783	11	73.3	1027	5	US-09-724-676A-20036	Sequence 20036, A
c 712	11	73.3	853	5	US-09-724-676A-3674	Sequence 3674, Ap	c 784	11	73.3	1027	5	US-09-724-676A-20036	Sequence 20036, A
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c 714	11	73.3	861	5	US-09-724-676A-25950	Sequence 25950, A	c 786	11	73.3	1050	6	US-10-057-498-184	Sequence 184, App
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c 753	11	73.3	996	5	US-09-724-676A-26444	Sequence 26444, A	c 825	11	73.3	1182	6	US-10-152-319A-1903	Sequence 1903, Ap
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c 755	11	73.3	996	5	US-09-724-676A-26451	Sequence 26451, A	c 827	11	73.3	1185	5	US-09-724-676A-24655	Sequence 24655, A
c 756	11	73.3	999	5	US-09-724-676A-14541	Sequence 14541, A	c 828	11	73.3	1186	5	US-09-724-676A-42340	Sequence 42340, A
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c 869	11	73.3	1327	5	US-09-724-676-6495	Sequence 6495, Ap	942	11	73.3	1332	6	US-10-131-815A-443	Sequence 443, App
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c 875	11	73.3	1332	6	US-10-131-823A-443	Sequence 443, App	948	11	73.3	1335	5	US-09-724-676-9017	Sequence 9017, Ap
c 876	11	73.3	1332	6	US-10-131-824A-443	Sequence 443, App	949	11	73.3	1335	5	US-09-724-676A-9017	Sequence 14546, A
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985	11	73.3	1444	5	US-09-724-676-14550	Sequence 14550, A
986	11	73.3	1444	5	US-09-724-676A-14550	Sequence 14550, A
c 987	11	73.3	1457	5	US-09-724-676-9011	Sequence 9011, Ap
c 988	11	73.3	1457	5	US-09-724-676A-9011	Sequence 9011, Ap
c 989	11	73.3	1473	5	US-09-724-676-3682	Sequence 3682, Ap
c 990	11	73.3	1473	5	US-09-724-676A-3682	Sequence 3682, Ap
c 991	11	73.3	1475	5	US-09-724-676-14528	Sequence 14528, A
c 992	11	73.3	1475	5	US-09-724-676A-14528	Sequence 14528, A
c 993	11	73.3	1476	5	US-09-724-676-25798	Sequence 25798, A
c 994	11	73.3	1476	5	US-09-724-676A-25798	Sequence 25798, A
c 995	11	73.3	1479	6	US-10-278-173-113	Sequence 113, App
c 996	11	-73.3	1479	6	US-10-278-536-19	Sequence 19, Appl
c 997	11	73.3	1479	6	US-10-302-267-171	Sequence 171, App
c 998	11	73.3	1481	5	US-09-724-676-10561	Sequence 10561, A
c 999	11	73.3	1481	5	US-09-724-676A-10561	Sequence 10561, A
c1000	11	73.3	1486	5	US-09-724-676-10560	Sequence 10560, A

ALIGNMENTS

RESULT 1

US-09-513-999C-13316/c

Sequence 13316, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.052.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 13316

LENGTH: 352

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 298

OTHER INFORMATION: k=g or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: 330

OTHER INFORMATION: r=a or g

US-09-513-999C-13316

Query Match 100.0%; Score 15; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15

Db 149 CCTTCTCCCTGTT 135

RESULT 2

US-10-264-237-1036

Sequence 1036, Application US/10264237

GENERAL INFORMATION:

APPLICANT: Birse et al.

RESULT 3

US-09-620-607B-1245/c

Sequence 1245, Application US/09620607B

GENERAL INFORMATION:

APPLICANT: Nehls, Michael

APPLICANT: Zambrowicz, Brian

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Novel Mutated Mammalian Cells and

FILE REFERENCE: LEX-0032-USA

CURRENT APPLICATION NUMBER: US/09/620,607B

CURRENT FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/144942

PRIOR FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 1848

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1245

LENGTH: 248

TYPE: DNA

ORGANISM: Mus musculus

US-09-620-607B-1245

Query Match 93.3%; Score 14; DB 5; Length 248;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCTGTT 15

Db 88 CTTCTCCCTGTT 75

RESULT 4

US-09-724-676-38339

Sequence 38339, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Comugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Comugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 38339

LENGTH: 908

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-38339

Query Match 93.3%; Score 14; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

Db 444 CCTTCTCCCCCTGT 457

RESULT 5

US-09-724-676A-38339

; Sequence 38339, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 38339

; LENGTH: 908

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-38339

Query Match

Best Local Similarity 93.3%; Score 14; DB 5; Length 908;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

Db 444 CCTTCTCCCCCTGT 457

RESULT 6

US-09-724-676-24274/c

; Sequence 24274, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 24274

; LENGTH: 1030

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676-24274

Query Match

Best Local Similarity 93.3%; Score 14; DB 5; Length 1030;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

Db 692 CCTTCTCCCCCTGT 679

RESULT 7

US-09-724-676A-24274/c

; Sequence 24274, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24274
; LENGTH: 1030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24274

Query Match 93.3%; Score 14; DB 5; Length 1030;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

Db 692 CCTTCTCCCCCTGT 679

RESULT 8

US-09-724-676-2247/c

; Sequence 2247, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2247

; LENGTH: 1509

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676-2247

Query Match

Best Local Similarity 93.3%; Score 14; DB 5; Length 1509;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

Db 831 CCTTCTCCCCCTGT 818

RESULT 9

US-09-724-676A-2247/c

; Sequence 2247, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2247

; LENGTH: 1509

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-2247

Query Match

Best Local Similarity 93.3%; Score 14; DB 5; Length 1509;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
|||||

Db 831 CCTTCTCCCCCTGT 818

RESULT 10

US-09-724-676-2234/c

; Sequence 2234, Application US/09724676

; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2234
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2234

Query Match 93.3%; Score 14; DB 5; Length 1667;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
Db 989 CCTTCTCCCCCTGT 976

RESULT 11
US-09-724-676A-2234/c
; Sequence 2234, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2234
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2234

Query Match 93.3%; Score 14; DB 5; Length 1667;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
Db 989 CCTTCTCCCCCTGT 976

RESULT 12
US-09-724-676-2221/c
; Sequence 2221, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2221
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2221

Query Match 93.3%; Score 14; DB 5; Length 1712;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
Db 1034 CCTTCTCCCCCTGT 1021

RESULT 13
US-09-724-676A-2221/c
; Sequence 2221, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2221
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2221

Query Match 93.3%; Score 14; DB 5; Length 1712;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
Db 1034 CCTTCTCCCCCTGT 1021

RESULT 14
US-09-724-676-2240/c
; Sequence 2240, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2240
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14
Db 831 CCTTCTCCCCCTGT 818

RESULT 15
US-09-724-676A-2240/c
; Sequence 2240, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2240
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;
Best Local Similarity 100.0%; Pred. No. 26;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTCTCCGCCCTGT 14
Db 831 CCTTCTCCGCCCTGT 818

Search completed: December 11, 2002, 20:30:16
Job time : 97.5 secs

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